



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 133719

To: Jeffrey Parkin
Location: rem/3d39/3c18
Art Unit: 1648
Wednesday, September 29, 2004

Case Serial Number: 10/084813

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:00:23 ; Search time 16.2 Seconds
(without alignments)
57.362 Million cell updates/sec

Title: US-10-084-813-13
Perfect score: 96
Sequence: 1 SQYQFWNFQTLKIVLG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	54	4	US-08-833-752-11
2	96	100.0	352	3	US-08-466-343D-2
3	96	100.0	352	3	US-09-087-232A-13
4	96	100.0	352	3	US-08-861-105-14
5	96	100.0	352	3	US-08-575-967A-2
6	96	100.0	352	3	US-09-045-583-52
7	96	100.0	352	4	US-09-517-605-5
8	96	100.0	352	4	US-09-534-185-52
9	96	100.0	352	4	US-08-833-752-5
10	96	100.0	352	4	US-09-502-783A-2
11	96	100.0	352	4	US-09-796-202-1
12	82	85.4	21	3	US-08-907-468-11
13	74	77.1	354	4	US-08-724-984A-2
14	47	49.0	355	4	US-09-886-319A-13
15	45	46.9	355	3	US-09-045-583-53
16	45	46.9	355	4	US-09-534-185-53
17	43.5	45.3	352	4	US-09-489-039A-13500
18	43	44.8	172	4	US-09-621-976-4131
19	43	44.8	344	3	US-08-681-192-2
20	42	43.8	460	3	US-08-935-283-4
21	42	43.8	460	3	US-09-594-185-4
22	42	43.8	727	4	US-09-540-236-3023
23	41	42.7	160	4	US-09-328-352-6593
24	41	42.7	255	4	US-09-491-577-2
25	41	42.7	363	4	US-09-252-991A-25052
26	40	41.7	254	4	US-09-134-001C-4582
27	40	41.7	311	4	US-09-134-001C-5171

28	40	41.7	316	4	US-09-489-039A-8904	Sequence 8904, Ap
29	40	41.7	355	1	US-08-012-988A-2	Sequence 2, Appli
30	40	41.7	355	1	US-08-450-393A-5	Sequence 5, Appli
31	40	41.7	355	3	US-08-446-669-5	Sequence 5, Appli
32	40	41.7	355	4	US-09-239-938-1	Sequence 1, Appli
33	40	41.7	355	4	US-08-833-752-9	Sequence 9, Appli
34	40	41.7	355	4	US-09-886-319A-14	Sequence 14, Appli
35	40	41.7	355	5	PCT-US95-00476-5	Sequence 5, Appli
36	40	41.7	371	3	US/08/622	INFORMATION FOR
37	40	41.7	371	4	US-09-165-922A-10	Sequence 10, Appli
38	40	41.7	659	4	US-09-252-991A-26013	Sequence 26013, A
39	40	41.7	2037	4	US-09-543-681A-5538	Sequence 5538, Ap
40	39	40.6	92	4	US-09-328-352-5171	Sequence 5171, Ap
41	39	40.6	448	4	US-09-134-000C-3794	Sequence 3794, Ap
42	39	40.6	452	4	US-09-530-836-6	Sequence 6, Appli
43	39	40.6	485	4	US-09-134-000C-6031	Sequence 6031, Ap
44	39	40.6	598	2	US-08-853-659A-53	Sequence 53, Appli
45	39	40.6	664	4	US-09-377-497-70	Sequence 70, Appli

ALIGNMENTS

RESULT 1
US-08-833-752-11
; Sequence 11, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-833-752-11

Query Match 100.0%; Score 96; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWNFQTLKIVLG 18
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Db 9 SQYQFWNFQTLKIVLG 26
|||

RESULT 2

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US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGMR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-2
Query Match 100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWNFQTLKIVILG 18
|||
Db 185 SOYQFWNFQTLKIVILG 202

RESULT 3
US-08-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435

US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:

US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435

US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-861-105-14

Query Match 100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 5
US-08-575-967A-2
; Sequence 2, Application US/08575967A
; Patent No. 6265184
; GENERAL INFORMATION:
; APPLICANT: Gray et al.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,967A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy R.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-52

Query Match 100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 7
US-09-517-605-5
; Sequence 5, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-605-5

Query Match 100.0%; Score 96; DB 4; Length 352;
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; Best Local Similarity 100.0%; Pred. No. 3.8e-08; Indels 0; Gaps 0;
; Matches 18; Conservative 0; Mismatches 0;
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QY 1 SOYQFWKFNFTLKIVILG 18
; |||||
Db 185 SOYQFWKFNFTLKIVILG 202

RESULT 8
US-09-534-185-52
; Sequence 52, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
;
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD, LLP
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

Query Match 100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNFTLKIVILG 18
; |||||
Db 185 SOYQFWKFNFTLKIVILG 202

RESULT 9
US-08-833-752-5
; Sequence 5, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
```

```
;
;
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-752-5

Query Match 100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNFTLKIVILG 18
; |||||
Db 185 SOYQFWKFNFTLKIVILG 202

RESULT 10
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match 100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNFTLKIVILG 18
; |||||
Db 185 SOYQFWKFNFTLKIVILG 202

RESULT 11
US-09-796-202-1
; Sequence 1, Application US/09796202
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Patent No. 6548636
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796.202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 12
US-08-907-468-11
Sequence 11, Application US/08907468
Patent No. 6057102
GENERAL INFORMATION:
APPLICANT: Landau, Nathaniel R.
APPLICANT: Koup, Richard A.
APPLICANT: Liu, Rong
APPLICANT: Paxton, William
TITLE OF INVENTION: HIV CORECEPTOR MUTANTS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/907,468
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-005 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1694
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-907-468-11

Query Match 85.4%; Score 82; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQYQFWKNFQTLKIV 15
Db 7 SQYQFWKNFQTLKIV 21

RESULT 13
US-08-724-984A-2
Sequence 2, Application US/08724984A
Patent No. 6388055
GENERAL INFORMATION:
APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-
TITLE OF INVENTION: CCR5 Receptor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSES: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,984A
FILING DATE: October 3, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEFAX: 610 270 5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 354
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-724-984A-2

Query Match 77.1%; Score 74; DB 4; Length 354;
Best Local Similarity 76.5%; Pred. No. 0.00017;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVIL 17
Db 187 QYHFWRKSFQTLKRWIL 203

RESULT 14
US-09-886-319A-13
Sequence 13, Application US/09886319A
Patent No. 6586185
GENERAL INFORMATION:
APPLICANT: Wolf, Eckard
APPLICANT: Werner, Sabine
APPLICANT: Halle, Jorn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Gopelt, Andreas
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
FILE REFERENCE: 50125/014002

us-10-084-813-13.ra1

Tue Sep 28 15:49:56 2004

; CURRENT APPLICATION NUMBER: US/09/886,319A
 ; CURRENT FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: US 60/222,081
 ; PRIOR FILING DATE: 2000-08-01
 ; PRIOR APPLICATION NUMBER: DE 10030149.5
 ; PRIOR FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 355
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-886-319A-13

Query Match 49.0%; Score 47; DB 4; Length 355;
 Best Local Similarity 61.5%; Pred. No. 5;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 WKFNQFTKLVILG 18
 |||||:|:
 DB 195 WKRFQALKNLFG 207

RESULT 15
 ; US-09-045-583-53
 ; Sequence 53, Application US/09045583
 ; Patent No. 6287805
 ; GENERAL INFORMATION:
 ; APPLICANT: Graham, Gerard J. et al.
 ; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/045,583
 ; FILING DATE: 20-MAR-98
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: MNT-044
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 53:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 355 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; US-09-045-583-53

Query Match 46.9%; Score 45; DB 3; Length 355;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 YQFWRNFQTKLVILG 18
 :|||:|:
 DB 192 FQQWKLFLQALKNLFG 207

RESULT 16
 ; US-09-534-185-53
 ; Sequence 53, Application US/09534185
 ; Patent No. 6403767
 ; GENERAL INFORMATION:
 ; APPLICANT: Graham, Gerard J. et al.
 ; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
 ; Heptahelical Receptor Superfamily and Uses
 ; Therefor
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/534,185
 ; FILING DATE: 24-Mar-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/045,583
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: MNT-044
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 53:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 355 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
 ; US-09-534-185-53

Query Match 46.9%; Score 45; DB 4; Length 355;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 YQFWRNFQTKLVILG 18
 :|||:|:
 DB 192 FQQWKLFLQALKNLFG 207

RESULT 17
 ; US-09-489-039A-13500
 ; Sequence 13500, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 13500
 ; LENGTH: 352

```
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13500

Query Match      45.3%; Score 43.5; DB 4; Length 352;
Best Local Similarity 43.5%; Pred. No. 19;
Matches 10; Conservative 3; Mismatches 3; Indels 7; Gaps 1;

QY  2 QYQFW-----KNFQTLKIVL 17
    |||:|||||:
Db   196 QLRFWQAGSLDIRTQTLKIVL 218

RESULT 18
US-09-621-976-4131
; Sequence 4131, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4131
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -30...-1
US-09-621-976-4131

Query Match      44.8%; Score 43; DB 4; Length 172;
Best Local Similarity 57.1%; Pred. No. 11;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY  4 QFWKNFQTLKIVL 17
    :|||:||||:|
Db   74 EFRKNFELRLDVL 87

RESULT 19
US-08-681-192-2
; Sequence 2, Application US/08681192
; Patent No. 6287801
; GENERAL INFORMATION:
; APPLICANT: BERGSM, DERK
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: SARAU, HENRY
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNFD578
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,192
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: ATG50014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5031
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-681-192-2

Query Match      44.8%; Score 43; DB 3; Length 344;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  5 FWKNFQTLKIVI 16
    |||:||||:|
Db   195 FWKHFLLKQNI 206

RESULT 20
US-08-935-263-4
; Sequence 4, Application US/08935263A
; Patent No. 6117669
; GENERAL INFORMATION:
; APPLICANT: Furuichi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
; APPLICANT: Kiyasu, Tatsuya
; APPLICANT: Nagahashi, Yoshie
; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
; FILE REFERENCE: Biotin Genes
; CURRENT APPLICATION NUMBER: US/08/935,263A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: EP 96115540.5
; EARLIER FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Kurthia sp.
US-08-935-263-4

Query Match      43.8%; Score 42; DB 3; Length 460;
Best Local Similarity 54.5%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  3 YQFWKNFQTLK 13
    |||:||||:|
Db   127 YQYWKNDPVK 137

RESULT 21
US-09-594-185-4
; Sequence 4, Application US/09594185
; Patent No. 6365388
; GENERAL INFORMATION:
; APPLICANT: Furuichi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
```

; APPLICANT: Kiyasu, Tateuya
 ; APPLICANT: Nagahashi, Yoshie
 ; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
 ; FILE REFERENCE: Biotin Genes
 ; CURRENT APPLICATION NUMBER: US/09/594,185
 ; CURRENT FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: 08/935,263
 ; PRIOR FILING DATE: 1997-09-22
 ; PRIOR APPLICATION NUMBER: EP 96115540.5
 ; PRIOR FILING DATE: 1996-09-27
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 460
 ; TYPE: PRT
 ; ORGANISM: Kurthia sp.
 ; US-09-594-185-4

Query Match 43.8%; Score 42; DB 4; Length 460;
 Best Local Similarity 54.5%; Pred. No. 45;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YQFWKNFQTLK 13
 Db 127 YQWKNDPVK 137

RESULT 22
 US-09-540-236-3023
 ; Sequence 3023, Application US/09540236
 ; Patent No. 6673910
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
 ; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
 ; CURRENT APPLICATION NUMBER: US/09/540,236
 ; CURRENT FILING DATE: 2000-04-04
 ; NUMBER OF SEQ ID NOS: 3840
 ; SEQ ID NO 3023
 ; LENGTH: 727
 ; TYPE: PRT
 ; ORGANISM: M. catarrhalis
 ; US-09-540-236-3023

Query Match 43.8%; Score 42; DB 4; Length 727;
 Best Local Similarity 37.5%; Pred. No. 74;
 Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 YQFWKNFQTLK 17
 Db 167 QLEWKNQTLSLTI 182

RESULT 23
 US-09-328-352-6593
 ; Sequence 6593, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 6593
 ; LENGTH: 160
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter baumannii
 ; US-09-328-352-6593

Query Match 42.7%; Score 41; DB 4; Length 160;

Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YQFWKNFQ 10
 Db 146 YVFWKNYQ 153

RESULT 24
 US-09-491-577-2
 ; Sequence 2, Application US/09491577
 ; Patent No. 6610511
 ; GENERAL INFORMATION:
 ; APPLICANT: Yale University
 ; APPLICANT: Carlson, John R.
 ; APPLICANT: Kim, Hunhyong
 ; APPLICANT: Clyne, Peter J.
 ; APPLICANT: Marr, Coral G.
 ; TITLE OF INVENTION: No. 6610511el Family of Odorant Receptor Genes in Drosophila
 ; FILE REFERENCE: 44574-5061-US
 ; CURRENT APPLICATION NUMBER: US/09/491,577
 ; CURRENT FILING DATE: 2000-01-25
 ; EARLIER APPLICATION NUMBER: US 60/117,132
 ; EARLIER FILING DATE: 1999-01-25
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 255
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; US-09-491-577-2

Query Match 42.7%; Score 41; DB 4; Length 255;
 Best Local Similarity 53.3%; Pred. No. 35;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 YQFWKNFQTLK 17
 Db 48 YKLWSTFVTLFIL 62

RESULT 25
 US-09-252-991A-25052
 ; Sequence 25052, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25052
 ; LENGTH: 363
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-25052

Query Match 42.7%; Score 41; DB 4; Length 363;
 Best Local Similarity 60.0%; Pred. No. 51;
 Matches 9; Conservative 2; Mismatches 0; Indels 4; Gaps 1;

QY 4 QFWKNFQTLK 18
 Db 237 KFWKHQFQ----VILG 247

RESULT 26

US-09-134-001C-4582
; Sequence 4582, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4582
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4582
Query Match 41.7%; Score 40; DB 4; Length 254;
Best Local Similarity 53.8%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 SOYQWKNFQTLK 13
||| |||
Db 9 SOYPLNQLNLYK 21
||| |||
RESULT 27
US-09-134-001C-5171
; Sequence 5171, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5171
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5171
Query Match 41.7%; Score 40; DB 4; Length 311;
Best Local Similarity 38.5%; Pred. No. 63;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 6 WKNFQTLKIVILG 18
||| |||
Db 271 WPNFATILWVVG 283
||| |||
RESULT 28
US-09-489-039A-8904
; Sequence 8904, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8904
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8904
Query Match 41.7%; Score 40; DB 4; Length 316;
Best Local Similarity 61.5%; Pred. No. 64;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 6 WKNFQTLKIVILG 18
||| |||
Db 226 WINVQGLKVEILG 238
||| |||
RESULT 29
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
; TITLE OF INVENTION: alpha)/RANTES Receptor.
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,988A
; FILING DATE: 19930128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-012-988A-2
Query Match 41.7%; Score 40; DB 1; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 6 WKNFQTLKIVILG 18
||| |||
Db 195 WKLQALKNLFG 207
||| |||
RESULT 30
US-08-450-393A-5
; Sequence 5, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel

;; APPLICANT: Coughlin, Shaun
;; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
;; TITLE OF INVENTION: PROTEIN RECEPTORS
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
;; STREET: 5 Palo Alto Square
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94306-2155
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/450,393A
;; FILING DATE: May 25, 1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cseerr, Luann
;; REGISTRATION NUMBER: 31,822
;; REFERENCE/DOCKET NUMBER: UCAL-237/02US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-843-5165
;; TELEFAX: 415-8857-0663
;; TELEX: 380816CooleyPA
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 355 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-450-393A-5

Query Match 41.7%; Score 40; DB 1; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18
||| ||| : :
Db 195 WKLFQALKLNLF 207

RESULT 31
US-08-446-669-5
;; Sequence 5, Application US/08446669
;; Patent No. 6132987
;; GENERAL INFORMATION:
;; APPLICANT: Charo, Israel
;; APPLICANT: Coughlin, Shaun
;; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
;; TITLE OF INVENTION: PROTEIN RECEPTORS
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
;; STREET: 5 Palo Alto Square
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94306-2155
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/446,669
;; FILING DATE: May 25, 1995
;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Neeley, Richard
;; REGISTRATION NUMBER: 30,092
;; REFERENCE/DOCKET NUMBER: UCAL-237/01US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-843-5000
;; TELEFAX: 415-857-0663
;; TELEX: 380816CooleyPA
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 355 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-446-669-5

Query Match 41.7%; Score 40; DB 3; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18
||| ||| : :
Db 195 WKLFQALKLNLF 207

RESULT 32
US-09-239-938-1
;; Sequence 1, Application US/09239938
;; Patent No. 6329510
;; GENERAL INFORMATION:
;; APPLICANT: Qin, Shixin
;; APPLICANT: Newman, Walter
;; APPLICANT: Kassam, Nasim
;; APPLICANT: LeukoSite, Inc.
;; TITLE OF INVENTION: ANTI-CCR1 ANTIBODIES AND METHODS OF USE
;; TITLE OF INVENTION: THEREFOR
;; FILE REFERENCE: LKS97-13
;; CURRENT APPLICATION NUMBER: US/09/239,938
;; CURRENT FILING DATE: 1999-01-29
;; NUMBER OF SEQ ID NOS: 1
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 1
;; LENGTH: 355
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-09-239-938-1

Query Match 41.7%; Score 40; DB 4; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18
||| ||| : :
Db 195 WKLFQALKLNLF 207

RESULT 33
US-08-833-752-9
;; Sequence 9, Application US/08833752
;; Patent No. 6448175
;; GENERAL INFORMATION:
;; APPLICANT: SAMSON, MICHEL
;; APPLICANT: PARMENTIER, MARC
;; APPLICANT: VASSART, GILBERT
;; APPLICANT: LIBERT, FREDERICK
;; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Kocbe, Martens, Olson & Bear
;; STREET: 620 Newport Center Drive 16th Floor

```

; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6448375e
US-08-833-752-9
Query Match 41.7%; Score 40; DB 4; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVLG 18
||| ||| :
Db 195 WKLFQALKNLFG 207

RESULT 34
US-09-886-319A-14
; Sequence 14, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886,319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR FILING DATE: 2000-08-01
; PRIOR FILING DATE: 2000-08-01
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-319A-14
Query Match 41.7%; Score 40; DB 4; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVLG 18
||| ||| :
Db 195 WKLFQALKNLFG 207
```

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RESULT 35
PCT-US95-00476-5
; Sequence 5, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 58555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-00476-5
Query Match 41.7%; Score 40; DB 5; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVLG 18
||| ||| :
Db 195 WKLFQALKNLFG 207

RESULT 36
US/08/622
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US/08/622,679D-10
Query Match 41.7%; Score 40; DB 3; Length 371;
Best Local Similarity 40.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIV 15
||| ||| :
Db 319 NQYFWDDFHPSEVV 333
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Search completed: September 28, 2004, 09:21:32
Job time : 17.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:51:21 ; Search time 52.525 seconds
(without alignments)
118.345 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126
Sequence: 1 QWDFGNTMCQLLTGLYFIGFPS 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep 29Jan04 : *
1: genesep1980a : *
2: genesep1990a : *
3: genesep2000a : *
4: genesep2000a : *
5: genesep2000a : *
6: genesep2003as : *
7: genesep2003bs : *
8: genesep2004s : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	126	100.0	22	AAB88994	Aab88994 HIV gp120
2	126	100.0	184	AAW27406	Aaw27406 Inactive
3	126	100.0	215	AAW27408	Aaw27408 Inactive
4	126	100.0	215	AAW88238	Aaw88238 HIV-1 co-
5	126	100.0	268	ADC10142	Adc10142 Human NOV
6	126	100.0	268	ADC10144	Adc10144 Human NOV
7	126	100.0	332	AAW26766	Aaw26766 Human che
8	126	100.0	352	AAW27407	Aaw27407 Human CCR
9	126	100.0	352	AAW27123	Aaw27123 Human che
10	126	100.0	352	AAW27125	Aaw27125 Macaque c
11	126	100.0	352	AAW07602	Aaw07602 Human G-P
12	126	100.0	352	AAW23835	Aaw23835 Human CC
13	126	100.0	352	AAW88232	Aaw88232 HIV-1 co-
14	126	100.0	352	AAW80128	Aaw80128 Human G-P
15	126	100.0	352	AAW79089	Aaw79089 Amino aci
16	126	100.0	352	AAW07046	Aaw07046 Human G-P
17	126	100.0	352	AAW07048	Aaw07048 Human G-P
18	126	100.0	352	AAW80111	Aaw80111 Human CCR
19	126	100.0	352	AAW04321	Aaw04321 Human che
20	126	100.0	352	AAW07037	Aaw07037 Human G-P
21	126	100.0	352	AAW07039	Aaw07039 Human G-P
22	126	100.0	352	AAW46858	Aab46858 Human HDG
23	126	100.0	352	AAW56342	Abb56342 Non-endog
24	126	100.0	352	AAW883354	Aab883354 Human CCR
25	126	100.0	352	AAW882948	Aab882948 Human HIV

26	126	100.0	352	AAU97150	Aau97150 Human G-P
27	126	100.0	352	AAU97152	Aau97152 Human G-P
28	126	100.0	352	AAW52829	Aam52829 Human CCR
29	126	100.0	352	AAW52828	Aam52828 Human CC
30	126	100.0	352	ABG70597	Abg70597 Human G-P
31	126	100.0	352	ABG92883	Abg92883 Human imm
32	126	100.0	352	ABG92880	Abg92880 Human G-P
33	126	100.0	352	AAE35808	Aae35808 Human G-P
34	126	100.0	352	AAE35811	Aae35811 Human G-P
35	126	100.0	352	ABB81054	Abb81054 G-protein
36	126	100.0	352	ABB08343	Abb08343 Human che
37	126	100.0	352	ABG75540	Abg75540 Human G-P
38	126	100.0	352	ABR58602	AbR58602 Human can
39	126	100.0	352	AAO29514	Aao29514 Human C-C
40	126	100.0	352	ABU61654	Abu61654 Human G-P
41	126	100.0	352	ABP97728	Abp97728 Amino aci
42	126	100.0	352	ABP81933	Abp81933 Human C-C
43	126	100.0	352	ADC03341	Adc03341 Human che
44	126	100.0	352	ADC03359	Adc03359 Macaque c
45	126	100.0	371	AAW23834	Aaw23834 Human CC

ALIGNMENTS

RESULT 1
AAB88994
ID AAB88994 standard; peptide; 22 AA.
XX
AC AAB88994;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #87.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX
PN WC200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023505.
XX
PR 27-AUG-1999; 99US-0151270P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions.
XX
PS Claim 21; Page 38; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4, and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the virus.
CC The present sequence is an example of a peptide of the invention

Sequence 22 AA;

Query Match 100.0%; Score 126; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFPS 22

Db 1 QWDFGNTMCLLTGLYFIGFPS 22

RESULT 2
AAW27406
ID AAW27406 standard; protein; 184 AA.

XX AC AAW27406;

XX DT 14-APR-1998 (first entry)

XX DE Inactive human CCR5.

XX KW Inactive; human Cys-Cys chemokine receptor-5; CCR5;
KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
KW predisposition; resistance; diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
KW atherosclerosis; autoimmune disorder.

XX OS Homo sapiens.

XX FN WO9732019-A2.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-BE000023.

XX PR 01-MAR-1996; 96EP-00870021.

XX PR 06-AUG-1996; 96EP-00870102.

XX FA (EURO-) EUROSREEN SA.

XX PI Samson M, Parmentier M, Vassart G, Libert F;

XX DR WPI; 1997-479829/44.

XX DR N-PSDB; AAT90116.

XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
XX to diagnose, prevent and/or treat inflammatory disorders, autoimmune
XX disease and viral infection.

XX PS Claim 1; Fig 1a; 94pp; English.

XX CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor
CC 5 (CCRS), which is not a receptor of human immunodeficiency virus type 1
CC or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to diagnose, treat
CC and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,
CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,
CC viral infections, especially HIV-1 or HIV-2 infection, cancer,
CC atherosclerosis and autoimmune disorders. Subjects that express the
CC inactive receptor have a predisposition, or resistance to HIV-1 and/or
XX HIV-2

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 126; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCLLTGLYFIGFPS 22
Db 93 QWDFGNTMCLLTGLYFIGFPS 114

RESULT 3
AAW27408
ID AAW27408 standard; protein; 215 AA.

XX AC AAW27408;

XX DT 14-APR-1998 (first entry)

XX DE Inactive human CCR5.

XX KW Inactive; human Cys-Cys chemokine receptor 5; CCR5;
KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
KW predisposition; resistance; diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
KW atherosclerosis; autoimmune disorder.

XX OS Homo sapiens.

XX FN WO9732019-A2.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-BE000023.

XX PR 01-MAR-1996; 96EP-00870021.

XX PR 06-AUG-1996; 96EP-00870102.

XX PA (EURO-) EUROSREEN SA.

XX PI Samson M, Parmentier M, Vassart G, Libert F;

XX DR WPI; 1997-479829/44.

XX DR N-PSDB; AAT90118.

XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
XX to diagnose, prevent and/or treat inflammatory disorders, autoimmune
XX disease and viral infection.

XX PS Claim 7; Fig 1d-e; 94pp; English.

XX CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor
CC 5 (CCRS), which lacks the last 3 transmembrane regions and the regions
CC involved in G protein-coupling. CCR5 or its cDNA can be used to diagnose,
CC treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,
CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,
CC viral infections, especially human immunodeficiency virus type 1 or type
CC 2 (HIV-1 or HIV-2) infection, cancer, atherosclerosis and autoimmune
CC disorders. Subjects that express the inactive receptor have a
CC predisposition, or resistance to HIV-1 and/or HIV-2

XX SQ Sequence 215 AA;

Query Match 100.0%; Score 126; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCLLTGLYFIGFPS 22
Db 93 QWDFGNTMCLLTGLYFIGFPS 114

RESULT 4

AAW88238

ID AAW88238 standard; protein; 215 AA.

XX AC AAW88238;

XX DT 15-MAR-1999 (first entry)

XX DE HIV-1 co-receptor CCR5 variant CCR5-delta32.

XX KW HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;
XX gene therapy; human.

XX OS Homo sapiens.

XX FT Key

XX FT Domain

XX FT Location/Qualifiers

XX FT 32..56

XX FT /note= "transmembrane domain 1"

FT Domain 67..87
 FT /note= "transmembrane domain 2"
 FT Domain 103..124
 FT /note= "transmembrane domain 3"
 FT Domain 142..167
 FT /note= "transmembrane domain 4"

FN WO9854317-A1.

PD 03-DEC-1998.

PF 29-MAY-1998; 98WO-EP003437.

PR 30-MAY-1997; 97US-0048057P.

PA (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.

PI Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;

PP WPI; 1999-059835/05.

PR N-PSDB; AAV84159.

PT New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection.

PS Disclosure; Page 38-39; 55pp; English.

CC This is the amino acid sequence of a CCR5 variant protein, designated CCR5-delta32, that includes the first 4 transmembrane domains of wild-type CCR5 (see AAV88232), but lacks transmembrane domains 5-7. CCR5 serves as a co-receptor for infection by macrophage-tropic (M-tropic) strains of HIV-1. Individuals homozygous for the CCR5-delta32 mutation are resistant to HIV-1 infection, but heterozygous individuals are susceptible. The invention additionally relates to the identification of variant CCR5s (see AAV88231), which lack transmembrane domains 3-7 of CCR5. The detection of CCR5 variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AIDS. Probes and primers (see AAV84127-36) are provided for use in diagnostic methods for detecting the presence of such variants. A method is provided for inhibiting HIV-1 infection of a cell expressing the CCR5 receptor. This involves introducing a nucleic acid encoding a CCR5 variant into the cell, thereby reducing the number of functional CCR5 molecules present on the cell surface

XX Sequence 215 AA;

Query Match 100.0%; Score 126; DB 2; Length 215;

Best Local Similarity 100.0%; Pred.No.1.5e-11; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0;

Cy 1 QWDFGNTMCLLGLYFIIGFFS 22

Db 93 QWDFGNTMCLLGLYFIIGFFS 114

RESULT 5

ADC10142

ID ADC10142 standard; protein; 268 AA.

XX ADC10142;

AC ADC10142;

XX 18-DEC-2003 (first entry)

DT Human NOVX polypeptide SEQ ID NO: 162.

DE Human NOVX polypeptide SEQ ID NO: 162.

XX cytostatic; anidiabetic; anorectic; cerebroprotective; neuroprotective;

XX antiinflammatory; gene therapy; antisense therapy; thymomimetic; NOVX;

XX pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;

XX inflammatory disorder; chromosome mapping; tissue typing;

XX predictive medicine.

XX Homo sapiens.

OS

XX WO2003000842-A2.
 XX 03-JAN-2003.
 XX 04-JUN-2002; 2002WO-US017443.
 XX 04-JUN-2001; 2001US-0295607P.
 XX 04-JUN-2001; 2001US-0295661P.
 XX 06-JUN-2001; 2001US-0296404P.
 XX 06-JUN-2001; 2001US-0296418P.
 XX 07-JUN-2001; 2001US-0296575P.
 XX 11-JUN-2001; 2001US-0297414P.
 XX 12-JUN-2001; 2001US-0295573P.
 XX 12-JUN-2001; 2001US-0297567P.
 XX 14-JUN-2001; 2001US-0298285P.
 XX 15-JUN-2001; 2001US-0298528P.
 XX 18-JUN-2001; 2001US-0299133P.
 XX 19-JUN-2001; 2001US-0299230P.
 XX 21-JUN-2001; 2001US-0299949P.
 XX 22-JUN-2001; 2001US-0300177P.
 XX 26-JUN-2001; 2001US-0300883P.
 XX 28-JUN-2001; 2001US-0301530P.
 XX 28-JUN-2001; 2001US-0301550P.
 XX 03-JUL-2001; 2001US-0302951P.
 XX 31-JUL-2001; 2001US-0308890P.
 XX 14-SEP-2001; 2001US-0322297P.
 XX 25-SEP-2001; 2001US-0324659P.
 XX 03-DEC-2001; 2001US-0337477P.
 XX 14-DEC-2001; 2001US-0341562P.
 XX 21-FEB-2002; 2002US-0358656P.
 XX 21-FEB-2002; 2002US-0359123P.
 XX 22-FEB-2002; 2002US-0358978P.
 XX 22-FEB-2002; 2002US-0359034P.
 XX 22-FEB-2002; 2002US-0359035P.
 XX 27-FEB-2002; 2002US-0359121P.
 XX 27-FEB-2002; 2002US-0359964P.
 XX 01-MAR-2002; 2002US-0360858P.
 XX 12-MAR-2002; 2002US-0363430P.
 XX 12-MAR-2002; 2002US-0363765P.
 XX 10-APR-2002; 2002US-0371348P.
 XX 10-MAY-2002; 2002US-0379444P.
 XX 04-JUN-2002; 2002US-00379444.

(CURA-) CURAGEN CORP.

Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
 Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
 Gerlach VL, Gorman L, Guo X, Herrmann UB, Hjalt T, Ji W, Kekuda R;
 Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
 Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
 Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
 Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
 Burgess CE, Lepley DM;

WPI: 2003-210149/20.

N-PSDB; ADC10141.

PT New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory or CNS diseases.

PS Claim 1; SEQ ID NO 162; 772pp; English.

XX The invention relates to novel isolated polypeptides, mature form of the CC polypeptide, a sequence that is 95% identical to the polypeptide or the CC polypeptide comprising one or more conservative substitutions. The NOVX CC polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and CC endocrine, CNS and inflammatory disorders. They can also be used in CC various detection and screening assays, chromosome mapping, tissue typing

CC and predictive medicine. This sequence corresponds to one of the
 CC polypeptides of the invention.

SQ Sequence 268 AA;

Query Match 100.0%; Score 126; DB 7; Length 268;
 Best Local Similarity 100.0%; Pred. No. 1.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLTYFGFSS 22
 |||||
 Db 93 QWDFGNTMCQLLTGLTYFGFSS 114

RESULT 6

ADCI0144
 ID ADCI0144 standard; protein; 268 AA.

AC ADCI0144;

DT 18-DEC-2003 (first entry)

DE Human NOVX polypeptide SEQ ID NO: 164.

XX cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
 KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
 KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
 KW inflammatory disorder; chromosome mapping; tissue typing;
 KW predictive medicine.

XX Homo sapiens.

XX WO2003000842-A2.

XX 03-JAN-2003.

XX 04-JUN-2002; 2002WO-US017443.

XX 04-JUN-2001; 2001US-0295607P.

XX 04-JUN-2001; 2001US-0295661P.

XX 06-JUN-2001; 2001US-0286404P.

XX 06-JUN-2001; 2001US-0286418P.

XX 07-JUN-2001; 2001US-0296575P.

XX 11-JUN-2001; 2001US-0297414P.

XX 12-JUN-2001; 2001US-0295573P.

XX 12-JUN-2001; 2001US-0297567P.

XX 14-JUN-2001; 2001US-0298285P.

XX 15-JUN-2001; 2001US-0298528P.

XX 18-JUN-2001; 2001US-0299133P.

XX 19-JUN-2001; 2001US-0299230P.

XX 21-JUN-2001; 2001US-0299949P.

XX 22-JUN-2001; 2001US-0300177P.

XX 26-JUN-2001; 2001US-0300883P.

XX 28-JUN-2001; 2001US-0301530P.

XX 28-JUN-2001; 2001US-0301550P.

XX 03-JUL-2001; 2001US-0302951P.

XX 31-JUL-2001; 2001US-0308890P.

XX 14-SEP-2001; 2001US-0322297P.

XX 25-SEP-2001; 2001US-0324669P.

PR 04-JUN-2002; 2002US-00379444.

XX (CURA-) CURAGEN CORP.

XX Aggee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;

PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;

PI Gerlach VL, German L, Guo X, Herrmann JM, Hjalte T, Ji W, Kekuda R;

PI Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;

PI Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;

PI Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;

PI Sytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;

PI Burgess CE, Lepley DM;

XX WPI; 2003-210149/20.

DR N-PSDB; ADCI0143.

XX New isolated NOVX polypeptides and nucleic acid molecules useful for

PT treating, preventing and diagnosing pathological conditions with NOVX-

PT associated disorders, such as cancer, obesity, diabetes and inflammatory

PT or CNS diseases.

XX Claim 1; SEQ ID NO 164; 772pp; English.

XX The invention relates to novel isolated polypeptides, mature form of the

CC polypeptide, a sequence that is 95% identical to the polypeptide or the

CC polypeptide comprising one or more conservative substitutions. The NOVX

CC polypeptide is useful for treating or preventing a pathology associated

CC with the polypeptide e.g. disorders associated with aberrant expression

CC or activity of the polypeptide, such as cancer, diabetes, obesity, and

CC endocrine, CNS and inflammatory disorders. They can also be used in

CC various detection and screening assays, chromosome mapping, tissue typing

CC and predictive medicine. This sequence corresponds to one of the

XX polypeptides of the invention.

SQ Sequence 268 AA;

Query Match 100.0%; Score 126; DB 7; Length 268;

Best Local Similarity 100.0%; Pred. No. 1.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLTYFGFSS 22

Db 93 QWDFGNTMCQLLTGLTYFGFSS 114

RESULT 7

AAW26766

ID AAW26766 standard; protein; 332 AA.

XX AAW26766;

XX 21-MAY-1998 (first entry)

XX Human chemokine receptor MMLR-CCR.

XX Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human;

XX monocyte; macrophage; chemotaxis; haematopoiesis; infection;

XX inflammation; proliferative disease; cardiovascular disease; tumour;

XX rheumatoid arthritis; alveolitis; atherosclerosis; diabetes;

XX chronic granulomatous disease; asthma; myasthenia gravis; shock;

XX inflammatory bowel disease; toxic shock syndrome; septic shock;

XX Chediak-Higashi syndrome; therapy; diagnosis.

XX Homo sapiens.

XX Key 107..128

XX Peptide /note="conserved peptide"

XX Misc-difference 121

XX /note="a claimed polypeptide has isoleucine at residue 121"

XX WO9741225-A2.


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XX PD 06-NOV-1997.
XX PF 25-APR-1997; 97WO-US006993.
XX PR 26-APR-1996; 96US-00638081.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Au-Young J, Bandman O, Coleman R, Wilde CG;
XX WPI; 1997-549729/50.
XX DR N-PSDB; AAT99542.
XX PT Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful
XX to study, diagnose and treat, e.g. infection, inflammation, solid tumour
XX and proliferative and cardiovascular disease.
XX PS Claim 8; Page 37-38; 59pp; English.
XX CC This protein comprises human MMLR-CCR, a novel C-C chemokine receptor
XX associated with monocyte/macrophage infiltration and chemotaxis and
XX haematopoiesis. The amino acid sequence was deduced from a cDNA clone
XX (see AAT99542) obtained from a cDNA library made from mononuclear cells
XX collected on day 2 of a mixed lymphocyte culture, i.e. cells associated
XX with inflammation and immunomodulation. Another novel chemokine receptor,
XX MPHG-CCR (see AAW36767), is also claimed. MMLR-CCR contains 7
XX transmembrane spanning segments connected by a series of intracellular
XX and extracellular loops. MMLR-CCR and MPHG-CCR can be used to study,
XX diagnose and treat disease states in which normal leukocyte function is
XX perturbed by normal leukopoiesis or inappropriate activation via
XX chemokine agonists or antagonists, such as infection, inflammation,
XX proliferative disease, tumorigenesis, autoimmune disease, abnormal cell
XX proliferation, solid tumours, cardiovascular disease, rheumatoid
XX arthritis, alveolitis, atherosclerosis, chronic granulomatous disease,
XX asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic
XX shock syndrome, septic shock and Chediak-Higashi syndrome
XX SQ Sequence 332 AA;
Query Match 100.0%; Score 126; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.4e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIQFFS 22
Db 84 QWDFGNTMCQLLTGLYFIQFFS 105

RESULT 8
AAW27407
ID AAW27407 standard; protein; 352 AA.
AC AAW27407;
XX 14-APR-1998 (first entry)
XX Human CCR5.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Domain 1..32 /label= Extracellular_domain
XX Domain 56..67 /label= Intracellular_domain
XX Domain 89..112 /label= Extracellular_domain
XX Domain 125..145 /label= Intracellular_domain
XX Domain 166..191 /label= Extracellular_domain
XX Domain 213..235 /label= Intracellular_domain
XX Domain 259..280 /label= Extracellular_domain
XX Domain 301..352 /label= Intracellular_domain
XX

Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
atherosclerosis; autoimmune disorder.

Homo sapiens.
WO9732019-A2.
04-SEP-1997.
28-FEB-1997; 97WO-BE000023.
XX

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PR 01-MAR-1996; 96EP-00870021.
PR 06-AUG-1996; 96EP-00870102.
XX (EURO-) EUROSCREEN SA.
XX Samson M, Parmentier M, Vassart G, Libert F;
XX WPI; 1997-479829/44.
XX DR N-PSDB; AAT90117.
XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful
XX to diagnose, prevent and/or treat inflammatory disorders, autoimmune
XX disease and viral infection.
XX Claim 4; Fig 1b-c; 94pp; English.
XX The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
XX which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but
XX not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,
XX interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
XX chemokines. Active CCR-5 is also a receptor of human immunodeficiency
XX virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to
XX diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
XX arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
XX psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
XX atherosclerosis and autoimmune disorders
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 126; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIQFFS 22
Db 93 QWDFGNTMCQLLTGLYFIQFFS 114

RESULT 9
AAW27123
ID AAW27123 standard; protein; 352 AA.
XX AC AAW27123;
XX 14-DEC-1997 (first entry)
XX Human chemokine receptor 89C.
XX Chemokine receptor 89C; atherosclerosis; rheumatoid arthritis; tumour;
XX asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
XX diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
XX modulator; antibody; human.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Domain 1..32 /label= Extracellular_domain
XX Domain 56..67 /label= Intracellular_domain
XX Domain 89..112 /label= Extracellular_domain
XX Domain 125..145 /label= Intracellular_domain
XX Domain 166..191 /label= Extracellular_domain
XX Domain 213..235 /label= Intracellular_domain
XX Domain 259..280 /label= Extracellular_domain
XX Domain 301..352 /label= Extracellular_domain
XX

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PN WO9722698-A2.
 PD 26-JUN-1997.
 XX
 PF 20-DEC-1996; 96WO-US020759.
 XX
 PR 20-DEC-1995; 95US-00575967.
 PR 07-JUN-1996; 96US-00661393.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Gray PW, Schweickart VL, Raport CU;
 XX
 DR WPI; 1997-341689/31.
 DR N-PSDB; AAT85161.
 XX
 PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
 PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
 PT tumours, viral infections, auto-immune diseases, etc.
 XX
 PS Claim 16; Page 47-48; 65pp; English.
 XX
 CC This polypeptide sequence comprises novel human chemokine receptor 88C, a
 CC G protein coupled receptor that is involved in leukocyte trafficking. Its
 CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
 CC macrophage library. It shows 62% identity to CCR1. Chemokine receptor
 CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
 CC and their polypeptide fragments can be produced in transformed host
 CC cells. The receptors, peptides comprising one or more of the
 CC extracellular or intracellular domains, and anti-receptor antibodies can
 CC be used to modulate receptor activities, particularly ligand and G
 CC protein binding, and are potentially useful in the treatment
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune response,
 CC abnormal haematopoietic processes etc
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
 DB 93 QWDFGNTMCQLLTGLYFIFGFS 114
 RESULT 10
 ID AAW27125 standard; protein; 352 AA.
 XX
 AC AAW27125;
 XX
 DT 14-DEC-1997 (first entry)
 XX
 DE Macaque chemokine receptor 88C.
 XX
 KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
 KW asthma; viral infection; AIDS; inflammation; auto-immune disease; therapy;
 KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
 KW modulator; antibody.
 XX
 OS Macaca sp.
 XX
 PN WO9722698-A2.
 XX
 PD 26-JUN-1997.
 XX
 PF 20-DEC-1996; 96WO-US020759.
 XX
 PR 20-DEC-1995; 95US-00575967.
 PR 07-JUN-1996; 96US-00661393.
 XX

PA (ICOS-) ICOS CORP.
 XX
 PI Gray PW, Schweickart VL, Raport CU;
 XX
 DR WPI; 1997-341689/31.
 DR N-PSDB; AAT85161.
 XX
 PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
 PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
 PT tumours, viral infections, auto-immune diseases, etc.
 XX
 PS Claim 36; Page 57-58; 65pp; English.
 XX
 CC This polypeptide sequence comprises macaque chemokine receptor 88C, a G
 CC protein coupled receptor that is involved in leukocyte trafficking. Its
 CC amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR
 CC amplification. It shows 97% identity to human 88C (AAW27123). 88C
 CC receptors and their polypeptide fragments can be produced in transformed
 CC host cells. The receptors, peptides comprising one or more of the
 CC extracellular or intracellular domains, and anti-receptor antibodies can
 CC be used to modulate receptor activities, particularly ligand and G
 CC protein binding, and are potentially useful in the treatment
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune response,
 CC abnormal haematopoietic processes etc. A hybridoma that produces an
 CC antibody that specifically binds to macaque 88C is claimed
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
 DB 93 QWDFGNTMCQLLTGLYFIFGFS 114
 RESULT 11
 ID AAW07602 standard; protein; 352 AA.
 XX
 AC AAW07602;
 XX
 DT 26-FEB-1997 (first entry)
 XX
 DE Human G-protein chemokine receptor HDGMR10.
 XX
 KW G-protein chemokine receptor; HDGMR10; signal transduction;
 KW haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9639437-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 06-JUN-1995; 95WO-US007173.
 XX
 PR 06-JUN-1995; 95WO-US007173.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Li Y, Ruben SM;
 XX
 DR WPI; 1997-043072/04.
 DR N-PSDB; AAT44042.
 XX
 PT Human G-protein chemokine receptor, HDGMR10 - useful to identify
 PT (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and
 PT acute inflammation, rheumatoid arthritis, etc.
 XX

PS Claim 1; Page 44-46; 61pp; English.

XX Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7

CC -transmembrane protein involved in signal transduction. Its amino acid

CC sequence was deduced from a cDNA clone (AA744042) isolated from a human

CC monocyte library. Isolation of the cDNA allows prodrn. of recombinant

CC HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant

CC receptor can be used to identify agonists or antagonists of the receptor;

CC such cpds. can be used to treat conditions related to the under- and over

CC -expression of G-protein chemokine receptors

XX

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMQLLTGLYFIQFFS 22

Db 93 QWDFGNTMQLLTGLYFIQFFS 114

RESULT 12

AAW23835

ID AAW23835 standard; protein; 352 AA.

AC AAW23835;

XX

XX 08-JUN-1998 (first entry)

DT Human CC chemokine receptor 5 (CCR5).

DE

DE Human CC chemokine receptor 5; CCR5; G-protein coupled receptor;

KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.

KW

XX Homo sapiens.

XX

Key Location/Qualifiers

Domain 29..55

FT /label= I

FT /note= "transmembrane domain"

FT 104..126

FT /label= III

FT /note= "transmembrane domain"

FT 109..120

FT /note= "extracellular loop-1 (Claim 19)"

FT 143..171

FT /label= IV

FT /note= "transmembrane domain"

FT 187..210

FT /note= "extracellular loop-2 (Claim 19)"

FT 194..219

FT /label= V

FT /note= "transmembrane domain"

FT 238..258

FT /label= VI

FT /note= "transmembrane domain"

FT 261..276

FT /note= "extracellular loop-3 (Claim 19)"

FT 277..300

FT /label= VII

FT /note= "transmembrane domain"

XX

XX WO9745543-A2.

XX

XX 04-DEC-1997.

XX

XX 28-MAY-1997; 97WO-US009586.

XX

XX 28-MAY-1996; 96US-0018508P.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;

PI Broder CC, Kennedy PE;

XX

DR WPI; 1998-032650/03.

DR N-PSDB; AAT76920.

XX

XX CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion

PT between HIV and a target cell.

XX

XX Claim 68; Fig 1C; 70pp; English.

XX

CC This protein sequence comprises of a novel human macrophage-selective CC

CC chemokine receptor that has been designated CCR5. The sequence was

CC deduced from an isolated cDNA clone (see AAT76920). An Alai27Leu variant

CC (see W238340 of CCR5 was also identified. The susceptibility of human

CC macrophages to HIV infection depends on cell surface expression of CD4

CC and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-

CC protein coupled cell surface molecules. It plays an essential role in the

CC membrane fusion step of infection by some HIV isolates. The establishment

CC of stable, non-human cell lines and transgenic mammals having cells that

CC coexpress human CD4 and CCR5 provides valuable tools for research of HIV

CC infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding

CC agents capable of blocking membrane fusion between HIV and target cells

CC represent potential anti-HIV therapeutics for macrophage tropic strains

CC of HIV

XX

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMQLLTGLYFIQFFS 22

Db 93 QWDFGNTMQLLTGLYFIQFFS 114

RESULT 13

AAW8232

ID AAW8232 standard; protein; 352 AA.

XX

AC AAW8232;

XX

XX 15-MAR-1999 (first entry)

DT HIV-1 co-receptor CCR5.

DE

DE HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;

KW Gene therapy; human.

KW

XX Homo sapiens.

XX

Key Location/Qualifiers

Domain 32..56

FT /note= "transmembrane domain 1"

FT 67..87

FT /note= "transmembrane domain 2"

FT Misc-difference 101

FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA

FT (Stop) in CCR5m303"

FT 103..124

FT /note= "transmembrane domain 3"

FT 142..167

FT /note= "transmembrane domain 4"

FT 200..223

FT /note= "transmembrane domain 5"

FT 236..260

FT /note= "transmembrane domain 6"

FT 275..301

FT /note= "transmembrane domain 7"

XX

XX WO9854317-A1.

XX

PD 03-DEC-1998.
 XX 29-MAY-1998; 98WO-EP003437.
 XX 30-MAY-1997; 97US-0048057P.
 PR (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
 XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
 XX WPI; 1999-059835/05.
 XX N-PSDB; AAV84126.

XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 PT resistance of CCR5-expressing cells to HIV-1 infection.
 PT Disclosure; Page 34-35; 55pp; English.

XX This is the amino acid sequence of wild-type human CCR5, which serves as
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of
 CC HIV-1. The invention relates to the identification of a CCR5 variant (see
 CC AAV84231), designated CCR5m303, comprising the first two transmembrane
 CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
 CC presence of the CCR5m303 variant with the wild-type CCR5 allele shows a
 CC positive correlation with resistance to infection with M-tropic HIV-1
 CC strains, and may indicate slower progression of the disease. The
 CC detection of CCR5 variants may be used to identify individuals at lower
 CC risk of infection relative to the general population who, if infected,
 CC may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
 CC 36) are provided for use in diagnostic methods for detecting the presence
 CC of such variants. A method is provided for inhibiting HIV-1 infection of
 CC a cell expressing the CCR5 receptor. This involves introducing a nucleic
 CC acid encoding a CCR5 variant into the cell, thereby reducing the number
 CC of functional CCR5 molecules present on the cell surface

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFES 22
 DB 93 QWDFGNTWCQLLTGLYFIGFES 114

RESULT 14
 AAY80128
 ID AAY80128 standard; protein; 352 AA.

XX AAY80128;

DT 19-MAY-2000 (first entry)

DE Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.

XX Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;
 KW diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
 KW tumour; infection; leukaemia; psoriasis; allergy;
 KW T-cell mediated autoimmune disease; atherogenesis; anaphylaxis;
 KW inflammation; allergic reaction; silicosis; sarcoidosis;
 KW rheumatoid arthritis; hyper-eosinophilia syndrome.

XX Homo sapiens.

XX US6025154-A.

PN 15-FEB-2000.

PD 06-JUN-1995; 95US-00466343.

XX 06-JUN-1995; 95US-00466343.

XX

(HUMA-) HUMAN GENOME SCI INC.

XX Li Y, Ruben SM;

XX WPI; 2000-181807/16.

XX N-PSDB; AAZ51481.

XX Isolated nucleic acid encoding human G-protein chemokine receptor useful
 PT for diagnostic assays, scientific research and screening for compounds
 PT which bind to and activate or inhibit activation of the receptor
 PT polypeptides.

XX Claim 1; Fig 1; 22pp; English.

XX The present sequence represents a human G-protein chemokine receptor
 CC designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
 CC screening for compounds which bind to and either: (1) activate the
 CC HDGNR10 polypeptides causing stimulation of haematopoiesis, wound
 CC healing, coagulation, and angiogenesis; treatment of solid tumours,
 CC chronic infections, leukaemia, T-cell mediated autoimmune diseases,
 CC or (2) inhibit activation of the HDGNR10 polypeptides which is useful for
 CC preventing and/or treating allergy, atherogenesis, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
 CC E-mediated allergic reactions, prostaglandin-independent fever, bone
 CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
 CC hyper-eosinophilia syndrome. The polynucleotides are also useful for
 CC diagnostic assays for detecting diseases related to mutations in the
 CC nucleic acid sequences encoding the polypeptides and for detecting an
 CC altered level of the soluble form of the receptor polypeptides. The
 CC polynucleotides are also useful for in vitro purposes related to
 CC scientific research, synthesis of DNA and manufacture of DNA vectors

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFES 22
 DB 93 QWDFGNTWCQLLTGLYFIGFES 114

RESULT 15
 AAG79089
 ID AAG79089 standard; protein; 352 AA.

XX AAG79089;

XX 10-DEC-2001 (first entry)

XX Amino acid sequence of human CCR5 protein.

XX Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
 KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
 XX Homo sapiens.

XX WO200164752-A2.

XX 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US006322.

XX 02-MAR-2000; 2000US-00517605.

XX (UYNY) UNIV NEW YORK STATE.

XX (UYNI -) UNIV NIJMEGEN.

XX Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;

XX WPI; 2001-602565/68.

XX An antibody for the treatment or prevention of HIV-infection comprises a
 PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of
 PT DC-SIGN due to concomitant conformational change.
 XX
 PS Disclosure; Page 118-119; 131pp; English.

XX The specification describes an antibody which is specific for an
 CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
 CC is exposed upon gp120 binding of DC-SIGN due to concomitant
 CC conformational change. DC-SIGN is a receptor that is specifically
 CC expressed on dendritic cells and facilitates infection of T lymphocytes
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
 CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
 CC with high affinity. The antibody of the invention inhibits the trans
 CC enhancement of HIV entry into a T cell or macrophage facilitated by
 CC dendritic cells. The antibody is useful to treat or prevent HIV
 CC infection. The present sequence represents a human CCR5 protein, which is
 CC a translocation promoting agent that interacts with CD4. This receptor
 CC functions in HIV-1 entry into cells
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFICGFFS 22
 |||||
 Db 93 QWDFGNTMCQLLTGLYFICGFFS 114

RESULT 16

AAE07046
 ID AAE07046 standard; protein; 352 AA.

AC AAE07046;

XX 16-OCT-2001 (first entry)

DE Human G-protein chemokine receptor (CCRS) HDGNR10 protein #1.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

Key	Location/Qualifiers
Domain	1..36
Domain	/label= Extracellular_domain
Domain	37..305
Domain	/label= Transmembrane_domain
Domain	37..58
Domain	/label= Transmembrane_domain
Domain	/note= "Segment 1"
Domain	59..67
Domain	/label= Intracellular_loop_1
Domain	68..88
Domain	/label= Transmembrane_domain
Domain	/note= "Segment 2"
Domain	89..102
Domain	/label= Extracellular_loop_1
Domain	103..124
Domain	/label= Transmembrane_domain
Domain	/note= "Segment 3"
Domain	125..141

FT	Domain	
FT	Domain	/label= Intracellular_loop_2
FT	Domain	142..166
FT	Domain	/label= Transmembrane_domain
FT	Domain	/note= "Segment 4"
FT	Domain	167..195
FT	Domain	/label= Extracellular_loop_2
FT	Domain	196..223
FT	Domain	/label= Transmembrane_domain
FT	Domain	/note= "Segment 5"
FT	Domain	224..235
FT	Domain	/label= Intracellular_loop_3
FT	Domain	236..260
FT	Domain	/label= Transmembrane_domain
FT	Domain	/note= "Segment 6"
FT	Domain	261..274
FT	Domain	/label= Extracellular_loop_3
FT	Domain	287..305
FT	Domain	/label= Transmembrane_domain
FT	Domain	/note= "Segment 7"
FT	Domain	306..352
FT	Domain	/label= Intracellular_domain

WO200158916-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US004153.

09-FEB-2000; 2000US-0181258P.

09-MAR-2000; 2000US-0187999P.

22-SEP-2000; 2000US-0234336P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Roschke V, Li Y, Ruben SM;

WPI; 2001-488966/53.

N-PSDB; AAD13282.

Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

Claim 102; Fig 1; 518pp; English.

The invention relates to human G-protein chemokine receptor (CCRS) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemia) and wound healing. The present sequence is human CCR5 HDGNR10 protein

Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
|||||
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 17
AAE07048
ID AAE07048 standard; protein; 352 AA.

AC AAE07048;

DT 16-OCT-2001 (first entry)

DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
KW cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;
KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX WO200158916-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004153.

XX 09-FEB-2000; 2000US-0181258P.

PR 09-MAR-2000; 2000US-0187999P.

PR 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488966/53.

XX N-PSDB; AAD13299.

PT Isolated nucleic acid encoding a human G-protein chemokine receptor

PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune

PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and

PT neurodegenerative disorders.

XX Example 40; Page 504-505; 518pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5)
CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
CC useful for treating, preventing or ameliorating a disease or disorder
CC associated with inflammation, defective or aberrant chemotaxis of immune
CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
CC sarcoma) or defective or aberrant T-cell antigen presenting cell
CC interaction. The disease or disorder may also be an infectious disease
CC (e.g. a viral infection such as an early stage HIV infection, a
CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
CC disease or disorder may be associated with aberrant CCR5 expression, lack
CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
CC protein, antibodies, agonists and antagonists are also useful in the
CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
CC urogenital); immune disorders (Addison's disease, allergies, autoimmune

CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The
CC present sequence is human CCR5 HDGNR10 protein

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22

|||||

DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 18

AAAG80111

ID AAG80111 standard; protein; 352 AA.

XX AAG80111;

XX 17-JAN-2002 (first entry)

DE Human CCR5 protein.

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW antirheumatic; antiarthritic.

XX Homo sapiens.

XX WO200172830-A2.

XX 04-OCT-2001.

XX 02-APR-2001; 2001WO-EP003708.

XX 31-MAR-2000; 2000DE-01016013.

XX (IPPP-) IPF PHARM GMBH.

XX (FORS/) FORSMANN U.

XX Forssmann W, Adermann K, Heitland A, Spodberg N;

XX WPI; 2001-626256/72.

XX Diagnostic agent containing two or more receptor-specific ligands, useful
XX for detecting tumors, inflammation etc., also therapeutic use of ligand
XX inhibitors.

XX Disclosure; Page 10; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antiasthmatic,
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC proliferation of chemokine receptors (CR), which control migration and
CC proliferation of these cells. AAG8045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCOLLTGLYFIFGFFS 114

RESULT 19
 AAE04321
 ID AAE04321 standard; protein; 352 AA.
 XX AC AAE04321;
 XX DT 04-SEP-2001 (first entry)
 XX DE Human chemokine receptor (CKR), CC-CKR-5 related protein #2.
 XX KW Human; transformed mammalian cell; CD4; reporter gene; translocation;
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
 KW chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor;
 KW CC-CKR-5; envelope glycoprotein; anti-HIV.
 XX OS Homo sapiens.
 XX FN US6258527-B1.
 XX PD 10-JUL-2001.
 XX PF 21-MAY-1997; 97US-00861105.
 XX PR 20-MAY-1996; 96US-0017157P.
 PR 19-JUN-1996; 96US-0020043P.
 PR 19-MAY-1997; 97US-00858660.
 XX PA (AARO-) AARON DIAMOND AIDS RES CENT.
 PA (UJNY) UNIV NEW YORK STATE.
 XX PI Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;
 DR WPI; 2001-417127/44.
 DR N-PSDB; AAD08577.
 XX Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
 PT and HIV LTR for identification of drugs and antibodies for treatment of
 PT HIV.
 XX PS Disclosure; Col 47-50; 37pp; English.
 CC The present invention relates to a transformed mammalian cell that
 CC contains a gene encoding CD4, a construct encoding a reporter gene under
 CC the regulation of an human immuno deficiency virus (HIV) long terminal
 CC repeat (LTR) and that has been transduced with a vector encoding a human
 CC chemokine receptor (CKR) where the CD4 and the CKR are present on the
 CC cell surface of transformed mammalian cell. The invention is useful for
 CC identifying drugs or antibodies that interfere with the translocation of
 CC HIV into transformed mammalian cell or for identifying a human chemokine
 CC receptor that facilitates the infection of a particular HIV strain into
 CC the transformed mammalian cell. Compounds identified can be used to treat
 CC cellular dysfunction and to prevent or combat HIV infection. The present
 CC sequence is a human chemokine receptor (CKR), CC-CKR-5 related protein.
 CC CC-CKR-5 is the principal cofactor for entry mediated by the envelope
 CC glycoproteins of primary macrophage-tropic strains of HIV-1
 XX SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFFS 22

DB 93 QWDFGNTMCOLLTGLYFIFGFFS 114

RESULT 20
 AAE07037
 ID AAE07037 standard; protein; 352 AA.
 XX AC AAE07037;
 XX DT 16-OCT-2001 (first entry)
 XX DE Human G-protein chemokine receptor (CKR5) HDGNR10 protein #1.
 XX KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antineoplastic; vasodilator; vulnery;
 KW cytoskeletal; immunosuppressive; nocotropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX OS Homo sapiens.
 XX FN Key Location/Qualifiers
 FH Domain 1..36
 FT /label= Extracellular_domain
 FT 37..305
 FT /label= Transmembrane_domain
 FT 37..58
 FT /label= Transmembrane_domain
 FT /note= "Segment 1"
 FT 59..67
 FT /label= Intracellular_loop_1
 FT 68..88
 FT /label= Transmembrane_domain
 FT /note= "Segment 2"
 FT 89..102
 FT /label= Extracellular_loop_1
 FT 103..124
 FT /label= Transmembrane_domain
 FT /note= "Segment 3"
 FT 125..141
 FT /label= Intracellular_loop_2
 FT 142..166
 FT /label= Transmembrane_domain
 FT /note= "Segment 4"
 FT 167..195
 FT /label= Extracellular_loop_2
 FT 196..223
 FT /label= Transmembrane_domain
 FT /note= "Segment 5"
 FT 224..235
 FT /label= Intracellular_loop_3
 FT 236..260
 FT /label= Transmembrane_domain
 FT /note= "Segment 6"
 FT 261..274
 FT /label= Extracellular_loop_3
 FT 287..305
 FT /label= Transmembrane_domain
 FT /note= "Segment 7"
 FT 306..352
 FT /label= Intracellular_domain
 XX WO200158915-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004152.

PR 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2001-488965/53.
 DR N-PSDB; AAD13181.
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX Claim 102; Fig 1; 495pp; English.
 CC The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No. 97183. CCR5
 CC HDGNR10 antibodies are useful for treating, preventing or ameliorating a
 CC disease or disorder associated with inflammation, defective or aberrant
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen
 CC presenting cell interaction. The disease or disorder may also be an
 CC infectious disease (e.g. a viral infection such as an early stage HIV
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative
 CC disorder. The disease or disorder may be associated with aberrant CCR5
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or
 CC lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food
 CC additive or preservative to increase or decrease storage capabilities.
 CC CCR5 HDGNR10 DNA are useful for chromosome identification and in gene
 CC therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists
 CC are also useful in the diagnosis, treatment and prevention of cancer
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,
 CC liver, lung, urogenital), immune disorders (Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis); cardiovascular disorders (myocardial ischaemias) and wound
 CC healing
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2,6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCQLLTGLTYFGFSS 22
 DB 93 QWDFGNTWCQLLTGLTYFGFSS 114
 RESULT 21
 AAE07039
 ID AAE07039 standard; protein; 352 AA.
 XX
 AC AAE07039;
 XX
 DT 16-OCT-2001 (first entry)
 DT Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
 DE Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 XX human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; neutropenic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

OS Homo sapiens.
 XX WC200158915-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004152.
 XX 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2001-488965/53.
 DR N-PSDB; AAD13198.
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX Example 40; Page 486-487; 495pp; English.
 CC The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or
 CC ameliorating a disease or disorder associated with inflammation, defective
 CC chemotaxis of immune cells, HIV infection (such as
 CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
 CC aberrant T-cell antigen presenting cell interaction. The disease or
 CC disorder may also be an infectious disease (e.g. a viral infection such
 CC as an early stage HIV infection, a cytomegalovirus infection, or a
 CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
 CC a neurodegenerative disorder. The disease or disorder may be associated
 CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
 CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
 CC is used as a food additive or preservative to increase or decrease
 CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
 CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
 CC antibodies, agonists and antagonists are also useful in the diagnosis,
 CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
 CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
 CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular
 CC disorders (myocardial ischaemias) and wound healing
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2,6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCQLLTGLTYFGFSS 22
 DB 93 QWDFGNTWCQLLTGLTYFGFSS 114
 RESULT 22
 AAB46858
 ID AAB46858 standard; protein; 352 AA.
 XX
 AC AAB46858;
 XX
 DT 16-AUG-2001 (revised)
 DT 02-AUG-2001 (revised)
 DT 04-MAY-2001 (first entry)
 XX Human HDGNR10 protein.
 XX Human HDGNR10; human; G-protein chemokine receptor; antiinflammatory;

immunomodulatory; anticoagulant; antiallergic; immunosuppressive; cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic; vasoprotic; gene therapy; haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour; infection; leukemia; growth factor activity; T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis; anaphylaxis; malignancy; inflammation; histamine; IGE; silicosis; shock; immunoglobulin E-mediated allergic reaction; rheumatoid arthritis; prostaglandin-independent fever; bone marrow failure; sarcoidosis; hyper-eosinophilic syndrome; vulnery.

OS Homo sapiens.
XX WO200177172-A2.
XX XX
XX 18-OCT-2001.
XX XX
XX 05-APR-2001; 2001WO-US011098.
XX XX
XX 07-APR-2000; 2000US-0195747P.
XX XX
XX (AREN-) ARENA PHARM INC.
XX XX
XX Lehmann-Bruinsma K, Liaw CW, Lin I;
XX WPI; 2001-648759/74.
XX N-PSDB; ABI97978.
XX XX
XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions of GPCRs.
XX XX
XX Claim 1; Page 277-278; 394pp; English.
XX XX
XX The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR
XX Sequence 352 AA;
SQ

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 24
AAB83354
ID AAB83354 standard; protein; 352 AA.
XX AAB83354;
XX XX
XX 09-OCT-2001 (first entry)
XX XX
XX Human CCR5 protein sequence.
XX XX
XX Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
XX human immunodeficiency virus; anti-inflammatory disease; human.
XX Homo sapiens.
XX EP1118858-A2.
XX XX
XX 25-JUL-2001.
XX XX
XX 03-JAN-2001; 2001EP-00300020.
XX PF
XX 12-JAN-2000; 2000GB-00000659.
XX PR
XX 12-JAN-2000; 2000GB-00000661.

immunomodulatory; anticoagulant; antiallergic; immunosuppressive; cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic; vasoprotic; gene therapy; haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour; infection; leukemia; growth factor activity; T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis; anaphylaxis; malignancy; inflammation; histamine; IGE; silicosis; shock; immunoglobulin E-mediated allergic reaction; rheumatoid arthritis; prostaglandin-independent fever; bone marrow failure; sarcoidosis; hyper-eosinophilic syndrome; vulnery.

OS Homo sapiens.
XX US2001000241-A1.
XX XX
XX 12-APR-2001.
XX XX
XX 29-NOV-2000; 2000US-00725285.
XX XX
XX 06-JUN-1995; 95US-00466343.
XX 18-NOV-1998; 98US-00195662.
XX 23-JUN-1999; 99US-00339912.
XX XX
XX (LIYY/) LI Y.
XX (RUBE/) RUBEN S M.
XX XX
XX Li Y, Ruben SM;
XX XX
XX WPI; 2001-226317/23.
XX N-PSDB; AAF26390.
XX XX
XX New human G-protein chemokine receptor polypeptides and polynucleotides, useful for identifying (ant)agonists to the G-protein chemokine receptor.
XX XX
XX Claim 1a; Page 15; 22pp; English.
XX XX
XX This invention describes a novel receptor polypeptide (I) selected from (i) a fully defined 329 amino acid sequence (ii) fully disclosed in the specification; and (iii) a polypeptide encoded by the cDNA contained in a plasmid, and fragments, analogs and derivatives of the polypeptide. The products of the invention have antiinflammatory, immunomodulatory, anticoagulant, antiallergic, immunosuppressive, vulnery, cytostatic, antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic activity and can be used for gene therapy. The G-protein chemokine receptors, HDGMR10, (I) are useful for screening for compounds which activate or inhibit activation of (I). The products of the invention can also be used for stimulating haematopoiesis, wound healing, coagulation, angiogenesis, treating solid tumours, chronic infections, leukemia, T-cell mediated autoimmune diseases, parasitic infections, psoriasis, and stimulating growth factor activity. HDGMR10 is useful for treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E (IGE)-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-eosinophilic syndrome. (N.B. This record was resubmitted to correct errors in the keyword formatting)

XX Sequence 352 AA;
SQ

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 23
ABB56342
ID ABB56342 standard; protein; 352 AA.
XX XX
XX ABB56342;
XX XX

PR 12-JAN-2000; 2000GB-00000663.
 XX (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX
 PI Dobbs S, Perros M, Rickett GA;
 XX
 DR WPI; 2001-477088/52.
 DR N-PSDB; AAF87099.
 XX
 PT Determining if an agent can modulate CCR5-gp120 interaction, comprises
 PT incubating the agent with CCR5 and gp120 and determining if the agent
 PT modulates the interaction.
 XX
 PS Claim 1; Page 110; 113pp; English.
 XX
 CC This sequence represents the human CCR5 protein sequence. The invention
 CC relates to a method for determining whether an agent is capable of
 CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
 CC with gp120, comprising incubating the agent with CCR5 and gp120 and
 CC determining whether the agent modulates the interaction, where gp120 is
 CC associated with CD4, and where the interaction is a low affinity binding.
 CC The method is used to identify an agent capable of modulating the
 CC interaction of CCR5 with gp120. An agent identified by the method is used
 CC to prepare a pharmaceutical composition for the treatment of a disease or
 CC condition associated with CCR5 and gp120 interaction, to treat a subject
 CC with a disease or condition associated with CCR5 and gp120 interaction,
 CC and for preparing a pharmaceutical for treating human immunodeficiency
 CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
 CC is commercially useful, amenable to high throughput screening, and
 CC detects interaction of gp120 with cells expressing only CCR5
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
 DB 93 QWDFGNTWCQLLTGLYFIFGFS 114
 RESULT 25
 AAB82948
 ID AAB82948 standard; protein; 352 AA.
 XX
 AC AAB82948;
 XX
 DT 21-DEC-2001 (first entry)
 XX
 DE Human HIV-1 co-receptor CCR5.
 XX
 KW CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
 KW infection; therapy; vaccine; anti-HIV-1.
 XX
 CS Homo sapiens.
 XX
 FH Key . Location/Qualifiers
 FT Binding-site 2..18
 FT /note= "binds to HIV-1 gp120"
 XX
 FN WO200164710-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US0066599.
 XX
 PR 29-FEB-2000; 2000US-0185667P.
 PR 19-MAY-2000; 2000US-0205839P.
 PR 07-FEB-2001; 2001US-0267231P.
 XX
 PA (PROG-) PROGENICS PHARM INC.

PA (AARO-) AARON DIAMOND AIDS RES CENT.
 XX
 PI Dragic T, Olson WC;
 XX
 DR WPI; 2001-611273/70.
 DR N-PSDB; AAH26903.
 XX
 PT Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-
 PT receptor) amino terminal domain including negatively charged and two
 PT sulfated tyrosine residues is useful for treating HIV infection in
 PT humans.
 XX
 PS Claim 1; Page 30; 163pp; English.
 XX
 CC The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids
 CC 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding
 CC site that determines the specificity of the interaction between CCR5 and
 CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the
 CC CCR5 N-terminus is required for gp120 binding and may critically modulate
 CC the susceptibility of target cells to HIV-1 infection in vivo. The
 CC invention provides claimed sulfated peptides (see AAB82947) that are
 CC based on the CCR5 N-terminal region and which are effective for
 CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed
 CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+
 CC cells from becoming infected with HIV, of treating a subject whose CD4+
 CC cells are infected with HIV, and of identifying an agent which inhibits
 CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried
 CC out in a subject, especially a human, infected (therapeutic method), not
 CC infected with HIV (prophylactic method), or in a subject who is not
 CC infected with, but has been exposed to, HIV
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
 DB 93 QWDFGNTWCQLLTGLYFIFGFS 114
 RESULT 26
 AAU97150
 ID AAU97150 standard; protein; 352 AA.
 XX
 AC AAU97150;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 KW hyperproliferative disease; neurological disease; receptor.
 XX
 CS Homo sapiens.
 XX
 FN US2002048786-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 09-FEB-2001; 2001US-00779879.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 XX (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.
 PA (LIYV/) LI Y.
 PA (RUBE/) RUBEN S M.

XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2002-434754/46.
 DR N-PSDB; ABK51853.
 XX
 XX New nucleic acid encoding an antibody specific for the G-protein
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 PT inflammation.
 XX
 XX Claim 61; Fig 1; 180pp; English.
 PS
 XX The present invention relates to the isolation of a novel human G-protein
 CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
 CC sequences encoding it. The invention also describes antibodies that bind
 CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide
 CC sequences encoding the antibodies. The antibodies are useful for treating
 CC or preventing inflammation, defective or aberrant chemotaxis of immune
 CC cells and T-cell/antigen-presenting cell interactions, infections and
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 CC associated with aberrant or deficient expression of the CCR5 receptor or
 CC its ligands. The antibodies are also useful to determine CCR5 expression,
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other
 CC hyperproliferative diseases. The polynucleotide sequences encoding human
 CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
 CC recombinant receptor, and in the treatment of a wide range of diseases
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 CC present sequence represents human G-protein chemokine receptor (CCR5)
 CC HDGNR10 #1
 XX
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QWDFGNTMCOLLTGLYFIFGPPS 22
 DB 93 QWDFGNTMCOLLTGLYFIFGPPS 114

RESULT 27
 AAU97152
 ID AAU97152 standard; protein; 352 AA.
 AC AAU97152;
 XX
 XX 13-AUG-2002 (first entry)
 DT
 XX Human G-protein chemokine receptor (CCR5) HDGNR10 #2.
 DE
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 KW hyperproliferative disease; neurological disease; receptor.
 XX
 XX Homo sapiens.
 OS
 XX US2002048786-A1.
 PN
 XX 25-APR-2002.
 PD
 XX 09-FEB-2001; 2001US-00779879.
 PF
 XX 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 XX (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.

PA (LIY/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2002-434754/46.
 DR N-PSDB; ABK51870.
 XX
 XX New nucleic acid encoding an antibody specific for the G-protein
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 PT inflammation.
 XX
 XX Disclosure; Page 165-166; 180pp; English.
 PS
 XX The present invention relates to the isolation of a novel human G-protein
 CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
 CC sequences encoding it. The invention also describes antibodies that bind
 CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide
 CC sequences encoding the antibodies. The antibodies are useful for treating
 CC or preventing inflammation, defective or aberrant chemotaxis of immune
 CC cells and T-cell/antigen-presenting cell interactions, infections and
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 CC associated with aberrant or deficient expression of the CCR5 receptor or
 CC its ligands. The antibodies are also useful to determine CCR5 expression,
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other
 CC hyperproliferative diseases. The polynucleotide sequences encoding human
 CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
 CC recombinant receptor, and in the treatment of a wide range of diseases
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 CC present sequence represents human G-protein chemokine receptor (CCR5)
 CC HDGNR10 #2
 XX
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QWDFGNTMCOLLTGLYFIFGPPS 22
 DB 93 QWDFGNTMCOLLTGLYFIFGPPS 114

RESULT 28
 AAM52829
 ID AAM52829 standard; protein; 352 AA.
 AC AAM52829;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX Human CCR5 Gln 55 variant.
 DE
 XX CCR5; CC chemokine receptor 5; human; HIV infection;
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
 KW drug screening; identification; variant.
 XX
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 55
 FT Misc-difference 58 /note= "Glu replaces wild-type Leu; encoded by CTG"
 FT Misc-difference 58 /note= "Encoded by AGC"
 FT
 XX WO200171346-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 21-MAR-2001; 2001WO-US0009155.
 PF

```

XX PR 21-MAR-2000; 2000US-0190946P.
XX PR 21-MAR-2000; 2000US-0190996P.
XX PR 21-MAR-2000; 2000US-0191299P.
XX PR 20-MAR-2001; 2001US-00813448.
XX PR 20-MAR-2001; 2001US-00813651.
XX PR 20-MAR-2001; 2001US-00813653.
XX PA (CONS-) CONSENSUS PHARM INC.
XX PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX DR N-PSDB; ABA02318.
XX DR WPI; 2002-010610/01.
XX PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,
XX PT comprises binding a molecule from library to a molecule having binding
XX PT property corresponding to CCR5 and identifying bound molecule.
XX PS Example 3; Fig 4B; 50pp; English.
XX CC The invention relates to a method for identifying a binding compound for
XX CC chemokine receptor 5 (CCR5). The method involves screening a library
XX CC of test molecules (particularly peptides) with immobilised CCR5, and then
XX CC identifying those molecules which bind. The invention also relates to
XX CC CCR5-binding molecules identified using the method of the invention,
XX CC methods for identifying consensus motifs for CCR5-binding peptides, a
XX CC transfer vector encoding tagged CCR5, a computer-aided method for
XX CC determining the relative binding affinity of a test molecule to CCR5 and
XX CC a computer aided drug screening assay that utilises the three-dimensional
XX CC structure of CCR5. Compounds identified using the methods of the
XX CC invention are useful for treating or preventing HIV (human
XX CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
XX CC syndrome) in a patient. The methods of the invention may also be used to
XX CC identify agonists or antagonists of the interaction of CCR5 with its
XX CC natural ligand, and to determine a binding motif for CCR5. The present
XX CC sequence represents a naturally occurring variant of human CCR5 in which
XX CC there is a glutamine, rather than a leucine, at position 55
XX SQ Sequence 352 AA;
XX Query Match 100.0%; Score 126; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 QWDFGNTMCQLLTGLYFIGFPS 22
XX DB 93 QWDFGNTMCQLLTGLYFIGFPS 114
XX RESULT 29
XX AAMS2828
XX ID AAM52828 standard; protein; 352 AA.
XX AC AAM52828;
XX DT 22-FEB-2002 (first entry)
XX DE Human CC chemokine receptor 5 (CCR5).
XX KW CCR5; CC chemokine receptor 5; human; HIV infection;
XX KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
XX KW drug screening; identification.
XX OS Homo sapiens.
XX FN WO200171346-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009155.
XX PR 21-MAR-2000; 2000US-0190946P.

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PR 21-MAR-2000; 2000US-0190996P.
PR 21-MAR-2000; 2000US-0191299P.
PR 20-MAR-2001; 2001US-00813448.
PR 20-MAR-2001; 2001US-00813651.
PR 20-MAR-2001; 2001US-00813653.
XX PA (CONS-) CONSENSUS PHARM INC.
XX PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX DR N-PSDB; ABA02317.
XX DR WPI; 2002-010610/01.
XX PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,
XX PT comprises binding a molecule from library to a molecule having binding
XX PT property corresponding to CCR5 and identifying bound molecule.
XX PS Example 3; Fig 4A; 50pp; English.
XX CC The invention relates to a method for identifying a binding compound for
XX CC chemokine receptor 5 (CCR5). The method involves screening a library
XX CC of test molecules (particularly peptides) with immobilised CCR5, and then
XX CC identifying those molecules which bind. The invention also relates to
XX CC CCR5-binding molecules identified using the method of the invention,
XX CC methods for identifying consensus motifs for CCR5-binding peptides, a
XX CC transfer vector encoding tagged CCR5, a computer-aided method for
XX CC determining the relative binding affinity of a test molecule to CCR5 and
XX CC a computer aided drug screening assay that utilises the three-dimensional
XX CC structure of CCR5. Compounds identified using the methods of the
XX CC invention are useful for treating or preventing HIV (human
XX CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
XX CC syndrome) in a patient. The methods of the invention may also be used to
XX CC identify agonists or antagonists of the interaction of CCR5 with its
XX CC natural ligand, and to determine a binding motif for CCR5. The present
XX CC sequence represents human CCR5
XX SQ Sequence 352 AA;
XX Query Match 100.0%; Score 126; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 QWDFGNTMCQLLTGLYFIGFPS 22
XX DB 93 QWDFGNTMCQLLTGLYFIGFPS 114
XX RESULT 30
XX ABG70597
XX ID ABG70597 standard; protein; 352 AA.
XX AC ABG70597;
XX DT 03-DEC-2002 (first entry)
XX DE Human G-protein chemokine receptor, HDGNR10.
XX KW Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;
XX KW haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour;
XX KW chronic infection; leukaemia; T-cell mediated autoimmune disease;
XX KW parasitic infection; psoriasis; growth factor activity; allergy;
XX KW atherogenesis; anaphylaxis; malignancy; inflammation; histamine;
XX KW immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis;
XX KW prostaglandin-independent fever; bone marrow failure; shock;
XX KW rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic;
XX KW immunosuppressive; antiparasitic; antipsoriatic; antiallergic;
XX KW antiarteriosclerotic; antiinflammatory; antirheumatic; antiarthritic;
XX KW antipyretic; receptor.
XX OS Homo sapiens.
XX DN US2002099176-A1.
XX

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PD 25-JUL-2002.
XX
XX
XX 25-JUN-1999; 99US-00339912.
XX
XX 06-JUN-1995; 95US-00466343.
XX
XX (LIYY/) LI Y.
XX (RUBE/) RUBEN S M.
XX
XX Li Y, Ruben SM;
XX
XX WPI; 2002-690494/74.
XX N-PSDB; ABS54272.
XX
XX Novel human G-protein chemokine receptor polypeptide useful for
XX identifying modulators for stimulating hematopoiesis, wound healing,
XX leukemia, for treating allergy, rheumatoid arthritis, shock and as
XX research agents.
XX
XX Claim 7; Fig 1; 22pp; English.
XX
XX The present invention relates to the isolation of human G-protein
XX chemokine receptor, HDGMR10 (CCR5 receptor), and the polynucleotide
XX sequence encoding it. HDGMR10 polypeptide and polynucleotide sequences
XX are useful for diagnosing a disease or a susceptibility to a disease
XX related to underexpression of HDGMR10. They are useful for identifying
XX modulators for stimulating haematopoiesis, wound healing, coagulation,
XX angiogenesis, to treat solid tumours, chronic infections, leukaemia, T-
XX cell mediated autoimmune diseases, parasitic infections, psoriasis, or
XX for stimulating growth factor activity. The sequences are also useful for
XX preventing and/or treating allergy, atherogenesis, anaphylaxis,
XX malignancy, chronic and acute inflammation, histamine and immunoglobulin
XX E (IGE)-mediated allergic reactions, prostatic and independent fever,
XX bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-
XX eosinophilic syndrome. Polynucleotide sequences encoding HDGMR10 can be
XX used in gene therapy to treat conditions related to underexpression of
XX HDGMR10. The present sequence represents human G-protein chemokine
XX receptor, HDGMR10
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 126; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
XX |||||
XX 93 QWDFGNTMCQLLTGLYFIFGFS 114
XX
XX
XX RESULT 31
XX ABG92883
XX ID ABG92883 standard; protein; 352 AA.
XX
XX AC ABG92883;
XX
XX 19-NOV-2002 (first entry)
XX
XX Human immunoglobulin variable heavy domain #1.
XX
XX Immunoglobulin; variable heavy chain; variable light chain; human;
XX G-protein chemokine receptor; CCR5; HDGMR10; cancer; inflammation;
XX immunologic deficiency syndrome; blood protein disorder; nephritis;
XX ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
XX histiocytosis; chemotaxis; infectious disease; autoimmune disease;
XX Addison's disease; dermatitis; rheumatoid arthritis; allergy;
XX neurodegenerative disorder; viral infection; poxvirus infection; HIV;
XX human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
XX Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
XX lymphocytopenia.
XX
XX Homo sapiens.
XX
XX

PN WO200264612-A2.
XX
XX PD 22-AUG-2002.
XX
XX PF 08-FEB-2002; 2002WO-US003634.
XX
XX 09-FEB-2001; 2001US-00779880.
XX 09-FEB-2001; 2001WO-US004153.
XX 12-JUN-2001; 2001US-0297257P.
XX 08-AUG-2001; 2001US-0310458P.
XX 12-OCT-2001; 2001US-0328447P.
XX 21-DEC-2001; 2001US-0341725P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Roschke V, Rosen CA, Ruben SM;
XX
XX WPI; 2002-643455/69.
XX N-PSDB; ABS68606.
XX
XX New human G-protein Chemokine Receptor gene (HDGMR10) useful for
XX treating, preventing, ameliorating or monitoring diseases or disorders
XX associated with aberrant expression of HDGMR10 e.g. cancer.
XX
XX Example 55; Fig 4; 562pp; English.
XX
XX The invention describes an isolated polynucleotide encoding a first
XX antibody at least 95-100% identical to a second antibody consisting of an
XX amino acid sequence comprising at least one, two or three CDR regions of
XX a variable heavy (VH) or variable light (VL) domain of the antibody
XX expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
XX XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,
XX XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
XX is useful treating, preventing, ameliorating, prognosing or monitoring
XX cancers or other diseases or disorders e.g. immunologic deficiency
XX syndromes such as blood protein disorders and ataxia telangiectasia,
XX inflammation associated disorders such as endotoxin lethality, nephritis
XX and inflammatory bowel disease, conditions associated with an increase in
XX certain haematopoietic cells such as histiocytosis, defective or aberrant
XX chemotaxis of immune cells or T-cell antigen presenting cell interaction,
XX an infectious disease, an autoimmune disease such as Addison's disease,
XX dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
XX disorder, a viral infection e.g. HIV infection, cytomegalovirus or
XX poxvirus infection, a pneumocystis carinii infection, Kaposi's sarcoma,
XX cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
XX disease or disorder associated with aberrant expression of novel human G-
XX protein chemokine receptor (CCR5) HDGMR10. This is the amino acid
XX sequence of human immunoglobulin sequence associated with the antibodies
XX against HDGMR10
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 126; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
XX |||||
XX 93 QWDFGNTMCQLLTGLYFIFGFS 114
XX
XX
XX RESULT 32
XX ABG92880
XX ID ABG92880 standard; protein; 352 AA.
XX
XX AC ABG92880;
XX
XX 19-NOV-2002 (first entry)
XX
XX Human G-protein chemokine receptor (CCR5) HDGMR10 #1.
XX
XX Immunoglobulin; variable heavy chain; variable light chain; human;
XX G-protein chemokine receptor; CCR5; HDGMR10; cancer; inflammation;
XX

immunologic deficiency syndrome; blood protein disorder; nephritis;
ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
histiocytosis; chemotaxis; infectious disease; autoimmune disease;
Addison's disease; dermatitis; rheumatoid arthritis; allergy;
neurodegenerative disorder; viral infection; poxvirus infection; HIV;
human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
lymphocytopenia.

Homo sapiens.

WC2000364612-A2.

22-AUG-2002.

08-FEB-2002; 2002WO-US003634.

09-FEB-2001; 2001US-00779880.

09-FEB-2001; 2001WO-US004153.

12-JUN-2001; 2001US-0297257P.

08-AUG-2001; 2001US-0310458P.

12-OCT-2001; 2001US-0328447P.

21-DEC-2001; 2001US-0341725P.

(HUMA-) HUMAN GENOME SCI INC.

Roschke V, Rosen CA, Ruben SM;

WPI; 2002-643455/69.

N-PSDB; ABS68553.

New human G-protein Chemokine Receptor gene (HDGNR10) useful for

treating, preventing, ameliorating or monitoring diseases or disorders

associated with aberrant expression of HDGNR10 e.g. cancer.

Disclosure; Fig 1A-B; 562pp; English.

The invention describes an isolated polynucleotide encoding a first
antibody at least 95-100% identical to a second antibody consisting of an
amino acid sequence comprising at least one, two or three CDR regions of
a variable heavy (VH) or variable light (VL) domain of the antibody
expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.1B8,
XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
is useful treating, preventing, ameliorating, prognosing or monitoring
cancers or other diseases or disorders e.g. immunologic deficiency
syndromes such as blood protein disorders and ataxia telangiectasia,
inflammation associated disorders such as endotoxin lethality, nephritis
and inflammatory bowel disease, conditions associated with an increase in
certain haematopoietic cells such as histiocytosis, defective or aberrant
chemotaxis of immune cells or T-cell antigen presenting cell interaction,
an infectious disease, an autoimmune disease such as Addison's disease,
dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
disorder, a viral infection e.g. HIV infection, cytomegalovirus or
poxvirus infection, a pneumocystis carinii infection, Kaposi's sarcoma,
cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
disease or disorder associated with aberrant expression of novel human G-
protein chemokine receptor (CCRS) HDGNR10. This is an amino acid sequence
of Human G-protein chemokine receptor (CCRS) HDGNR10 #1

Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22

Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114

RESULT 33

AAE25808

ID AAE25808 standard; protein; 352 AA.
XX
AC AAE25808;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human G-protein chemokine receptor (CCRS), HDGNR10 #1.
XX
KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
inflammation; viral infection; autoimmune disease; neurodegeneration;
rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
hyperproliferative disease; receptor.
XX
OS Homo sapiens.

US2002061834-A1.

23-MAY-2002.

09-FEB-2001; 2001US-00779880.

09-FEB-2000; 2000US-0181258P.

09-MAR-2000; 2000US-0187999P.

22-SEP-2000; 2000US-0234336P.

(ROSE/) ROSEN C A.

(ROSC/) ROSCHKE V.

(LIYY/) LI Y.

(RUBE/) RUBEN S M.

Rosen CA, Roschke V, Li Y, Ruben SM;

WPI; 2002-499674/53.

N-PSDB; AAD42409.

New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,

useful for treatment, prevention and diagnosis of e.g. cancer, also

related antibodies.

PS Claim 61; Page 163-164; 186pp; English.

XX The invention relates to human G-protein chemokine receptor (CCRS), CCR5
HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
antibodies are used for the treatment or prevention of inflammation,
defective or aberrant chemotaxis of immune cells or T cell antigen-
presenting cell interaction, viral infections (specifically human immune
deficiency (including its early stages), cytomegalovirus or pox viruses),
autoimmune disease, rheumatoid arthritis, neurodegeneration, pneumocystis
carinii infection, Kaposi's sarcoma or any condition associated with the
aberrant expression of CCR5 or their ligands. They are also used for the
detection, diagnosis, prognosis and monitoring of cancers or other
hyperproliferative diseases. The present sequence is human G-protein
chemokine receptor (CCRS), HDGNR10 DNA

Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22

Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114

RESULT 34

AAE25811

ID AAE25811 standard; protein; 352 AA.

XX AAE25811;

DT 24-FEB-2003 (first entry)

XX

DE Human G-protein chemokine receptor (CCR5), HDGMR10 #2.
 XX Human, G-protein chemokine receptor; CCR5; HDGMR10 protein; cancer;
 KW inflammation; viral infection; autoimmune disease; neurodegeneration;
 KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
 KW hyperproliferative disease; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002061834-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 09-FEB-2001; 2001US-00779880.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 PR 03-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 PA (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.
 PA (LIYV/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2002-499674/53.
 DR N-PSDB; AAD42426.
 XX
 PT New nucleic acid encoding antibodies to the human CCR5 receptor HDGMR10,
 PT useful for treatment, prevention and diagnosis of e.g. cancer, also
 PT related antibodies.
 XX
 PS Disclosure; Page 170; 186pp; English.
 XX
 CC The invention relates to human G-protein chemokine receptor (CCR5),
 CC HDGMR10 proteins and nucleic acid molecules encoding such proteins. CCR5
 CC antibodies are used for the treatment or prevention of inflammation,
 CC defective or aberrant chemotaxis of immune cells or T cell antigen-
 CC presenting cell interaction, viral infections (specifically human immune
 CC deficiency including its early stages), cytomegalovirus or pox viruses),
 CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
 CC carinii infection, Kaposi's sarcoma or any condition associated with
 CC aberrant expression of CCR5 or their ligands. They are also used for the
 CC detection, diagnosis, prognosis and monitoring of cancers or other
 CC hyperproliferative diseases. The present sequence is human G-protein
 CC chemokine receptor (CCR5), HDGMR10 DNA
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCLLTGLYFIFGFFS 114
 RESULT 35
 ABB81054
 ID ABB81054 standard; protein; 352 AA.
 XX
 AC ABB81054;
 XX
 XX 05-NOV-2002 (first entry)
 DT
 DE G-protein chemokine receptor, HDGMR10.
 XX
 KW 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGMR10;
 KW G-protein chemokine receptor; haematopoietic; immunosuppressant;
 KW antiparasitic; antiproliferative; antiallergic; antiinflammatory; cytostatic;
 KW antineumatic; antiarthritic; gene therapy; human; receptor.

XX Homo sapiens.
 OS
 PN US2002076745-A1.
 XX
 PD 20-JUN-2002.
 XX
 PF 18-NOV-1998; 98US-00195662.
 XX
 PR 06-JUN-1995; 95US-00466343.
 XX
 PA (LIYV/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Li Y, Ruben SM;
 XX WPI; 2002-598724/64.
 DR N-PSDB; AEN86542.
 XX
 PT New polynucleotide encoding a human G protein chemokine receptor HDGMR10,
 PT useful e.g. for treating tumors.
 XX
 PS Claim 7; Fig 1; 22pp; English.
 XX
 CC The invention relates to a novel human 7-transmembrane receptor, HDGMR10,
 CC which has been identified as a G-protein chemokine receptor. The GPCR
 CC HDGMR10 polypeptide can be expressed by standard recombinant methodology.
 CC Compounds that activate or inhibit the receptor polypeptide, optionally
 CC expressed from DNA in gene therapy vectors, are used to treat diseases
 CC that require: (a) activation of the receptor (e.g. stimulation of
 CC haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune
 CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the
 CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis
 CC etc). The present sequence represents the human HDGMR10 receptor
 CC polypeptide
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCLLTGLYFIFGFFS 114
 RESULT 36
 ABB08343
 ID ABB08343 standard; protein; 352 AA.
 XX
 AC ABB08343;
 XX
 XX 18-JUN-2002 (first entry)
 DT
 DE Human chemokine (C-C motif) receptor 5 polypeptide.
 XX
 KW Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;
 KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;
 KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;
 KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;
 KW chromosome 3p21.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 55
 FT /label= Leu, Gln
 FT Misc-difference 182
 FT /label= Phe, Leu
 FT Misc-difference 223
 FT /label= Arg, Gln
 XX

PN WO200177125-A2.
 XX 18-OCT-2001.
 PD 04-APR-2001; 2001WO-US010708.
 PF 05-APR-2000; 2000US-0194361P.
 PR (GENA-) GENAISANCE PHARM INC.
 PA
 XX Choi JY, Klieh SE, Koshy B;
 XX WPI; 2002-041282/05.
 DR N-PSDB; ABA97318, ABA97319.
 XX
 PT New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful
 PT to diagnose and treat diseases associated with its abnormal expression or
 PT function, including human immunodeficiency virus-1 infection.
 XX
 PS Claim 29; Fig 3; 61pp; English.
 CC The present sequence is that of a polypeptide encoded by the human
 CC chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see
 CC ABA97318, ABA97319). The specification describes haplotyping the CCR5
 CC gene of an individual by determining if the individual has one of the
 CC CCR5 haplotypes or haplotype pairs fully defined in the specification.
 CC The specification also describes an isolated polynucleotide comprising a
 CC nucleotide sequence which is a polymorphic variant of the reference CCR5
 CC gene sequence and comprises an isogene defined by a haplotype described
 CC in the specification and its encoded polypeptide. The methods of the
 CC invention are useful to diagnose and develop treatment for diseases
 CC associated with abnormal expression or function of the gene. The CCR5
 CC isogenes and the screened compounds are useful for treating human
 CC immunodeficiency virus (HIV)-1 infection and the progression to acquired
 CC immunodeficiency syndrome (AIDS). The invention has antiviral
 CC applications. The specification describes genotyping the CCR5 gene of an
 CC individual; predicting a haplotype pair for the CCR5 gene of an
 CC individual; identifying an association between a trait and a haplotype or
 CC haplotype pair of the CCR5 gene. The specification describes a
 CC composition comprising a genotyping oligonucleotide for detecting a CCR5
 CC polymorphism; a recombinant non-human organism transformed with CCR5
 CC polynucleotide expressing a CCR5 protein encoded by the variant sequence;
 CC an isolated antibody specific for the CCR5 polypeptide and a method for
 CC screening drugs targeting the CCR5 polypeptide
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
 DB 93 QWDFGNTWCQLLTGLYFIFGFS 114
 RESULT 37
 ABG75540
 ID ABG75540 standard; protein; 352 AA.
 XX ABG75540;
 AC
 XX 16-APR-2003 (first entry)
 DT Human G-protein chemokine receptor, HDGNR10, protein.
 XX Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor;
 KW HDGNR10; signal transduction; gene therapy; haematopoiesis;
 KW wound healing; coagulation; angiogenesis; tumour; chronic infection;
 KW leukaemia; T-cell mediated auto-immune disease; parasitic infection;
 KW psoriasis; growth factor; allergy; atherogenesis; anaphylaxis;
 KW malignancy; inflammation; histamine; IgE-mediated;
 KW prostaglandin-independent fever; bone marrow failure; silicosis;
 KW

KW sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.
 XX Homo sapiens.
 OS US2002132269-A1.
 PN 19-SEP-2002.
 PD 11-FEB-2000; 2000US-00502783.
 XX 06-JUN-1995; 95US-00466343.
 PF (HUMA-) HUMAN GENOME SCI INC.
 PR Li Y, Ruben SM;
 XX WPI; 2003-208944/20.
 DR N-PSDB; ABX10635.
 XX
 PT Novel human G-protein chemokine receptor polypeptide useful for
 PT diagnostic purposes and for identifying modulators of the polypeptide
 PT useful for treating leukemia, autoimmune diseases, psoriasis and allergic
 PT reactions.
 XX
 PS Claim 7; Fig 1; 22pp; English.
 CC The invention discloses a G-protein chemokine receptor (sometimes
 CC referred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the
 CC polynucleotide encoding it. G-protein chemokine receptors are involved in
 CC signal transduction pathways. The polynucleotide and polypeptide can be
 CC used to identify compounds which activate or inhibit activation of the
 CC protein and these compounds are useful for treating a patient having need
 CC to activate or inhibit a G-protein chemokine receptor. The compound is
 CC administered by providing to the patient DNA encoding the agonist or
 CC antagonist and expressing them in vivo (gene therapy). The
 CC polynucleotides and polypeptide are also useful for diagnosing a
 CC disease or susceptibility to a disease related to an under-expression of
 CC the protein, for chromosome identification or as immunogens for producing
 CC antibodies. Agonists are useful in stimulating haematopoiesis, wound
 CC healing, coagulation, angiogenesis, to treat solid tumours, chronic
 CC infections, leukaemia, T-cell mediated auto-immune diseases, parasitic
 CC infections, psoriasis and to stimulate growth factor activity.
 CC Antagonists are useful in the prevention and treatment of allergy,
 CC atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation,
 CC histamine and IgE-mediated allergic reactions, prostaglandin-independent
 CC fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis,
 CC shock and hyper-eosinophilic syndrome. The sequence presented is the
 CC human HDGNR10 protein
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
 DB 93 QWDFGNTWCQLLTGLYFIFGFS 114
 RESULT 38
 ABR58602
 ID ABR58602 standard; protein; 352 AA.
 XX ABR58602;
 AC
 XX 09-JUL-2003 (first entry)
 DT Human cancer related protein SEQ ID NO:259.
 DE Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 KW Human heart disease; atherosclerosis; endometriosis.
 KW

OS Homo sapiens.
 FN WO2003025138-A2.
 XX
 XX
 XX 27-MAR-2003.
 XX
 XX 17-SEP-2002; 2002WO-US029560.
 XX
 XX 17-SEP-2001; 2001US-0323469P.
 PR 20-SEP-2001; 2001US-0323887P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 08-FEB-2002; 2002US-0355145P.
 PR 08-FEB-2002; 2002US-0355257P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 XX (EOSB-) BOS BIOTECHNOLOGY INC.
 XX
 XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE,
 PI Zlotnick A;
 PI
 DR WPI; 2003-354600/33.
 DR N-PSDB; ACC72740.

XX New genes that are up-regulated or down-regulated in cancers, useful as
 PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
 PT therapeutic targets for screening drugs for treating these diseases.
 PT
 XX

PS Claim 12; Page 745; 767pp; English.

XX The present invention describes an isolated nucleic acid molecule, which
 CC comprises the sequence of any of the genes that are up-regulated or down-
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
 CC acute lymphocytic leukemia). ACC72641 to ACC72660 represent cancer-
 CC related gene nucleotide sequences which encode the proteins given in
 CC ABR5521 to ABR58709. Also described: (1) determining the presence or
 CC absence of a pathological cell in a patient; (2) an expression vector
 CC comprising a nucleic acid molecule described above; (3) a host cell
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
 CC of (4); (6) specifically targeting a compound to a pathological cell in a
 CC patient by administering to the patient the antibody above; and (7) a
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or
 CC therapeutic targets. In particular, the nucleic acid is useful for
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
 CC pancreas, prostate, skin and uterus), wounds, ischemia, heart diseases,
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in
 CC drug screening, particularly for identifying agents for treating these
 CC pathologies
 XX

SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 6; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 Db |||||
 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 39
 AAO29514
 ID AAO29514 standard; protein; 352 AA.
 XX
 XX AAO29514;
 AC
 XX 27-AUG-2003 (first entry)
 DT
 XX Human C-C chemokine receptor type 5 (333) protein.
 DE
 XX Human; urological disorder; stress urinary incontinence; prostate cancer;
 KW benign prostatic hyperplasia; overactive bladder; oversensitive bladder;
 KW

KW overflow urinary incontinence; gene therapy; nephrotropic; prostatitis;
 KW kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.
 OS Homo sapiens.
 XX
 XX WO2003039475-A2.
 PN
 XX 15-MAY-2003.
 XX
 XX 07-NOV-2002; 2002WO-US035824.
 PF
 XX 07-NOV-2001; 2001US-0344552P.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX Silos-Santiago I;
 PI
 XX WPI; 2003-449396/42.
 DR N-PSDB; AAL59912.
 DR
 XX Identifying a compound, capable of treating urological disorder e.g.,
 PT benign prostatic hyperplasia, by assaying the ability of the compound to
 PT modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or
 PT polypeptide activity.
 XX
 PS Disclosure; Page 81; 87pp; English.

XX The invention relates to a method for treating an urological disorder
 CC which comprises assaying the ability of the compound to modulate 313,
 CC 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide
 CC activity. The method is useful for identifying a compound for treating an
 CC urological disorder comprising urinary incontinence e.g., overactive/
 CC oversensitive bladder, overflow urinary incontinence, stress urinary
 CC incontinence caused by dysfunction of the bladder, urethra or central/
 CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,
 CC prostate cancer or kidney disorders. It is also used in gene therapy. The
 CC present sequence is human C-C chemokine receptor type 5 (CCR5; 333)
 CC protein. This sequence is used to illustrate the method of the invention
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 6; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 Db |||||
 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 40
 ABU61654
 ID ABU61654 standard; protein; 352 AA.
 XX
 XX AC ABU61654;
 AC
 XX 08-AUG-2003 (first entry)
 DT
 XX Human G-protein chemokine receptor (HDGMR10) polypeptide.
 DE
 XX Human; G-protein chemokine receptor; receptor; HDGMR10;
 KW 7-transmembrane receptor.
 KW
 XX Homo sapiens.
 OS
 XX US2003023044-A1.
 PN
 XX 30-JAN-2003.
 PD
 XX 03-SEP-2002; 2003US-00232686.
 PF
 XX 06-JUN-1995; 95US-00466343.
 PR 18-NOV-1996; 98US-00195662.
 PR

```

PR 25-JUN-1999; 99US-00339912.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Li Y, Ruben SM;
XX
XX DR WPI; 2003-456307/43.
XX DR N-PSDB; ACA61721.
XX
XX PT Producing an antibody, involves immunizing an animal with a polypeptide
XX or with a polypeptide encoded by the human G-protein chemokine receptor
XX clone in AFCC 97183, and recovering the antibody.
XX
XX Claim 1; Fig 1; 23pp; English.
XX
XX The invention relates to a method of producing an antibody, involving
XX immunising an animal with a human G-protein chemokine receptor (HDGGR10)
XX polypeptide (also referred to as a human 7-transmembrane receptor) and
XX recovering an antibody which binds the polypeptide. The method is useful
XX for producing an antibody which binds specifically to the human G-protein
XX chemokine receptor polypeptide. This sequence represents the HDGGR10
XX polypeptide of the invention.
XX
XX SQ Sequence 352 AA;
XX
XX Query Match 100.0%; Score 126; DB 6; Length 352;
XX Best Local Similarity 100.0%; Pred. NO. 2.6e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
XX |||||
XX Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114
XX
XX Search completed: September 28, 2004, 09:03:37
XX Job time : 56.525 secs

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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:00:23 ; Search time 19.8 Seconds
(without alignments)
57.362 Million cell updates/sec

Title: US-10-084-813-12
Perfect score: 126
Sequence: 1 QWDFGNTMCOLLTGLYFIGFPS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	126	100.0	215	3	US-09-087-232A-17
3	126	100.0	215	4	US-08-833-752-6
4	126	100.0	352	3	US-08-466-343D-2
5	126	100.0	352	3	US-09-087-232A-13
6	126	100.0	352	3	US-08-861-105-14
7	126	100.0	352	3	US-08-575-987A-2
8	126	100.0	352	3	US-09-045-583-52
9	126	100.0	352	4	US-09-517-605-5
10	126	100.0	352	4	US-09-534-185-52
11	126	100.0	352	4	US-08-833-752-5
12	126	100.0	352	4	US-09-502-783A-2
13	126	100.0	352	4	US-09-796-202-1
14	87	69.0	344	3	US-08-466-343D-9
15	87	69.0	347	1	US-08-461-244-3
16	87	69.0	360	1	US-08-450-393A-4
17	87	69.0	360	3	US-08-446-869-4
18	87	69.0	360	3	US-09-045-583-50
19	87	69.0	360	4	US-09-534-185-50
20	87	69.0	360	4	US-08-833-752-7
21	87	69.0	360	4	US-09-131-827A-2
22	87	69.0	360	4	US-09-131-827A-20
23	87	69.0	360	5	PCT-US95-00476-4
24	87	69.0	374	1	US-08-450-393A-2
25	87	69.0	374	3	US-08-446-869-2
26	87	69.0	374	5	PCT-US95-00476-2
27	83	65.9	269	1	US-08-307-499-30

ALIGNMENTS

RESULT 1
US-08-833-752-4
; Sequence 4, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-752-4

Sequence 30, Appl
Sequence 2, Appl
Sequence 56, Appl
Sequence 56, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 2, Appl
Sequence 13, Appl
Sequence 9, Appl
Sequence 2, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 53, Appl
Sequence 53, Appl
Sequence 14, Appl
Sequence 5, Appl
Sequence 9, Appl

Query Match 100.0%; Score 126; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIGFPS 22

Db 93 QWDFGNTMCOLLTGLYFIGFPS 114

RESULT 2

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US-09-087-232A-17
; Sequence 17, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillient et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/09/087,232A
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-17

Query Match 100.0%; Score 126; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLTYFGFFS 22
DB 93 QWDFGNTMCQLLTGLTYFGFFS 114

RESULT 3
US-08-833-752-6
; Sequence 6, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833.752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-752-6

Query Match 100.0%; Score 126; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLTYFGFFS 22
DB 93 QWDFGNTMCQLLTGLTYFGFFS 114

RESULT 4
US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGMR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-2

Query Match 100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLTYFGFFS 22
```

Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 5

US-09-087-232A-13

Sequence 13, Application US/09087232A

Patent No. 6153431

GENERAL INFORMATION:

APPLICANT: Quilliant et al.

TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/087,232A

FILING DATE: 28 MAY 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/048,057

FILING DATE: 30 MAY 1997

ATTORNEY/AGENT INFORMATION:

NAME: KOLE, LISA B.

REGISTRATION NUMBER: 35,225

REFERENCE/DOCKET NUMBER: AP 31115

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 408-2628

TELEFAX: (212) 765-2519

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-087-232A-13

Query Match 100.0%; Score 126; DB 3; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.5e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22

Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 6

US-08-861-105-14

Sequence 14, Application US/08861105

Patent No. 6258527

GENERAL INFORMATION:

APPLICANT: LITMAN, DAN R.

APPLICANT: DENG, HONGKUI

APPLICANT: ELLMBIER, WILFRIED

APPLICANT: LANDAU, NATHANIEL R.

APPLICANT: LIU, RONG

TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH

MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC

USERS THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

STREET: Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/861,105

FILING DATE:

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/666,020

FILING DATE: 19-JUN-1996

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,319

FILING DATE: 13-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1049-1-004 N1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-861-105-14

Query Match 100.0%; Score 126; DB 3; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.5e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22

Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 7

US-08-575-967A-2

Sequence 2, Application US/08575967A

Patent No. 6265184

GENERAL INFORMATION:

APPLICANT: Gray et al.

TITLE OF INVENTION: Chemokine Receptor Materials and Methods

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/575,967A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 6265184and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELEPHONE: 206-485-1900
TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: /= "88C amino acid sequence"
US-08-575-967A-2

Query Match 100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFSS 22
DB 93 QWDFGNTMCQLLTGLYFIGFSS 114

RESULT 8

US-09-045-583-52
Sequence 52, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELEPHONE: (617)742-4214
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal
US-09-045-583-52

Query Match 100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFSS 22
DB 93 QWDFGNTMCQLLTGLYFIGFSS 114

RESULT 9

US-09-517-605-5
Sequence 5, Application US/09517605
Patent No. 6391567
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: van Kooyk, Yvette
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-517-605-5

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFSS 22
DB 93 QWDFGNTMCQLLTGLYFIGFSS 114

RESULT 10

US-09-534-185-52
Sequence 52, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELEPHONE: (617)742-4214
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 52:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 11
US-08-833-752-5
; Sequence 5, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: 5:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-752-5

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 12
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
; TITLE OF INVENTION: HDGNR10
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502.783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 13
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPN/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 14
US-08-466-343D-9
; Sequence 9, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-343D-9

Query Match 69.0%; Score 87; DB 3; Length 344;
Best Local Similarity 66.7%; Pred. No. 1.9e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIQFF 21
Db 88 EWVFGNAMCKLFTGLYHIGYF 108

RESULT 15
US-08-461-244-3
Sequence 3, Application US/08461244
Patent No. 5776729
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Vi, Li
APPLICANT: Ruben, Steven M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-244-3

Query Match 69.0%; Score 87; DB 1; Length 347;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIQFF 21
Db 92 EWVFGNAMCKLFTGLYHIGYF 112

RESULT 16
US-08-450-393A-4
Sequence 4, Application US/08450393A
Patent No. 5707815
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Csert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-393A-4

Query Match 69.0%; Score 87; DB 1; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIQFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 17
US-08-446-669-4
Sequence 4, Application US/08446669
Patent No. 6132987
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nealey, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-669-4

Query Match 69.0%; Score 87; DB 3; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIQFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 18
US-09-045-583-50
Sequence 50, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-Mar-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-50

Query Match 69.0%; Score 87; DB 3; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIQFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 19
US-09-534-185-50
Sequence 50, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptacelical Receptor Superfamily and Uses
Therefor
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIQFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 20
US-08-833-752-7
; Sequence 7, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6448375e
US-08-833-752-7

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFF 21
Db 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 21
US-09-131-827A-2
; Sequence 2, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: 60/055,659
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-2

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFF 21
Db 105 EWVFGNACKLFTGLYHIGYF 125

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFF 21
Db 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 22
US-09-131-827A-20
; Sequence 20, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: 60/055,659
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-20

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFF 21
Db 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 23
PCT-US95-00476-4
; Sequence 4, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001

TELEFAX: 310-977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-00476-4

Query Match 69.0%; Score 87; DB 5; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGF 21
DB 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 24
US-08-450-393A-2
Sequence 2, Application US/08450393A
Patent No. 5707815
GENERAL INFORMATION:
APPLICANT: Charo, Israel
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cseri, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-393A-2

Query Match 69.0%; Score 87; DB 1; Length 374;
Best Local Similarity 66.7%; Pred. No. 2.1e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGF 21
DB 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 25
US-08-446-669-2
Sequence 2, Application US/08446669

TELEFAX: 310-977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-00476-4

Query Match 69.0%; Score 87; DB 3; Length 374;
Best Local Similarity 66.7%; Pred. No. 2.1e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGF 21
DB 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 26
PCT-US95-00476-2
Sequence 2, Application PC/TUS9500476
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

```
;
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-00476-2

Query Match 69.0%; Score 87; DB 5; Length 374;
Best Local Similarity 66.7%; Pred. No. 2.1e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QWDFGNTWCQLLTGLYFIFGFF 21
Db 105 EWVFGNAMCKLFTGLYHIGVF 125

RESULT 27
US-08-307-499-30
; Sequence 30, Application US/08307499
; Patent No. 5651972
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,499
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/301,127
; FILING DATE:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-00476-2

Query Match 65.9%; Score 83; DB 3; Length 269;
Best Local Similarity 54.5%; Pred. No. 6e-05;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 20 QWIFGNILCKIMSVLYVGFSS 41

RESULT 28
US-09-299-268-30
; Sequence 30, Application US/09299268
; Patent No. 6217882
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/301,127
; FILING DATE:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US99-299-268-30

Query Match 65.9%; Score 83; DB 3; Length 269;
Best Local Similarity 54.5%; Pred. No. 6e-05;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QWDFGNTWCQLLTGLYFIFGFFS 22
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DB      |||||:|||||:|||||
        20 QWIFGNILCKMSVLVYVGFFS 41

RESULT 29
US-08-461-244-2
; Sequence 2, Application US/08461244
; Patent No. 576729
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yl, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461.244
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-244-2

Query Match          65.1%; Score 82; DB 1; Length 355;
Best Local Similarity 54.5%; Pred. No. 0.00011;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY      1 QWDFGNTWCQLLTGLYFIIGFFS 22
       |||||:|||||:|||||
       98 QWFGVTMCKVSGFYIIGFYIS 119

DB

RESULT 30
US-09-045-583-56
; Sequence 56, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534.185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045.583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 742-4214
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:

```

LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-534-185-56

Query Match 65.1%; Score 82; DB 4; Length 355;
Best Local Similarity 54.5%; Pred. No. 0.00016;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCKLLTGLYIFGFS 22
Db 98 QWVFGNCKRVSGFYIFGFS 119

RESULT 32

US-09-045-583-51
Sequence 51, Application US/09045583
Patent No. 6287805

GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.

TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/045,583

FILING DATE: 20-MAR-98

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNI-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 360 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-09-045-583-51

Query Match 64.3%; Score 81; DB 3; Length 360;
Best Local Similarity 65.0%; Pred. No. 0.00016;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCKLLTGLYIFG 20
Db 105 EWVFGNCKRVSGFYIFG 124

RESULT 33

US-09-534-185-51
Sequence 51, Application US/09534185
Patent No. 6403767

GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185

FILING DATE: 24-Mar-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/045,593

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNI-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 360 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 51:

US-09-534-185-51

Query Match 64.3%; Score 81; DB 4; Length 360;
Best Local Similarity 65.0%; Pred. No. 0.00016;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCKLLTGLYIFG 20
Db 105 EWVFGNCKRVSGFYIFG 124

RESULT 34

US-08-724-984A-2

Sequence 2, Application US/08724984A

Patent No. 6388055

GENERAL INFORMATION:

APPLICANT: Dark Bergsma, Mary Branner, and Usman Shabon

TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road, P.O. Box 1539

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM 486

OPERATING SYSTEM: WINDOWS FOR WORKGROUPS

SOFTWARE: MICROSOFT WORD

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/724,984A
; FILING DATE: October 3, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATGS0023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354
; TYPE: Amino Acid
; TOPOLOGY: Linear
; ORGANISM: Mus musculus
US-08-724-984A-2

Query Match 63.5%; Score 80; DB 4; Length 354;
Best Local Similarity 57.1%; Pred. No. 0.00023;
Matches 12; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFF 21
Db 95 EWIFGNIMCKVFTGVTHIYF 115

RESULT 35

US-09-886-319A-13
; Sequence 13, Application US/09886319A
; Patent No. 6585185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Joern-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886,319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-886-319A-13

Query Match 50.3%; Score 76; DB 4; Length 355;
Best Local Similarity 52.4%; Pred. No. 0.00093;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 WDFGNTMCOLLTGLYFIFGFFS 22
Db 99 WIFGDAMCKLLSGFYVLGLYS 119

RESULT 36

US-09-502-783A-9
; Sequence 9, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
; FILE REFERENCE: HDGNR10
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-502-783A-9

Query Match 58.7%; Score 74; DB 4; Length 329;
Best Local Similarity 54.5%; Pred. No. 0.0017;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFFS 22
Db 88 EWVFGNAMCKLFTGLYHIRYLA 109

RESULT 37

US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
; TITLE OF INVENTION: alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,988A
; FILING DATE: 19930128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-012-988A-2

Query Match 56.3%; Score 71; DB 1; Length 355;
Best Local Similarity 47.6%; Pred. No. 0.0053;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 WDFGNTMCOLLTGLYFIFGFFS 22
Db 99 WVFGDAMCKLLSGFYVLGLYS 119

RESULT 38
US-08-450-393A-5
; Sequence 5, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS: 14
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseer, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-450-393A-5
Query Match 56.3%; Score 71; DB 1; Length 355;
Best Local Similarity 47.6%; Pred. No. 0.0053;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 2 WDFGNTMCQLTGLYFIQFFS 22
Db 99 WVFSDAMCKILSGFYITGLYS 119
RESULT 39
US-08-446-669-5
; Sequence 5, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS: 14
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 35,207
; REFERENCE/DOCKET NUMBER: XAI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-450-393A-5

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-446-669-5
Query Match 56.3%; Score 71; DB 3; Length 355;
Best Local Similarity 47.6%; Pred. No. 0.0053;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 2 WDFGNTMCQLTGLYFIQFFS 22
Db 99 WVFSDAMCKILSGFYITGLYS 119
RESULT 40
US-09-045-583-53
; Sequence 53, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 35,207
; REFERENCE/DOCKET NUMBER: XAI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid

;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-53

Query Match 56.3%; Score 71; DB 3; Length 355;
Best Local Similarity 47.6%; Pred. No. 0.0053;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 WDFGNTMCOLLTGLYFIFGFFS 22
| | | | | | | | | | | | | | | | | | | | | |
Db 99 WIFGDAMCKILSGFYVTGLYS 119

Search completed: September 28, 2004, 09:21:31
Job time : 20.8 secs

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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:06:23 ; Search time 72.875 Seconds
(without alignments)
97.074 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFGNWCOLLTGLYFIFGFFS 22

Scoring table: BLOSUM62

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Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	100.0	22	14	US-10-084-813-12
2	126	100.0	184	9	US-09-938-719-4
3	126	100.0	184	9	US-02-939-226-4
4	126	100.0	184	9	US-09-938-703-4
5	126	100.0	184	16	US-10-661-798-4
6	126	100.0	184	16	US-10-612-791-4
7	126	100.0	215	9	US-09-938-719-6
8	126	100.0	215	9	US-09-938-226-6
9	126	100.0	215	9	US-09-938-703-6
10	126	100.0	215	16	US-10-661-798-6
11	126	100.0	215	16	US-10-612-791-8
12	126	100.0	215	16	US-10-612-791-6
13	126	100.0	215	16	US-10-612-791-18
14	126	100.0	332	14	US-10-095-876A-2
15	126	100.0	352	9	US-09-725-285-2

16 126 100.0 352 9 US-09-759-841-2 Sequence 2, Appli
17 126 100.0 352 9 US-03-779-879A-2 Sequence 2, Appli
18 126 100.0 352 9 US-09-779-879A-22 Sequence 22, Appli
19 126 100.0 352 9 US-09-779-880A-2 Sequence 2, Appli
20 126 100.0 352 9 US-09-779-880A-22 Sequence 22, Appli
21 126 100.0 352 9 US-09-813-653-15 Sequence 15, Appli
22 126 100.0 352 9 US-09-813-653-17 Sequence 17, Appli
23 126 100.0 352 9 US-09-796-202-1 Sequence 1, Appli
24 126 100.0 352 9 US-09-135-662A-2 Sequence 2, Appli
25 126 100.0 352 9 US-09-339-912A-2 Sequence 2, Appli
26 126 100.0 352 9 US-09-938-719-5 Sequence 2, Appli
27 126 100.0 352 9 US-09-939-226-5 Sequence 5, Appli
28 126 100.0 352 9 US-09-938-703-5 Sequence 5, Appli
29 126 100.0 352 9 US-09-502-783A-2 Sequence 2, Appli
30 126 100.0 352 10 US-09-734-221A-14 Sequence 14, Appli
31 126 100.0 352 11 US-09-826-509-477 Sequence 477, Appli
32 126 100.0 352 12 US-10-151-274-5 Sequence 5, Appli
33 126 100.0 352 13 US-10-106-623-2 Sequence 2, Appli
34 126 100.0 352 13 US-10-106-623-20 Sequence 20, Appli
35 126 100.0 352 14 US-10-232-686-2 Sequence 2, Appli
36 126 100.0 352 14 US-10-086-814-1 Sequence 1, Appli
37 126 100.0 352 14 US-10-067-800-2 Sequence 2, Appli
38 126 100.0 352 14 US-10-067-800-22 Sequence 22, Appli
39 126 100.0 352 14 US-10-290-058A-6 Sequence 6, Appli
40 126 100.0 352 14 US-10-225-567A-352 Sequence 352, Appli
41 126 100.0 352 14 US-10-323-314-1 Sequence 1, Appli
42 126 100.0 352 14 US-10-072-301-1 Sequence 1, Appli
43 126 100.0 352 14 US-10-164-649-52 Sequence 52, Appli
44 126 100.0 352 14 US-10-071-866-1 Sequence 1, Appli
45 126 100.0 352 14 US-10-135-839-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-084-813-12
; Sequence 12, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-12

Query Match 100.0%; Score 126; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNWCOLLTGLYFIFGFFS 22
DB 1 QWDFGNWCOLLTGLYFIFGFFS 22

RESULT 2

US-09-938-719-4
; Sequence 4, Application US/09938719
; Patent No. US20020106742A1

GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-719-4
Query Match 100.0%; Score 126; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
RESULT 3
US-09-938-226-4
Sequence 4, Application US/09939226
Patent No. US20020110805A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-939-226-4
Query Match 100.0%; Score 126; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
RESULT 4
US-09-938-703-4
Sequence 4, Application US/09938703
Patent No. US20020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-703-4

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Query Match      100.0%; Score 126; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QWDFGNTMCOLLTGLYFIGFFS 22
Db      93 QWDFGNTMCOLLTGLYFIGFFS 114

RESULT 5
US-10-661-798-4
; Sequence 4, Application US/10661798
; Publication No. US20040110127A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; APPLICANT: Frederic, Libert
; TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV En
; FILE REFERENCE: 9409/2023F
; CURRENT APPLICATION NUMBER: US/10/661,798
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: 09/938,703
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/626,939
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 08/833,752
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: 08/810,028
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: EP 96870021.1
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: EP 96870102.9
; PRIOR FILING DATE: 1996-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-798-4

Query Match      100.0%; Score 126; DB 16; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QWDFGNTMCOLLTGLYFIGFFS 22
Db      93 QWDFGNTMCOLLTGLYFIGFFS 114

RESULT 6
US-10-612-791-4
; Sequence 4, Application US/10612791
; Publication No. US20040161739A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; TITLE OF INVENTION: HIV Diagnostic Methods
; FILE REFERENCE: 9409/2023E
; CURRENT APPLICATION NUMBER: US/10/612,791
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/938,703
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/626,939
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 08/833,752
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: 08/810,028
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: EP 96870021.1
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; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: EP 96870102.9
; PRIOR FILING DATE: 1996-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-791-4

Query Match      100.0%; Score 126; DB 16; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QWDFGNTMCOLLTGLYFIGFFS 22
Db      93 QWDFGNTMCOLLTGLYFIGFFS 114

RESULT 7
US-09-938-719-6
; Sequence 6, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altmar, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-719-6

Query Match      100.0%; Score 126; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QWDFGNTMCOLLTGLYFIGFFS 22
Db      93 QWDFGNTMCOLLTGLYFIGFFS 114
```

RESULT 8
US-09-939-226-6
; Sequence 6, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6
Query Match 100.0%; Score 126; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIGFFS 114
RESULT 9
US-09-938-703-6
; Sequence 6, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6
Query Match 100.0%; Score 126; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIGFFS 114
RESULT 10
US-10-661-798-6
; Sequence 6, Application US/10661798
; Publication No. US20040110127A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; APPLICANT: Frederic, Libert
; TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV Ent
; FILE REFERENCE: 9409/2023F
; CURRENT APPLICATION NUMBER: US/10/661,798
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: 09/938,703
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/626,939
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 08/833,752
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: 08/810,028
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: EP 96870021.1
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: EP 96870102.9
; PRIOR FILING DATE: 1996-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-798-6
Query Match 100.0%; Score 126; DB 16; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIGFFS 22

Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 11

US-10-661-798-18

Query Match 100.0%; Score 126; DB 16; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 18, Application US/10661798
Publication No. US20040110127A1
GENERAL INFORMATION:
APPLICANT: Samson, Michael
APPLICANT: Parmentier, Marc
APPLICANT: Vassart, Gilbert
APPLICANT: Frederic, Libert
TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV En
TITLE OF INVENTION: a Cell
FILE REFERENCE: 9409/2023F
CURRENT APPLICATION NUMBER: US/10/661,798
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: 09/938,703
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 09/626,939
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 08/833,752
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: 08/810,028
PRIOR FILING DATE: 1997-03-03
PRIOR APPLICATION NUMBER: EP 96870021.1
PRIOR FILING DATE: 1996-03-01
PRIOR APPLICATION NUMBER: EP 96870102.9
PRIOR FILING DATE: 1996-08-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 215
TYPE: PRT
ORGANISM: Homo sapiens

US-10-661-798-18

Query Match 100.0%; Score 126; DB 16; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 6, Application US/10612791
Publication No. US20040161739A1
GENERAL INFORMATION:
APPLICANT: Samson, Michael
APPLICANT: Parmentier, Marc
APPLICANT: Vassart, Gilbert
TITLE OF INVENTION: HIV Diagnostic Methods
FILE REFERENCE: 9409/2023E
CURRENT APPLICATION NUMBER: US/10/612,791
CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: 09/938,703
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 09/626,939
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 08/833,752
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: EP 96870021.1
PRIOR FILING DATE: 1996-03-01
PRIOR APPLICATION NUMBER: EP 96870102.9
PRIOR FILING DATE: 1996-08-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 215
TYPE: PRT
ORGANISM: Homo sapiens

US-10-612-791-6

Query Match 100.0%; Score 126; DB 16; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 2, Application US/10095876A
Publication No. US20030148294A1
GENERAL INFORMATION:
APPLICANT: Au-Yang, Janice; Bandman, Olga
APPLICANT: Coleman, Roger; Wilde, Craig G.
TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
FILE REFERENCE: PF-0060-1 CON
CURRENT APPLICATION NUMBER: US/10/095,876A
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 08/638,081
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 332
TYPE: PRT

US-10-095-876A-2

Query Match 100.0%; Score 126; DB 16; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 2, Application US/10095876A
Publication No. US20030148294A1
GENERAL INFORMATION:
APPLICANT: Au-Yang, Janice; Bandman, Olga
APPLICANT: Coleman, Roger; Wilde, Craig G.
TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
FILE REFERENCE: PF-0060-1 CON
CURRENT APPLICATION NUMBER: US/10/095,876A
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 08/638,081
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 332
TYPE: PRT

US-10-095-876A-2

Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 13

US-10-612-791-18

Query Match 100.0%; Score 126; DB 16; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 18, Application US/10612791
Publication No. US20040161739A1
GENERAL INFORMATION:
APPLICANT: Samson, Michael
APPLICANT: Parmentier, Marc
APPLICANT: Vassart, Gilbert
TITLE OF INVENTION: HIV Diagnostic Methods
FILE REFERENCE: 9409/2023E
CURRENT APPLICATION NUMBER: US/10/612,791
CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: 09/938,703
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 09/626,939
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 08/833,752
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: 08/810,028
PRIOR FILING DATE: 1997-03-03
PRIOR APPLICATION NUMBER: EP 96870021.1
PRIOR FILING DATE: 1996-03-01
PRIOR APPLICATION NUMBER: EP 96870102.9
PRIOR FILING DATE: 1996-08-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 215
TYPE: PRT
ORGANISM: Homo sapiens

US-10-612-791-18

Query Match 100.0%; Score 126; DB 16; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 2, Application US/10095876A
Publication No. US20030148294A1
GENERAL INFORMATION:
APPLICANT: Au-Yang, Janice; Bandman, Olga
APPLICANT: Coleman, Roger; Wilde, Craig G.
TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
FILE REFERENCE: PF-0060-1 CON
CURRENT APPLICATION NUMBER: US/10/095,876A
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 08/638,081
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 332
TYPE: PRT

US-10-095-876A-2

Query Match 100.0%; Score 126; DB 16; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 2, Application US/10095876A
Publication No. US20030148294A1
GENERAL INFORMATION:
APPLICANT: Au-Yang, Janice; Bandman, Olga
APPLICANT: Coleman, Roger; Wilde, Craig G.
TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
FILE REFERENCE: PF-0060-1 CON
CURRENT APPLICATION NUMBER: US/10/095,876A
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 08/638,081
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 332
TYPE: PRT

US-10-095-876A-2

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-2

Query Match 100.0%; Score 126; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. No. 6e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 84 QWDFGNTMCQLLTGLYFIFGFFS 105

RESULT 15

US-09-725-285-2
Sequence 2, Application US/09725285
Patent No. US20010000241A1
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
FILE REFERENCE: 1488.1150003
CURRENT APPLICATION NUMBER: US/09/725,285
CURRENT FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 09/339,912
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Artificial Sequence: Genomic
FEATURE:
OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 16

US-09-759-841-2
Sequence 2, Application US/09759841
Patent No. US20010039026A1
GENERAL INFORMATION:
APPLICANT: Rickett, Graham A
APPLICANT: Dobbs, Susan
APPLICANT: Petros, Manoussos
TITLE OF INVENTION: Assay Method
FILE REFERENCE: PCl0348APME
CURRENT APPLICATION NUMBER: US/09/759,841
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: GB 0000661.9
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GB 0000663.5
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GB 0000659.3
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2

LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-759-841-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 17

US-09-779-879A-2
Sequence 2, Application US/09779879A
Patent No. US20020048786A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Roschke, Viktor
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.115000A
CURRENT APPLICATION NUMBER: US/09/779,879A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/234,336
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-879A-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 18

US-09-779-879A-22
Sequence 22, Application US/09779879A
Patent No. US20020048786A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Roschke, Viktor
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1489.115000A
CURRENT APPLICATION NUMBER: US/09/779,879A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/234,336
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENGTH: 352


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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-22

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 19
US-09-779-880A-2
; Sequence 2, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGHR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-2

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 20
US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGHR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens

; ORGANISM: Homo sapiens
US-09-779-880A-22

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 21
US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-15

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 22
US-09-813-653-17
; Sequence 17, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-813-653-17

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLTYFGFFS 22
DB 93 QWDFGNTMCQLLTGLTYFGFFS 114

RESULT 23

US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLTYFGFFS 22
DB 93 QWDFGNTMCQLLTGLTYFGFFS 114

RESULT 24

US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGHR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLTYFGFFS 22
DB 93 QWDFGNTMCQLLTGLTYFGFFS 114

RESULT 25

US-09-339-912A-2

; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGHR10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLTYFGFFS 22
DB 93 QWDFGNTMCQLLTGLTYFGFFS 114

RESULT 26

US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID-MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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/
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIQFFS 22
   |||||
Db 93 QWDFGNTMCQLLTGLYFIQFFS 114

RESULT 27
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-939-226-5

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIQFFS 22
   |||||
Db 93 QWDFGNTMCQLLTGLYFIQFFS 114

RESULT 28
US-09-938-703-5
; Sequence 5, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
```

```
/
/ VASSART, GILBERT
/ LIBERT, FREDERICK
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/ AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/938,703
/ FILING DATE: 24-Aug-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/626,939
/ FILING DATE: 2000-07-27
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: <Unknown>
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 352 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIQFFS 22
   |||||
Db 93 QWDFGNTMCQLLTGLYFIQFFS 114

RESULT 29
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. US20020132269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIQFFS 22
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DB 93 QWDFGNTMCQLLTGLTYFGFFS 114
|||||

RESULT 30

US-09-734-221A-14

; Sequence 14, Application US/09734221A

; Publication No. US20030096221A1

; GENERAL INFORMATION:

; APPLICANT: LITTMAN, DAN R.

; DENG, HONGKUI

; ELLMEIER, WILFRIED

; LANDAU, NATHANIEL R.

; LIU, RONG

; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; USES THEREOF

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/734,221A

; FILING DATE: 11-Dec-2000

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/666,020

; FILING DATE: 19-JUN-1996

; APPLICATION NUMBER: US 08/227,319

; FILING DATE: 13-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REFERENCE/DOCKET NUMBER: 1049-1-004 N2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-487-5800

; TELEFAX: 201-343-1684

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 352 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ORGANISM: Homo sapiens

; ORIGINAL SOURCE:

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-734-221A-14

Query Match 100.0%; Score 126; DB 10; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.3e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 31

US-09-826-509-477

; Sequence 477, Application US/09826509

; Publication No. US20030204073A1

DB 93 QWDFGNTMCQLLTGLTYFGFFS 114
|||||

Query Match 100.0%; Score 126; DB 10; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.3e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 32

US-10-151-274-5

; Sequence 5, Application US/10151274

; Publication No. US20030064071A1

; GENERAL INFORMATION:

; APPLICANT: Littman, Dan R.

; APPLICANT: Kwon, Douglas S.

; APPLICANT: van Kooyk, Yvette

; APPLICANT: Geljtenbeck, Theo

; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

; TITLE OF INVENTION: INTO

; FILE REFERENCE: 1049-1-017

; CURRENT APPLICATION NUMBER: US/10/151,274

; CURRENT FILING DATE: 2002-05-20

; PRIOR APPLICATION NUMBER: US/09/517,605

; PRIOR FILING DATE: 2000-03-02

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 5

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-151-274-5

Query Match 100.0%; Score 126; DB 12; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.3e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 33

US-10-106-623-2

; Sequence 2, Application US/10106623

; Publication No. US2002015088A1

; GENERAL INFORMATION:

; APPLICANT: Gray, Patrick W.

; APPLICANT: Schweickart, Vicky L.

; APPLICANT: Report, Carol J.

; TITLE OF INVENTION: Chemokine Receptor Materials and Methods

US-10-106-623-2

Query Match 100.0%; Score 126; DB 12; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.3e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

;
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2

Query Match 100.0%; Score 126; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 34
US-10-106-623-20
; Sequence 20, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002

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;
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-106-623-20

Query Match 100.0%; Score 126; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 35
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCRS) HDGNR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2

Query Match 100.0%; Score 126; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 36
US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814

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; CURRENT FILING DATE: 2002-02-28
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-084-813-12

Query Match 100.0%; Score 126; DB 14; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.3e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 37
 US-10-067-800-2
 ; Sequence 2, Application US/10067800
 ; Publication No. US20030100058A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Roschke, Viktor
 ; APPLICANT: Ruben, Steven, M.
 ; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGHR10
 ; FILE REFERENCE: 1488.1150001
 ; CURRENT APPLICATION NUMBER: US/10/067,800
 ; CURRENT FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: PCT/US01/04153
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 09/779,880
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/297,257
 ; PRIOR FILING DATE: 2001-06-12
 ; PRIOR APPLICATION NUMBER: 60/310,458
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/328,447
 ; PRIOR FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 60/341,725
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-067-800-2

Query Match 100.0%; Score 126; DB 14; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.3e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 38
 US-10-067-800-22
 ; Sequence 22, Application US/10067800
 ; Publication No. US20030100058A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Roschke, Viktor
 ; APPLICANT: Ruben, Steven, M.
 ; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGHR10
 ; FILE REFERENCE: 1488.1150001
 ; CURRENT APPLICATION NUMBER: US/10/067,800
 ; CURRENT FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: PCT/US01/04153
 ; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 09/779,880
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/297,257
 ; PRIOR FILING DATE: 2001-06-12
 ; PRIOR APPLICATION NUMBER: 60/310,458
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/328,447
 ; PRIOR FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 60/341,725
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 22
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-067-800-22

Query Match 100.0%; Score 126; DB 14; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.3e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 39
 US-10-290-058A-6
 ; Sequence 6, Application US/10290058A
 ; Publication No. US20030104455A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Silos-Santiago, Immaculada
 ; TITLE OF INVENTION: Methods and Compositions for Treating
 ; TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
 ; FILE REFERENCE: WPI01-289PRM
 ; CURRENT APPLICATION NUMBER: US/10/290,058A
 ; CURRENT FILING DATE: 2002-11-07
 ; PRIOR APPLICATION NUMBER: 60/344,552
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-290-058A-6

Query Match 100.0%; Score 126; DB 14; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.3e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 40
 US-10-225-567A-352
 ; Sequence 352, Application US/10225567A
 ; Publication No. US20030113798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lifespan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Burner, Glenn C.
 ; APPLICANT: Roush, Christine L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO. 352
; LENGTH 352
; TYPE: FRI
; ORGANISM: Homo sapiens
US-10-225-567A-352

Query Match      100.0%;   Score 126;   DB 14;   Length 352;
Best Local Similarity 100.0%;   Pred. NO. 6.3e-10;
Matches 22;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      1 QWDFGNTMCOLLTGLYFIGFFS 22
        |||||
Db      93 QWDFGNTMCOLLTGLYFIGFFS 114

Search completed: September 28, 2004, 09:44:41
Job time : 74.875 secs

```

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OM protein - protein search, using sw model
Run on: September 28, 2004, 08:57:36 ; Search time 11.825 Seconds
(without alignments)
178.961 Million cell updates/sec

Title: US-10-084-813-12
Perfect score: 126
Sequence: 1 QWDFGNTMCOLLGLYFIFGFFS 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	100.0	352	2 A43113	chemokine (C-C) re
2	87	69.0	360	2 JC2443	chemokine (C-C) re
3	87	69.0	374	2 I38450	chemokine (C-C) re
4	82	65.1	355	2 JC5067	G protein-coupled
5	76	60.3	355	2 I49339	macrophage inflam
6	74	58.7	356	2 I49340	MIP-1 alpha recept
7	71	56.3	355	2 A45177	chemokine (C-C) re
8	70	55.6	359	2 I49341	MIP-1 alpha recept
9	67	53.2	355	2 G02436	chemokine (C-C) re
10	66	52.4	360	2 A57160	chemokine (C-C) re
11	65	51.6	344	2 JC5942	chemokine receptor
12	65	51.6	360	2 JC4587	chemokine (C-C) re
13	60	47.6	354	2 I58186	chemokine (C-C) re
14	59	46.8	369	2 JC5068	probable G protein
15	56	44.4	355	2 JC4304	G protein-coupled
16	55	43.7	383	2 S55394	orphan G protein-c
17	53.5	42.5	328	2 I38973	G protein-coupled
18	53	42.1	378	2 A55735	G protein-coupled
19	53	42.1	422	2 JC7080	G protein-coupled
20	52	41.3	378	2 A45680	melanin-concentrat
21	52	41.3	378	2 B55735	G protein-coupled
22	51	40.5	352	1 S27357	lymphocyte-specifi
23	50	39.7	350	2 JN0621	complement C5a ana
24	50	39.7	359	2 A48921	G protein-coupled
25	50	39.7	435	2 T37324	interleukin-8 rece
26	50	39.7	448	2 T16256	probable JNK-activ
27	49.5	39.3	359	2 I51372	hypothetical prote
28	49	38.9	354	2 B55733	angiotensin II rec
29	49	38.9	367	2 JE0349	G protein-coupled
					interferon-inducib

30	49	38.9	398	2 A57510	mu opitoid receptor
31	49	38.9	425	2 A37512	thrombin receptor
32	49	38.9	427	2 S17148	alpha-thrombin rec
33	48.5	38.5	186	2 AG1086	hypothetical prote
34	48.5	38.5	706	2 A81848	probable TonB-depe
35	48	38.1	352	2 G00048	fusin (LESTRA) C
36	48	38.1	352	2 A5747	neuropeptide Y/pep
37	48	38.1	409	2 P5067	probable transport
38	48	38.1	409	2 F91091	probable transport
39	48	38.1	409	2 A85937	probable transport
40	48	38.1	420	2 I51667	thrombin receptor
41	48	38.1	482	2 S65766	G protein-coupled
42	48	38.1	937	2 T37241	olfactory channel
43	48	38.1	957	2 D88651	protein B0212.5 [i
44	47.5	37.7	370	2 J85549	heptamethyl P2Y5-
45	47	37.3	334	2 JC4681	bradykinin B1 rece

ALIGNMENTS

RESULT 1

A43113
chemokine (C-C) receptor 5 - human
N:Alternate names: C-C CKR-5; CCR5
C:Species: Homo sapiens (man)
C:Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000
C:Accession: A43113; S71808; A58834; A58832; G02653; A58833
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A:Title: Molecular cloning and functional expression of a new human CC-chemokine recepto
A:Reference number: A43113; MUID:96241590; PMID:8639485
A:Accession: A43113
A:Molecule type: mRNA
A:Residues: 1-352 <SAM1>
A:Cross-references: GB:X91492; NID:91262810; PIDN:CAA62796.1; PID:g1262811
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragost
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa
Nature 382, 722-725, 1996
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles (c
A:Reference number: S71808; MUID:96345670; PMID:8751444
A:Accession: S71808
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206;207-230 <SAM2>
A:Accession: A58834
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184, 'IKDSLHGAPAAACHGILLGNPKNSASVSK' <SAM3>
A:Cross-references: GB:X99393; NID:91524062; PIDN:CAA67767.1; PID:g1524063
A>Note: this frameshift mutation results in a non-functional receptor but confers a deg
rd may have had a selective advantage by conferring resistance to Yersinia plague infect
R:Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec
A:Reference number: A58832; MUID:96295970; PMID:8699119
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:91502408; PIDN:AAB17071.1; PID:g1502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadiere, C.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89, 'L', 91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine
A:Reference number: A58833; MUID:96291862; PMID:8663314

A/Accession: A50833
 A/Molecule type: mRNA
 A/Residues: 1-352 <RAP>
 A/Cross-references: GB:U54994; NID:G1457945; PIDN:BA050598.1; PID:G1457946
 C/Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A030574), MIP-1beta (see PIR:A030575) and dual-tropic strains of HIV-1 bind to a complex of chemokine (see PIR:A030576) and dual-tropic strains of HIV-1 bind to a complex of chemokine (see PIR:A030576).
 C/Genetics:
 A/Gene: GDB:CMKBR5; CCR5; CCR5; CCR5; CCR5; ChemR13
 A/Cross-references: GDB:1230510; OMIM:601373
 A/Map position: 3p21-3p21

C/Function:
 A/Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
 A/Note: probably acts to control granulocyte proliferation and differentiation
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F:2-56/Domain: transmembrane #status predicted <TM1>
 F:57-87/Domain: transmembrane #status predicted <TM2>
 F:103-124/Domain: transmembrane #status predicted <TM3>
 F:142-166/Domain: transmembrane #status predicted <TM4>
 F:193-218/Domain: transmembrane #status predicted <TM5>
 F:236-257/Domain: transmembrane #status predicted <TM6>
 F:285-300/Domain: transmembrane #status predicted <TM7>
 F:20-269/Domain: transmembrane #status predicted
 F:268/Binding site: carbohydrate bonds: #status predicted
 F:336.337.342/Binding site: phosphate (Ser) (covalent) #status predicted
 F:340.343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.08; Score 126; DB 2; Length 352;
 Best Local Similarity 100.08; Pred. No. 1.6e-11; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCCQLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCCQLTGLYFIFGFFS 114

RESULT 2
 JC2443

Chemokine (C-C) receptor 2, splice form B - human
 N/Alternate names: C-C CRK-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1 receptor
 C/Species: Homo sapiens (man)
 C/Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
 C/Accession: JC2443; 138463
 R/Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
 Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
 A/Title: CDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor
 A/Reference number: JC2443; MUID:94324942; PMID:8048929
 A/Accession: JC2443
 A/Molecule type: mRNA
 A/Residues: 1-360 <YAM>
 A/Cross-references: DDBJ:D29584; NID:G531246; PIDN:BA06253.1; PID:G531247
 R/Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A/Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors
 A/Reference number: A53477; MUID:94195821; PMID:8146186
 A/Accession: 138463
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-360 <RES>
 A/Cross-references: EMBL:U03905; NID:G472557; PIDN:AAA19120.1; PID:G472558
 C/Genetics:
 A/Gene: GDB:CMKBR2
 A/Cross-references: GDB:337364; OMIM:601267
 A/Map position: 3p21-3p21
 C/Superfamily: vertebrate rhodopsin
 F:43-70/Domain: transmembrane #status predicted <TM1>
 F:81-100/Domain: transmembrane #status predicted <TM2>
 F:115-136/Domain: transmembrane #status predicted <TM3>
 F:154-178/Domain: transmembrane #status predicted <TM4>
 F:207-226/Domain: transmembrane #status predicted <TM5>
 F:244-268/Domain: transmembrane #status predicted <TM6>
 F:287-309/Domain: transmembrane #status predicted <TM7>

Query Match 100.08; Score 126; DB 2; Length 352;
 Best Local Similarity 100.08; Pred. No. 1.6e-11; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCCQLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCCQLTGLYFIFGFFS 114

RESULT 2
 JC2443

Chemokine (C-C) receptor 2, splice form B - human
 N/Alternate names: C-C CRK-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1 receptor
 C/Species: Homo sapiens (man)
 C/Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
 C/Accession: JC2443; 138463
 R/Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
 Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
 A/Title: CDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor
 A/Reference number: JC2443; MUID:94324942; PMID:8048929
 A/Accession: JC2443
 A/Molecule type: mRNA
 A/Residues: 1-360 <YAM>
 A/Cross-references: DDBJ:D29584; NID:G531246; PIDN:BA06253.1; PID:G531247
 R/Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A/Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors
 A/Reference number: A53477; MUID:94195821; PMID:8146186
 A/Accession: 138463
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-360 <RES>
 A/Cross-references: EMBL:U03905; NID:G472557; PIDN:AAA19120.1; PID:G472558
 C/Genetics:
 A/Gene: GDB:CMKBR2
 A/Cross-references: GDB:337364; OMIM:601267
 A/Map position: 3p21-3p21
 C/Superfamily: vertebrate rhodopsin
 F:43-70/Domain: transmembrane #status predicted <TM1>
 F:81-100/Domain: transmembrane #status predicted <TM2>
 F:115-136/Domain: transmembrane #status predicted <TM3>
 F:154-178/Domain: transmembrane #status predicted <TM4>
 F:207-226/Domain: transmembrane #status predicted <TM5>
 F:244-268/Domain: transmembrane #status predicted <TM6>
 F:287-309/Domain: transmembrane #status predicted <TM7>

Query Match 100.08; Score 126; DB 2; Length 352;
 Best Local Similarity 100.08; Pred. No. 1.6e-11; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCCQLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCCQLTGLYFIFGFFS 114

RESULT 2
 JC2443

Chemokine (C-C) receptor 2, splice form B - human
 N/Alternate names: C-C CRK-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1 receptor
 C/Species: Homo sapiens (man)
 C/Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
 C/Accession: JC2443; 138463
 R/Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
 Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
 A/Title: CDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor
 A/Reference number: JC2443; MUID:94324942; PMID:8048929
 A/Accession: JC2443
 A/Molecule type: mRNA
 A/Residues: 1-360 <YAM>
 A/Cross-references: DDBJ:D29584; NID:G531246; PIDN:BA06253.1; PID:G531247
 R/Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A/Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors
 A/Reference number: A53477; MUID:94195821; PMID:8146186
 A/Accession: 138463
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-360 <RES>
 A/Cross-references: EMBL:U03905; NID:G472557; PIDN:AAA19120.1; PID:G472558
 C/Genetics:
 A/Gene: GDB:CMKBR2
 A/Cross-references: GDB:337364; OMIM:601267
 A/Map position: 3p21-3p21
 C/Superfamily: vertebrate rhodopsin
 F:43-70/Domain: transmembrane #status predicted <TM1>
 F:81-100/Domain: transmembrane #status predicted <TM2>
 F:115-136/Domain: transmembrane #status predicted <TM3>
 F:154-178/Domain: transmembrane #status predicted <TM4>
 F:207-226/Domain: transmembrane #status predicted <TM5>
 F:244-268/Domain: transmembrane #status predicted <TM6>
 F:287-309/Domain: transmembrane #status predicted <TM7>

Query Match 100.08; Score 126; DB 2; Length 352;
 Best Local Similarity 100.08; Pred. No. 1.6e-11; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCCQLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCCQLTGLYFIFGFFS 114

RESULT 2
 JC2443

F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:113-190/Disulfide bonds: #status predicted

Query Match 69.08; Score 87; DB 2; Length 360;
 Best Local Similarity 66.78; Pred. No. 1.4e-05; Indels 0; Gaps 0;
 Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCCQLTGLYFIFGFF 21
 DB 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 3
 I38450

Chemokine (C-C) receptor 2, splice form A - human
 N/Alternate names: C-C CRK-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1 receptor
 C/Species: Homo sapiens (man)
 C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
 C/Accession: 138450
 R/Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A/Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors
 A/Reference number: A53477; MUID:94195821; PMID:8146186
 A/Accession: 138450
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-374 <RES>
 A/Cross-references: EMBL:U03882; NID:G472555; PIDN:AAA19119.1; PID:G472556
 C/Genetics:
 A/Gene: GDB:CMKBR2
 A/Cross-references: GDB:337364; OMIM:601267
 A/Map position: 3p21-3p21
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
 F:44-68/Domain: transmembrane #status predicted <TM1>
 F:79-99/Domain: transmembrane #status predicted <TM2>
 F:115-136/Domain: transmembrane #status predicted <TM3>
 F:154-178/Domain: transmembrane #status predicted <TM4>
 F:208-226/Domain: transmembrane #status predicted <TM5>
 F:244-265/Domain: transmembrane #status predicted <TM6>
 F:292-309/Domain: transmembrane #status predicted <TM7>
 F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:32-277, 113-190/Disulfide bonds: #status predicted

Query Match 69.08; Score 87; DB 2; Length 374;
 Best Local Similarity 66.78; Pred. No. 1.5e-05; Indels 0; Gaps 0;
 Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCCQLTGLYFIFGFF 21
 DB 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 4
 JC5067

G protein-coupled receptor CRK-L1 - human
 N/Alternate names: chemokine receptor-like protein TER1; GPR-CY6
 C/Species: Homo sapiens (man)
 C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C/Accession: JC5067; G02776; G02387
 R/Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996
 A/Title: Molecular cloning and RNA expression of two new human chemokine receptor-like G protein-coupled receptors
 A/Reference number: JC5067; MUID:97040707; PMID:8886020
 A/Accession: JC5067
 A/Molecule type: DNA
 A/Residues: 1-355 <ZAB>
 A/Cross-references: EMBL:Z79782; NID:G1668735; PIDN:CA02142.1; PID:G1668736
 R/Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
 submitted to the EMBL Data Library, June 1996
 A/Reference number: H01714
 A/Accession: G02776
 A/Status: translated from GB/EMBL/DBJ

Query Match 69.08; Score 87; DB 2; Length 374;
 Best Local Similarity 66.78; Pred. No. 1.5e-05; Indels 0; Gaps 0;
 Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCCQLTGLYFIFGFF 21
 DB 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 4
 JC5067

G protein-coupled receptor CRK-L1 - human
 N/Alternate names: chemokine receptor-like protein TER1; GPR-CY6
 C/Species: Homo sapiens (man)
 C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C/Accession: JC5067; G02776; G02387
 R/Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996
 A/Title: Molecular cloning and RNA expression of two new human chemokine receptor-like G protein-coupled receptors
 A/Reference number: JC5067; MUID:97040707; PMID:8886020
 A/Accession: JC5067
 A/Molecule type: DNA
 A/Residues: 1-355 <ZAB>
 A/Cross-references: EMBL:Z79782; NID:G1668735; PIDN:CA02142.1; PID:G1668736
 R/Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
 submitted to the EMBL Data Library, June 1996
 A/Reference number: H01714
 A/Accession: G02776
 A/Status: translated from GB/EMBL/DBJ

Query Match 69.08; Score 87; DB 2; Length 374;
 Best Local Similarity 66.78; Pred. No. 1.5e-05; Indels 0; Gaps 0;
 Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCCQLTGLYFIFGFF 21
 DB 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 4
 JC5067

G protein-coupled receptor CRK-L1 - human
 N/Alternate names: chemokine receptor-like protein TER1; GPR-CY6
 C/Species: Homo sapiens (man)
 C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C/Accession: JC5067; G02776; G02387
 R/Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996
 A/Title: Molecular cloning and RNA expression of two new human chemokine receptor-like G protein-coupled receptors
 A/Reference number: JC5067; MUID:97040707; PMID:8886020
 A/Accession: JC5067
 A/Molecule type: DNA
 A/Residues: 1-355 <ZAB>
 A/Cross-references: EMBL:Z79782; NID:G1668735; PIDN:CA02142.1; PID:G1668736
 R/Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
 submitted to the EMBL Data Library, June 1996
 A/Reference number: H01714
 A/Accession: G02776
 A/Status: translated from GB/EMBL/DBJ

A.Molecule type: DNA
 A.Residues: 1-355 <NAP>
 A.Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
 R.Bonner, T.I.
 submitted to the EMBL Data Library, January 1996
 A.Reference number: H01154
 A.Accession: G02387
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-355 <BON>
 A.Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
 C.Comment: This protein belongs to the family of beta chemokine receptors.

C.Genetics:
 A.Gene: GDB:CMKBR8; CMKBR2; TER1; CKR-L1
 A.Cross-references: GDB:6053733; OMIM:601834
 A.Map position: 3p21-3p21
 C.Superfamily: vertebrate rhodopsin

C.Keywords: G protein-coupled receptor; transmembrane protein
 F136-63/Domain: transmembrane #status predicted <TM1>
 F136-94/Domain: transmembrane #status predicted <TM2>
 F108-123/Domain: transmembrane #status predicted <TM3>
 F147-171/Domain: transmembrane #status predicted <TM4>
 F200-222/Domain: transmembrane #status predicted <TM5>
 F233-260/Domain: transmembrane #status predicted <TM6>
 F281-304/Domain: transmembrane #status predicted <TM7>

Query Match 65.1%; Score 82; DB 2; Length 355;
 Best Local Similarity 54.5%; Pred. No. 7.9e-05;
 Matches 12; Conservative 6; Mismatches 4; Indels 0;

QY 1 QWDFGNTMCKLLTGLYIFGPF 22
 DB 98 QWFGTVMCKVSGFYIIGFYS 119

RESULT 5

I49339
 macrophage inflammatory protein-1 alpha receptor - mouse
 C.Species: Mus musculus (house mouse)
 C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
 C.Accession: I49339
 R.Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A.Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
 A.Reference number: I49339; MUID:95340546; PMID:7542241
 A.Accession: I49339
 A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA
 A.Residues: 1-355 <RES>
 A.Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
 C.Superfamily: vertebrate rhodopsin

Query Match 60.3%; Score 76; DB 2; Length 355;
 Best Local Similarity 52.4%; Pred. No. 0.00065;
 Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 WDFGNTMCKLLTGLYIFGPF 22
 DB 99 WIFGDAMCKLLSGFYIIGFYS 119

RESULT 6

I49340
 MIP-1 alpha receptor like-1 - mouse
 C.Species: Mus musculus (house mouse)
 C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
 C.Accession: I49340
 R.Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A.Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
 A.Reference number: I49339; MUID:95340546; PMID:7542241
 A.Accession: I49340
 A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA
 A.Residues: 1-355 <NAP>
 A.Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
 R.Bonner, T.I.
 submitted to the EMBL Data Library, January 1996
 A.Reference number: H01154
 A.Accession: G02387
 A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA
 A.Residues: 1-355 <RES>
 A.Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
 C.Superfamily: vertebrate rhodopsin

Query Match 58.7%; Score 74; DB 2; Length 356;
 Best Local Similarity 47.6%; Pred. No. 0.0013;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 WDFGNTMCKLLTGLYIFGPF 22
 DB 100 WIFGDAMCKVSGFYIIGFYS 120

RESULT 7

A45177
 chemokine (C-C) receptor 1 - human
 N.Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
 C.Species: Homo sapiens (man)
 C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C.Accession: A45177; I55671
 R.Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
 Cell 72, 415-425, 1993
 A.Title: Molecular cloning, functional expression, and signaling characteristics of a C-
 A.Reference number: A45177; MUID:93161416; PMID:7679328
 A.Accession: A45177

A.Status: nucleic acid sequence not shown
 A.Molecule type: mRNA
 A.Residues: 1-355 <NEO>
 A.Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 A.Experimental source: HL60 cells
 A.Note: sequence extracted from NCBI backbone (NCBIP:124876)
 R.Gao, J.

J. Exp. Med. 177, 1421-1427, 1993
 A.Title: Structure and functional expression of the human macrophage inflammatory 1 alp
 A.Reference number: I55671; MUID:93240122; PMID:7683036
 A.Accession: I55671

A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-355 <RES>
 A.Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

C.Genetics:
 A.Gene: GDB:CMKBR1; CMKR-1
 A.Cross-references: GDB:1138446; OMIM:601159
 A.Map position: 3p21-3p21
 C.Superfamily: vertebrate rhodopsin

C.Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; t
 F136-60/Domain: transmembrane #status predicted <TM1>
 F171-91/Domain: transmembrane #status predicted <TM2>
 F108-129/Domain: transmembrane #status predicted <TM3>
 F147-171/Domain: transmembrane #status predicted <TM4>
 F205-223/Domain: transmembrane #status predicted <TM5>
 F240-264/Domain: transmembrane #status predicted <TM6>
 F288-305/Domain: transmembrane #status predicted <TM7>
 F5/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F24-273,106-183/Disulfide bonds: #status predicted
 F345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 56.3%; Score 71; DB 2; Length 355;
 Best Local Similarity 47.6%; Pred. No. 0.0038;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 WDFGNTMCKLLTGLYIFGPF 22
 DB 99 WIFGDAMCKLLSGFYIIGFYS 119

RESULT 8

I49341
 MIP-1 alpha receptor like-2 - mouse
 C.Species: Mus musculus (house mouse)
 C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
 A.Accession: I49341

R;Geo, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
 A;Reference number: 149339; MUID:95340546; PMID:7542241
 A;Accession: 149341
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-359 <RES>
 A;Cross-references: EMBL:U28406; NID:G881551; PID:G881552
 A;Superfamily: vertebrate rhodopsin

Query Match 55.6%; Score 70; DB 2; Length 359;
 Best Local Similarity 40.9%; Pred. NO. 0.0054;
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFVIGFFS 22
 DB 102 EWFGHMKMLSGFYIALYS 123

RESULT 9
 G02436
 Chemokine (C-C) receptor 3 - human
 N;Alternate names: C-C CKR-3
 C;Species: Homo sapiens (man)
 C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
 C;Accession: G02436; A57237
 R;Ponath, P.D.
 submitted to the EMBL Data Library, February 1996
 A;Reference number: H01272
 A;Accession: G02436
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-355 <PON>
 A;Cross-references: EMBL:U49727; NID:G1477560; PID:AA09726.1; PID:G1477561
 R;Combadere, C.; Ahuja, S.K.; Murphy, P.M.
 J. Biol. Chem. 270, 16491-16494, 1995
 A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
 A;Reference number: A57237; MUID:95348056; PMID:7622448
 A;Accession: A57237
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>
 A;Cross-references: GB:U28694; NID:G1199579; PID:AA050469.1; PID:G1199580
 A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PID:AA050469.
 C;Genetics:
 A;Gene: GDB:CMKBR3
 A;Cross-references: GDB:579624; OMIM:601268
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;36-60/Domain: transmembrane #status predicted <TM1>
 F;71-91/Domain: transmembrane #status predicted <TM2>
 F;108-129/Domain: transmembrane #status predicted <TM3>
 F;147-171/Domain: transmembrane #status predicted <TM4>
 F;205-223/Domain: transmembrane #status predicted <TM5>
 F;240-261/Domain: transmembrane #status predicted <TM6>
 F;288-305/Domain: transmembrane #status predicted <TM7>
 F;24-273,106-183/Disulfide bonds: #status predicted
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 53.2%; Score 67; DB 2; Length 355;
 Best Local Similarity 52.4%; Pred. NO. 0.015;
 Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 WDFGNTMCLLTGLYFVIGFFS 22
 DB 99 WVFHGMCKLSSGFYHTGLIS 119

RESULT 10
 A57160
 Chemokine (C-C) receptor 4 - human

N;Alternate names: C-C CKR-4
 C;Species: Homo sapiens (man)
 C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 A;Accession: A57160
 R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W
 J. Biol. Chem. 270, 19495-19500, 1995
 A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cD
 A;Reference number: A57160; MUID:95370289; PMID:7642634
 A;Accession: A57160
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-360 <PON>
 A;Cross-references: GB:X85740; NID:G1370103; PID:CAA59743.1; PID:G971452
 A;Note: source clone K5-5
 C;Genetics:
 A;Gene: GDB:CMKBR4
 A;Cross-references: GDB:677463
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;40-65/Domain: transmembrane #status predicted <TM1>
 F;76-97/Domain: transmembrane #status predicted <TM2>
 F;112-133/Domain: transmembrane #status predicted <TM3>
 F;151-175/Domain: transmembrane #status predicted <TM4>
 F;208-226/Domain: transmembrane #status predicted <TM5>
 F;243-264/Domain: transmembrane #status predicted <TM6>
 F;291-308/Domain: transmembrane #status predicted <TM7>
 F;229-276,110-187/Disulfide bonds: #status predicted
 F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F;143/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;183,194/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 52.4%; Score 66; DB 2; Length 360;
 Best Local Similarity 40.9%; Pred. NO. 0.022; 5; Indels 0; Gaps 0;
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFVIGFFS 22
 DB 102 QWVFLGLCKMISWYLVGFYS 123

RESULT 11
 JC5942
 Chemokine receptor - human
 C;Species: Homo sapiens (man)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C;Accession: JC5942
 R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
 Biochem. Biophys. Res. Commun. 243, 264-268, 1998
 A;Title: Cloning and characterization of a novel human chemokine receptor.
 A;Reference number: JC5942; MUID:98139902; PMID:9473515
 A;Accession: JC5942
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-344 <PAN>
 A;Cross-references: GB:U97123; NID:G2897070; PID:AA039595.1; PID:G2897071
 C;Superfamily: vertebrate rhodopsin

Query Match 51.8%; Score 65; DB 2; Length 344;
 Best Local Similarity 55.6%; Pred. NO. 0.03;
 Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 GNTMCLLTGLYFVIGFFS 22
 DB 99 GDPCKILIGLVFVGLYS 116

RESULT 12
 JC4587
 Chemokine (C-C) receptor 4 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000

C/Accession: JC4587
 R/Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996
 A/Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
 A/Reference number: JC4587; MUID:96136324; PMID:8573157
 A/Accession: JC4587
 A/Molecule type: mRNA
 A/Residues: 1-360 <HOO>
 A/Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
 A/Experimental source: thymus
 C/Genetics:
 A/Gene: cc ckr-4
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F:2,183,194/Binding site: carboxyhydrate (Asn) (covalent) #status predicted
 F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 51.6%; Score 65; DB 2; Length 360;
 Best Local Similarity 40.9%; Pred. No. 0.031;
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 QWDFGNTMQLLTGLYFIFGFFS 22
 DB 102 QWVFLGLCKIVSMYLVGFYS 123

RESULT 13
 I58186
 Probable G protein-coupled receptor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
 C/Accession: I58186
 R/Harrison, J.K.; Barber, C.M.; Lynch, K.R.
 Neurosci. Lett. 169, 85-89, 1994
 A/Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and b
 A/Reference number: I58186; MUID:94323113; PMID:8047298
 A/Accession: I58186
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-354 <RES>
 A/Cross-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor

Query Match 47.6%; Score 60; DB 2; Length 354;
 Best Local Similarity 62.5%; Pred. No. 0.18;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 NTWCQLLTGLYFIFGFF 21
 DB 100 NAMCKLTATFFIFGFF 115

RESULT 14
 JC5068
 G protein-coupled receptor CXR-L3 - human
 C/Species: Homo sapiens (man)
 C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C/Accession: JC5068
 R/Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996
 A/Title: Molecular cloning and RNA expression of two new human chemokine receptor-like g
 A/Reference number: JC5067; MUID:97040707; PMID:8886020
 A/Accession: JC5068
 A/Molecule type: DNA
 A/Residues: 1-369 <ZAB>
 A/Cross-references: EMBL:Z79784; NID:g1668737; PIDN:CAB02144.1; PID:g1668738
 C/Comment: This protein belongs to the family of alpha chemokine receptors.
 C/Genetics:
 A/Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CXR-L3; GPR-CY4
 A/Cross-references: GDB:5370639; OMIM:601835

A/Map position: 6q27-6q27
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; transmembrane protein
 F:42-68/Domain: transmembrane #status predicted <TM1>
 F:79-99/Domain: transmembrane #status predicted <TM2>
 F:115-136/Domain: transmembrane #status predicted <TM3>
 F:160-180/Domain: transmembrane #status predicted <TM4>
 F:212-233/Domain: transmembrane #status predicted <TM5>
 F:250-271/Domain: transmembrane #status predicted <TM6>
 F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 46.8%; Score 59; DB 2; Length 369;
 Best Local Similarity 52.6%; Pred. No. 0.26;
 Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 WDFGNTMQLLTGLYFIFGFF 20
 DB 106 WVFSNATCKLLKGIYAINF 124

RESULT 15
 JC4304
 orphan G protein-coupled receptor - human
 N/Alternate names: V28 protein
 C/Species: Homo sapiens (man)
 C/Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
 C/Accession: JC4304
 R/Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
 Gene 163, 295-299, 1995
 A/Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to g
 A/Reference number: JC4304; MUID:96011651; PMID:7590284
 A/Accession: JC4304
 A/Molecule type: mRNA
 A/Residues: 1-355 <RAP>
 A/Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
 A/Experimental source: peripheral blood mononuclear cell
 C/Comment: This protein is a cell-surface receptor which recognizes extracellular signal
 C/Genetics:
 A/Gene: V28

A/Map position: 3pter-p21
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
 F:35-57/Domain: transmembrane #status predicted <TM1>
 F:66-88/Domain: transmembrane #status predicted <TM2>
 F:104-125/Domain: transmembrane #status predicted <TM3>
 F:146-165/Domain: transmembrane #status predicted <TM4>
 F:197-217/Domain: transmembrane #status predicted <TM5>
 F:230-254/Domain: transmembrane #status predicted <TM6>
 F:275-296/Domain: transmembrane #status predicted <TM7>

Query Match 44.4%; Score 56; DB 2; Length 355;
 Best Local Similarity 56.2%; Pred. No. 0.72;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 NTWCQLLTGLYFIFGFF 21
 DB 99 NAMCKTATFFIFGFF 114

RESULT 16
 S55594
 G protein-coupled receptor E1 - equine herpesvirus 2
 C/Species: equine herpesvirus 2
 C/Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
 C/Accession: S55594
 R/Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
 J. Mol. Biol. 249, 520-528, 1995
 A/Title: The DNA sequence of equine herpesvirus 2.
 A/Reference number: S55594; MUID:95302501; PMID:7783207
 A/Accession: S55594
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: DNA

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A;Residues: 1-383 <TEL>
A;Cross-references: GB:U20824; NID:9695172; PIDN:AA13788.1; PID:9695173
A;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 43.7%; Score 55; DB 2; Length 383;
Best Local Similarity 38.1%; Pred. No. 1.1;
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 2 WDFGNTWCQLLTGLYFIFGFFS 22
DB 138 WTFGSLCKLLRGVCNLSYS 158

RESULT 17
I38973
G protein-coupled receptor 7 - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Jul-2000
C;Accession: I38973
R;O'Dowd, B.F.; Scheideler, M.A.; Nguyen, T.; Cheng, R.; Rasmussen, J.S.; Zastawny, R.;
Genomics 28, 84-91, 1995
A;Title: The cloning and chromosomal mapping of two novel human opicoid-somatostatin-like
A;Reference number: A57647; MUID:96070436; PMID:7590751
A;Accession: I38973
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-328 <RES>
A;Cross-references: EMBL:U22491; NID:9553232; PIDN:AA150197.1; PID:9553233
C;Genetics:
A;Gene: GDB:GPR7
A;Cross-references: GDB:371714; OMIM:600730
A;Map position: 10q11.2-10q21.1
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 42.5%; Score 53.5; DB 2; Length 328;
Best Local Similarity 35.5%; Pred. No. 1.6;
Matches 11; Conservative 4; Mismatches 7; Indels 9; Gaps 1;

QY 1 QMDFGNTWCQLLTGLYFIFGFFS 22
DB 101 QMDFGNTWCQLLTGLYFIFGFFS 131

RESULT 18
A55735
G protein-coupled receptor EB11 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C;Accession: A55735
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: A55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:L31580; NID:9468340; PIDN:AAA74232.1; PID:9468341
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 42.1%; Score 53; DB 2; Length 378;
Best Local Similarity 42.9%; Pred. No. 2.2;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 WDFGNTWCQLLTGLYFIFGFFS 22
DB 122 WDFGNTWCQLLTGLYFIFGFFS 142

RESULT 19
A55735
G protein-coupled receptor EB11 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Accession: A55735
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: A55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:L31581; NID:9468319; PIDN:AAA74231.1; PID:9468320
R;Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995

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JC7080
melanin-concentrating hormone receptor [validated] - human
N;Alternate names: MCHR; orphan somatostatin-like receptor 1 (SLC-1)
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: JC7080
R;Shimomura, Y.; Mori, M.; Sugo, T.; Ishibashi, Y.; Abe, M.; Kurokawa, T.; Onda, H.; Nis
Biochem. Biophys. Res. Commun. 261, 622-626, 1999
A;Title: Isolation and identification of melanin-concentrating hormone as the endogenous
A;Reference number: JC7080; MUID:99373129; PMID:10441476
A;Accession: JC7080
A;Molecule type: mRNA
A;Residues: 1-422 <SHI>
A;Note: It is uncertain whether Met-1, Met-6 or Met-70 is the initiation codon
C;Superfamily: neurokinin 1 receptor
C;Keywords: hormone receptor; transmembrane protein

Query Match 42.1%; Score 53; DB 2; Length 422;
Best Local Similarity 57.1%; Pred. No. 2.5;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 WDFGNTWCQLLTGL 15
DB 178 WHFGTMTLTITAM 191

RESULT 20
A45680
G protein-coupled peptide receptor EBI 1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A45680
R;Birkenbach, M.; Josefsen, K.; Yalamanchilli, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p
A;Reference number: A45680; MUID:93188173; PMID:8363238
A;Accession: A45680
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-378 <BIR>
A;Cross-references: GB:L08176; NID:9183484; PID:9183485
A;Experimental source: B-lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBI:127094, NCBI:127095)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 41.3%; Score 52; DB 2; Length 378;
Best Local Similarity 42.9%; Pred. No. 3.1;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 WDFGNTWCQLLTGLYFIFGFFS 22
DB 122 WDFGNTWCQLLTGLYFIFGFFS 142

RESULT 21
B55735
Lymphocyte-specific G protein-coupled receptor EB11 - human
N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Accession: B55735; S52443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: B55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:L31581; NID:9468319; PIDN:AAA74231.1; PID:9468320
R;Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995

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A;Description: The expression of the chemokine receptor BLR2/EBI1 is specifically transcribed in the brain.
 A;Reference number: S52443
 A;Accession: S52443
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 21-378

 A;Cross-references: EMBL:X84702
 C;Genetics:
 A;Gene: GDB:CMKBR7; EBI1; BLR2; CCR7
 A;Cross-references: GDB:342065; OMIM:600242
 A;Map position: 17q12-17q21.2
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor

Query Match 41.3%; Score 52; DB 2; Length 378;
 Best Local Similarity 42.9%; Pred. No. 3.1;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 WDFGNTWCOLLTGLYFIGFPGS 22
 Db 122 WVFQVHFCKLIFAIYKMSFFS 142

RESULT 22

S27357
 Complement C5a anaphylatoxin receptor - dog
 C;Species: Canis lupus familiaris (dog)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: S27357
 R;Perret, J.J.; Raspe, E.; Vassart, G.; Parmentier, M.
 Biochem. J. 288, 911-917, 1992
 A;Title: Cloning and functional expression of the canine anaphylatoxin C5a receptor. Evl
 A;Reference number: S27357; MUID:93111969; PMID:1472004
 A;Accession: S27357

A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-352 <PER>
 A;Cross-references: EMBL:X65860; NID:g878; PIDN:CAA46690.1; PID:g879
 C;Function:
 A;Description: mediates the inflammatory and chemotactic responses of polymorphonuclear

C;Superfamily: vertebrate rhodopsin
 C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorph
 F;1-38/Domain: extracellular #status predicted <EX1>
 F;39-62/Domain: transmembrane #status predicted <TM1>
 F;63-72/Domain: intracellular #status predicted <IN1>
 F;73-95/Domain: transmembrane #status predicted <TM2>
 F;96-111/Domain: extracellular #status predicted <EX2>
 F;112-133/Domain: transmembrane #status predicted <TM3>
 F;134-150/Domain: intracellular #status predicted <IN2>
 F;151-175/Domain: transmembrane #status predicted <TM4>
 F;176-208/Domain: extracellular #status predicted <EX3>
 F;209-229/Domain: transmembrane #status predicted <TM5>
 F;230-244/Domain: intracellular #status predicted <IN3>
 F;245-266/Domain: transmembrane #status predicted <TM6>
 F;267-285/Domain: extracellular #status predicted <EX4>
 F;286-309/Domain: transmembrane #status predicted <TM7>
 F;310-352/Domain: intracellular #status predicted <IN4>
 F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.5%; Score 51; DB 1; Length 352;
 Best Local Similarity 33.3%; Pred. No. 4.1;
 Matches 7; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 WDFGNTWCOLLTGLYFIGFPGS 22
 Db 103 WFFGNACRILPSLLNNYA 123

RESULT 23

JN0621
 G protein-coupled receptor type B - bovine
 C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
 C;Accession: JN0621
 R;Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
 Biochem. Biophys. Res. Commun. 194, 504-511, 1993
 A;Title: Identification of novel members of G-protein coupled receptor superfamily expr
 A;Reference number: JN0621; MUID:93326166; PMID:8392843
 A;Accession: JN0621
 A;Molecule type: mRNA

A;Residues: 1-350 <MAT>
 A;Cross-references: GB:S63848; NID:g399710; PIDN:AAB27547.1; PID:g399711
 A;Experimental source: tongue taste papillae
 C;Comment: This protein is involved in modulating taste sensitivity or regeneration of t
 C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
 F;42-66/Domain: transmembrane #status predicted <TM1>
 F;60-99/Domain: transmembrane #status predicted <TM2>
 F;114-135/Domain: transmembrane #status predicted <TM3>
 F;154-175/Domain: transmembrane #status predicted <TM4>
 F;200-222/Domain: transmembrane #status predicted <TM5>
 F;242-265/Domain: transmembrane #status predicted <TM6>
 F;284-306/Domain: transmembrane #status predicted <TM7>
 F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.7%; Score 50; DB 2; Length 350;
 Best Local Similarity 38.1%; Pred. No. 5.8;
 Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 WDFGNTWCOLLTGLYFIGFPGS 22
 Db 105 WVLGKIMCKVTSALYTNFVS 125

RESULT 24

A48921
 Interleukin-8 receptor type B - mouse
 N;Alternate names: G-protein coupled receptor GPCR16
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
 C;Accession: A48921; A53677; I49348; I55421; H48909; I53774
 R;Cerretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert,
 Genomics 18, 410-413, 1993
 A;Title: The murine homologue of the human interleukin-8 receptor type B maps near the i
 A;Reference number: A48921; MUID:94117014; PMID:8288247
 A;Accession: A48921
 A;Molecule type: DNA
 A;Residues: 1-359 <CER>
 A;Cross-references: GB:L23637; NID:g435093; PIDN:AAA39305.1; PID:g435094
 R;Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
 J. Biol. Chem. 269, 18263-18266, 1994

A;Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding t
 A;Reference number: A53677; MUID:94308043; PMID:7518426
 A;Accession: A53677
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-359 <SUZ>
 A;Cross-references: GB:L26549
 A;Note: sequence extracted from NCBI backbone (NCBIP:149812)
 R;Lee, J.; Cacialano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
 J. Immunol. 155, 2159-2164, 1995
 A;Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
 A;Reference number: I49348; MUID:95363183; PMID:7636264
 A;Accession: I49348
 A;Status: preliminary; translated from GB/EMBL/DBSJ
 A;Molecule type: DNA

A;Residues: 1-359 <RES>
 A;Cross-references: EMBL:U31207; NID:g950174; PIDN:AAC52239.1; PID:g950175
 R;Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
 J. Biol. Chem. 269, 29355-29358, 1994

A;Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression
 A;Reference number: I55421; MUID:95050766; PMID:7961509
 A;Accession: I55421
 A;Status: preliminary; translated from GB/EMBL/DBSJ
 A;Molecule type: DNA

A:Residues: 1-359 <RE2>
A:Cross-references: GB:U13239; NID:G293665; PIDN:AAA62109.1; PID:G293666
R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.
Genomics 18, 173-184, 1993
A:Title: Identification, chromosomal location, and genome organization of mammalian G-protein coupled receptor 18, 173-184, 1993
A:Reference number: A48909; MUID:94116980; PMID:8288218
A:Accession: H48909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 145-258 <WL>
A:Cross-references: GB:U20337; NID:G438800; PIDN:AAA16953.1; PID:G438801
R:Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.
Gene 142, 297-300, 1994
A:Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.
A:Reference number: I53774; MUID:94252584; PMID:8194768
A:Accession: I53774
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <RE3>
A:Cross-references: GB:U17630; NID:G493671; PIDN:BA04536.1; PID:G493672
C:Genetics:
A:Gene: t18rb
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:49-74/Domain: transmembrane #status predicted <TM1>
F:84-106/Domain: transmembrane #status predicted <TM2>
F:120-141/Domain: transmembrane #status predicted <TM3>
F:163-182/Domain: transmembrane #status predicted <TM4>
F:213-234/Domain: transmembrane #status predicted <TM5>
F:251-271/Domain: transmembrane #status predicted <TM6>
F:308-328/Domain: transmembrane #status predicted <TM7>
Query Match 39.7%; Score 50; DB 2; Length 359;
Best Local Similarity 33.3%; Pred. No. 6;
Matches 7; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
QY 2 WDFGNTMCOQLTGLY 22
DB 111 WTFGSLTKIFSVKVFYS 131
RESULT 25
T37324
A:Title: Probable JNK-activating protein kinase (EC 2.7.1.1) JNK-1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T37324
R:Kawasaki, M.; Hisamoto, N.; Iino, Y.; Yamamoto, M.; Ninomiya-Tsuji, J.; Matsumoto, K.
EMBO J. 18, 3604-3615, 1999
A:Title: A Caenorhabditis elegans JNK signal transduction pathway regulates coordinated
A:Reference number: Z21688; MUID:99321749; PMID:10393177
A:Accession: T37324
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-435 <KAW>
A:Cross-references: EMBL:AB024086; NID:G5668698; PIDN:BA082641.1; PID:G5668699
C:Genetics:
A:Gene: jnk-1
C:Function:
A:Description: activation of JNK-1
A:Pathway: JNK signaling pathway
A:Note: JNK pathway functions in type-D GABAergic motor neurons and thereby modulates co-ordinated movement
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; signal transduction
Query Match 39.7%; Score 50; DB 2; Length 435;
Best Local Similarity 60.0%; Pred. No. 7.3;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 WDFGNTMCOQLTGLY 16
DB 307 WSLGITVQLVTGLY 321

RESULT 26
T16256
A:Title: Hypothetical protein F35C8.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Jan-2000
C:Accession: T16256
R:Wu, X.
Submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid F35C8.
A:Reference number: Z18486
A:Accession: T16256
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-448 <WUX>
A:Cross-references: EMBL:U40941; NID:G1072184; PID:G1072189; PIDN:AAA81711.1; CESP:F35C8
C:Genetics:
A:Gene: CESP:F35C8.3
A:Introns: 70/1; 37/1; 134/1; 162/3; 201/3; 253/3; 308/3; 362/3; 393/3; 413/3
C:Superfamily: Kinase-related transforming protein; protein kinase homology
Query Match 39.7%; Score 50; DB 2; Length 448;
Best Local Similarity 60.0%; Pred. No. 7.5;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 WDFGNTMCOQLTGLY 16
DB 320 WSLGITVQLVTGLY 334
RESULT 27
I51372
A:Title: angiotensin II receptor - turkey
C:Species: Meleagris gallopavo (common turkey)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Nov-1999
C:Accession: I51372; FN0449
R:Murphy, T.J.; Nakamura, Y.; Takeuchi, K.; Alexander, R.W.
Mol. Pharmacol. 44, 1-7, 1993
A:Title: A cloned angiotensin receptor isoform from the turkey adrenal gland is pharmacologically distinct from the turkey angiotensin II (AII) receptor
A:Reference number: I51372; MUID:93341466; PMID:8341266
A:Accession: I51372
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <MUR>
A:Cross-references: GB:U23203; NID:G349735; PIDN:AAA03560.1; PID:G349736
R:Carasia, R.V.; McIlroy, P.J.; Kowalski, K.I.; Tilly, J.L.
Biochem. Biophys. Res. Commun. 191, 1073-1080, 1993
A:Title: Isolation of turkey adrenocortical cell angiotensin II (AII) receptor partial cDNA
A:Reference number: FN0449; MUID:93221469; PMID:7916599
A:Accession: FN0449
A:Molecule type: mRNA
A:Residues: 53-91; C, 93-162, SSFVIVY, 171-291 <CAR>
A:Cross-references: GB:S58041; NID:G299373; PIDN:AA826041.1; PID:G299374
A:Experimental source: liver
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; transmembrane protein
F:53-64/Domain: intracellular #status predicted <IN1>
F:65-86/Domain: transmembrane #status predicted <TM1>
F:87-102/Domain: extracellular #status predicted <EX1>
F:103-134/Domain: transmembrane #status predicted <TM2>
F:125-142/Domain: intracellular #status predicted <IN2>
F:143-162/Domain: transmembrane #status predicted <TM3>
F:163-192/Domain: extracellular #status predicted <EX2>
F:193-214/Domain: transmembrane #status predicted <TM4>
F:215-238/Domain: intracellular #status predicted <IN3>
F:239-262/Domain: transmembrane #status predicted <TM5>
F:263-274/Domain: extracellular #status predicted <EX3>
F:275-291/Domain: transmembrane #status predicted <TM6>
F:136/Binding site: phosphate (Ser) (covalent) #status predicted
F:141,233/Binding site: phosphate (Thr) (covalent) #status predicted
F:176,188/Binding site: carbohydrate (Asn) (covalent) #status predicted


```

Query Match      39.3%; Score 49.5; DB 2; Length 359;
Best Local Similarity 50.0%; Pred. No. 7.1;
Matches 9; Conservative 4; Mismatches 1; Gaps 1;

QY 1 QWDFGNTWCQLLT-GLYF 17
Db 93 QWPGNCLCKLASAGISF 110

RESULT 28
B55733
G protein-coupled receptor GPR2 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 26-Aug-1999
C:Accession: B55733
R:Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, H.H.Q.; Tsui, L.
Genomics 23, 609-618, 1994
A:Title: Cloning of human genes encoding novel G protein-coupled receptors.
A:Reference number: A55733; MUID:95154831; PMID:7851889
A:Accession: B55733
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <MAR>
A:Cross-references: GB:U13667
C:Genetics:
A:Gene: GDB:GPR2
A:Cross-references: GDB:371708; OMIM:600240
A:Map position: 17q21.1-17q21.3
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match      38.9%; Score 49; DB 2; Length 354;
Best Local Similarity 36.8%; Pred. No. 8.4;
Matches 7; Conservative 4; Mismatches 0; Gaps 0;

QY 2 WDFGNTWCQLLTGLYFIFGF 20
Db 98 WSLGSATCRITSLGYSASF 116

RESULT 29
JE0349
interferon-inducible protein 10 (IP-10) receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C:Accession: JE0349
R:Tamaru, M.; Tomimaga, Y.; Yatsunami, K.; Narumi, S.
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A:Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its
A:Reference number: JE0349; MUID:99009219; PMID:9790904
A:Molecule type: mRNA
A:Residues: 1-367 <TAM>
A:Cross-references: DDBJ:AB003174; NID:g3798731; PIDN:BAA34045.1; PID:g3798732
C:Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C:Superfamily: vertebrate rhodopsin

Query Match      38.9%; Score 49; DB 2; Length 367;
Best Local Similarity 36.4%; Pred. No. 8.7;
Matches 8; Conservative 6; Mismatches 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGF 22
Db 115 QWVFGGLCKVGAUFINFYA 136

RESULT 30
A57510
mu opioid receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999
C:Accession: A57510; I48665; S66513; I49300
R:Kaufman, D.L.; Keith Jr., D.E.; Anton, B.; Tian, J.; Magendzo, K.; Newman, D.; Tran, T

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J. Biol. Chem. 270, 15877-15883, 1995
A:Title: Characterization of the murine mu opioid receptor gene.
A:Reference number: A57510; MUID:95318184; PMID:7797593
A:Accession: A57510
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-398 <KAU>
A:Cross-references: GB:U19380
R:Min, B.H.; Augustin, L.B.; Felsheim, R.F.; Fuchs, J.A.; Loh, H.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 9081-9085, 1994
A:Title: Genomic structure analysis of promoter sequence of a mouse mu opioid receptor y
A:Reference number: I48665; MUID:94377496; PMID:8090773
A:Accession: I48665
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-398 <RES>
A:Cross-references: EMBL:U10561; NID:9555696; PIDN:AAB60673.1; PID:9565069
R:Roosi, G.C.; Pan, Y.X.; Brown, G.P.; Pasternak, G.W.
FEBS Lett. 369, 192-196, 1995
A:Title: Antisense mapping the MOR-1 opioid receptor: evidence for alternative splicing
A:Reference number: I49300; MUID:95377399; PMID:7649256
A:Accession: S66513
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-398 <ROS>
A:Cross-references: EMBL:U26915; NID:g1055230; PIDN:AAA81170.1; PID:g1055231
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C:Genetics:
A:Gene: MOR-1
A:Introns: 95/2; 213/1; 386/3
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran

Query Match      38.9%; Score 49; DB 2; Length 398;
Best Local Similarity 28.6%; Pred. No. 9.5;
Matches 6; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 WDFGNTWCQLLTGLYFIFGF 22
Db 133 WPGNLCIKVISIDYINMET 153

RESULT 31
A37912
thrombin receptor precursor - human
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C:Accession: A37912
R:Vu, T.K.H.; Hung, D.T.; Wheaton, V.I.; Coughlin, S.R.
Cell 64, 1057-1068, 1991
A:Title: Molecular cloning of a functional thrombin receptor reveals a novel proteolytic
A:Reference number: A37912; MUID:91168254; PMID:1672265
A:Molecule type: mRNA
A:Residues: 1-425 <VUA>
A:Cross-references: GB:M62424; NID:g339676; PIDN:AAA36743.1; PID:g339677
C:Genetics:
A:Gene: GDB:F2R
A:Cross-references: GDB:I127737; OMIM:187930
A:Map position: 5q13-5q13
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-425/Product: thrombin receptor #status predicted <MAT>

Query Match      38.9%; Score 49; DB 2; Length 425;
Best Local Similarity 23.8%; Pred. No. 10;
Matches 5; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 2 WDFGNTWCQLLTGLYFIFGF 22
Db 168 WQFGSELCFVTAFCNNYA 189

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Tue Sep 28 15:49:55 2004

us-10-084-813-12.rpr

Page 12

Job time : 13.075 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:55:11 ; Search time 6.875 Seconds
(without alignments)
166.624 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFGNVTCQLLGLYFIFGFFS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	100.0	352	1	CKR5_CERAE
2	126	100.0	352	1	CKR5_CERP
3	126	100.0	352	1	CKR5_CERTO
4	126	100.0	352	1	CKR5_GORGO
5	126	100.0	352	1	CKR5_HUMAN
6	126	100.0	352	1	CKR5_HYLE
7	126	100.0	352	1	CKR5_HYML
8	126	100.0	352	1	CKR5_HYLS
9	126	100.0	352	1	CKR5_MACMU
10	126	100.0	352	1	CKR5_PANTR
11	126	100.0	352	1	CKR5_PAPHA
12	126	100.0	352	1	CKR5_PONPY
13	126	100.0	352	1	CKR5_PYGBI
14	126	100.0	352	1	CKR5_PYGNE
15	126	100.0	352	1	CKR5_TRAFR
16	126	100.0	352	1	CKR5_TRAPH
17	89	70.6	353	1	CKR8_MOUSE
18	87	69.0	374	1	CKR2_HUMAN
19	86	68.3	373	1	CKR2_RAT
20	84	66.7	354	1	CKR5_RAT
21	83	65.9	289	1	VC03_SPVKA
22	83	65.9	370	1	VK02_SPVKA
23	83	65.9	373	1	CKR2_MOUSE
24	82	65.1	355	1	CKR8_HUMAN
25	82	65.1	356	1	CKR8_MACMU
26	81	64.3	360	1	CKR2_MOUSE
27	80	63.5	354	1	CKR5_MOUSE
28	79	62.7	358	1	CKR2_CAVPO
29	76	60.3	355	1	CKR1_MOUSE
30	75	59.5	359	1	CKR3_RAT
31	74	58.7	356	1	CKR1_MOUSE
32	71	56.3	355	1	CKR1_HUMAN
33	71	56.3	355	1	CKR1_MACMU

34	70	55.6	359	1	CKR3_MOUSE
35	67	53.2	355	1	CKR3_HUMAN
36	66	52.4	342	1	CKR6_CERAE
37	66	52.4	360	1	CKR4_HUMAN
38	65	51.6	342	1	CKR6_HUMAN
39	65	51.6	342	1	CKR6_MACNE
40	65	51.6	342	1	CKR6_PANTR
41	65	51.6	343	1	CKR6_VACFA
42	65	51.6	343	1	CKR6_VACMU
43	65	51.6	360	1	CKR4_MOUSE
44	61	48.4	381	1	Q33L_CAVPK
45	60	47.6	354	1	VQ31_MOUSE

ALIGNMENTS

RESULT 1

CKR5_CERAE
ID CKR5_CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMXBR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC Murayama Y., Matsunaga S., Inoue-Murayama M.;
RA "cDNA sequence of African green monkey CCR-5 chemokine receptor
gene.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U83324; AAC51795.1; -;
CC EMBL; U83325; AAC51796.1; -;
CC EMBL; AB015944; BAA31328.1; -;
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
CC PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
Polymorphism.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

```

FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 4 (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 5 (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 6 (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 7 (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT VARIANT 302 352 7 (POTENTIAL).
FT SEQUENCE 352 AA; 40561 MW; 7F52E690C72EC29A CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 2
CKR5_CERY ID CKR5_CERY STANDARD; PRT; 352 AA.
AC QTV42;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Cercopithecus pygerythrus (Vervet monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopitheciinae.
OX NCBI_TaxID=60710;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=100;
RX MEDLINE=99335215; PubMed=10408730;
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with HIV
RT carrier status in African nonhuman primates."
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC or send an email to license@isb-sib.ch)
CC
CC EMBL; AF035222; AAD44015.1;
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
DR KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 4 (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 5 (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 6 (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 7 (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DISULFID 302 352 7 (POTENTIAL).
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 15 15 SULFATION (BY SIMILARITY).
FT SEQUENCE 352 AA; 40558 MW; EF17D67C8CC3DB0 CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 3
CKR5_CERTO ID CKR5_CERTO STANDARD; PRT; 352 AA.
AC Q62743; Q62744; Q62745; Q62746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopitheciinae.
OX NCBI_TaxID=95311;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Isolate 079, 085, 087, and 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabey
RT naturally infected in west Africa: a comparison of coreceptor usage
RT of primary SIVsm, HIV-2, and SIVmac."
RL Virology 246:113-124(1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC
CC EMBL; AF035222; AAD44015.1;
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.

```

increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; AF051902; AAC39830.1; -
 DR EMBL; AF051903; AAC39831.1; -
 DR EMBL; AF051904; AAC39832.1; -
 DR EMBL; AF051905; AAC39833.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 2 (POTENTIAL).
 FT TRANSMEM 69 89 3 (POTENTIAL).
 FT DOMAIN 90 102 4 (POTENTIAL).
 FT TRANSMEM 103 124 5 (POTENTIAL).
 FT DOMAIN 125 141 6 (POTENTIAL).
 FT TRANSMEM 142 166 7 (POTENTIAL).
 FT DOMAIN 167 198 8 (POTENTIAL).
 FT TRANSMEM 199 219 9 (POTENTIAL).
 FT DOMAIN 220 235 10 (POTENTIAL).
 FT TRANSMEM 236 260 11 (POTENTIAL).
 FT DOMAIN 261 277 12 (POTENTIAL).
 FT TRANSMEM 278 301 13 (POTENTIAL).
 FT DOMAIN 302 352 14 (POTENTIAL).
 FT TRANSMEM 353 360 15 (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 FT VARIANT 2 2 D -> E (IN ISOLATE 087).
 FT VARIANT 3 3 Y -> D (IN ISOLATE 079).
 FT VARIANT 25 25 V -> G (IN ISOLATE 087).
 FT VARIANT 100 100 M -> K (IN ISOLATE 079).
 FT VARIANT 107 107 L -> V (IN ISOLATE 089).
 FT VARIANT 134 134 V -> G (IN ISOLATE 079).
 FT VARIANT 146 146 V -> L (IN ISOLATE 085 AND 089).
 FT VARIANT 340 340 T -> I (IN ISOLATE 079).
 SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGPF 22
 DB 93 QWDFGNTMCQLLTGLYFIFGPF 114

RESULT 4
 CKR5_GORGO STANDARD; PRT; 352 AA.
 AC P56439;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
 GN CKR5 OR CMKR5.
 OS Gorilla gorilla gorilla (lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 OX NCBI_TaxID=9595;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9726867; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharron M., Sanson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RA "Differential utilization of CKR5 by macrophage and T cell tropic
 simian immunodeficiency virus strains";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by

CC-chemokine receptor gene.";
RL Biochemistry 35:3362-3367(1996).
[2]
RN
RP
SEQUENCE FROM N.A.
RX MEDLINE=96291862; PubMed=8663314;
RA Report C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
RT "Molecular cloning and functional characterization of a novel human
CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";
RL J. Biol. Chem. 271:17161-17166(1996).
[3]
RN
RP
SEQUENCE FROM N.A.
RX MEDLINE=96295970; PubMed=8699119;
RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
RT "Cloning and functional expression of CC CKR5, a human monocyte CC
chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
RANTES.";
RL J. Leukoc. Biol. 60:147-152(1996).
[4]
RN
RP
SEQUENCE FROM N.A.
RX McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gao J., la Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinski K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[5]
RN
RP
SEQUENCE FROM N.A.
RX MEDLINE=98001387; PubMed=9343222;
RA Kubmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
[6]
RN
RP
SEQUENCE FROM N.A., AND VARIANT ARG-178.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
[7]
RN
RP
SEQUENCE FROM N.A.
RX MEDLINE=98049523; PubMed=9388201;
RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
with 5' end heterogeneity, dual promoter usage, and evidence for
RT polymorphisms within the regulatory regions and noncoding exons.";
RL J. Biol. Chem. 272:30662-30671(1997).
[8]
RN
RP
SEQUENCE FROM N.A., AND VARIANT ARG-178.
RX Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
RA Debre P.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[9]
RN
RP
SEQUENCE FROM N.A.
RX Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
[10]
RN
RP
CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE=96260017; PubMed=8649511;
RA Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
RA di Marzio P., Broder C., Spector R.E., Hill C.M., Davis C.B.,
RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
RT "Identification of a major co-receptor for primary isolates of
HIV-1.";
RL Nature 381:661-666(1996).
[11]
RN
RP
CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE=96260018; PubMed=8649512;

RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
RA Nagashima K.A., Cayan C., Maddon P.J., Koup R.A., Moore J.P.,
RA Paxton W.A.;
RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
CC-CCR-5.";
RL Nature 381:667-673(1996).
[12]
RN
RP
SUBMISSION.
RX MEDLINE=99189752; PubMed=1009882;
RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
entry.";
RL Cell 96:667-676(1999).
[13]
RN
RP
FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and Rantes and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation. Acts as co-receptor with CD4 for primary non-
CC syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1
CC virus. It promotes Env-mediated fusion of the virus.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Found in promyelocytic cells.
CC -!- PTM: Sulfation contributes to the efficiency of HIV-1 entry.
CC -!- PTM: Modified by O-linked glycosylation, but not by N-linked
CC glycosylation.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; X91492; CAA62796.1; -
CC EMBL; U54994; AAC50598.1; -
CC EMBL; U57840; AAB17071.1; -
CC EMBL; U58266; AAB57793.1; -
CC EMBL; U83326; AAC51797.1; -
CC EMBL; AF011500; AAB65700.1; -
CC EMBL; AF011501; AAB65701.1; -
CC EMBL; AF011502; AAB65702.1; -
CC EMBL; AF011503; AAB65703.1; -
CC EMBL; AF011505; AAB65705.1; -
CC EMBL; AF011506; AAB65706.1; -
CC EMBL; AF011507; AAB65707.1; -
CC EMBL; AF011508; AAB65708.1; -
CC EMBL; AF011509; AAB65709.1; -
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CC EMBL; AF011516; AAB65716.1; -
CC EMBL; AF011517; AAB65717.1; -
CC EMBL; AF011518; AAB65718.1; -
CC EMBL; AF011519; AAB65719.1; -
CC EMBL; AF011520; AAB65720.1; -
CC EMBL; AF011521; AAB65721.1; -
CC EMBL; AF011522; AAB65722.1; -
CC EMBL; AF011523; AAB65723.1; -
CC EMBL; AF011524; AAB65724.1; -
CC EMBL; AF011525; AAB65725.1; -
CC EMBL; AF011526; AAB65726.1; -
CC EMBL; AF011527; AAB65727.1; -
CC EMBL; AF011528; AAB65728.1; -
CC EMBL; AF011529; AAB65729.1; -
CC EMBL; AF011530; AAB65730.1; -
CC EMBL; AF011531; AAB65731.1; -
CC EMBL; AF011532; AAB65732.1; -

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 EMBL; AF011534; AAB65734.1; --
 EMBL; AF011535; AAB65735.1; --
 EMBL; AF011536; AAB65736.1; --
 EMBL; AF011537; AAB65737.1; --
 EMBL; AF011538; AAB65738.1; --
 EMBL; AF011539; AAB65739.1; --
 EMBL; AF011540; AAB65740.1; --
 EMBL; AF011541; AAB65741.1; --
 EMBL; AF011542; AAB65742.1; --
 EMBL; AF011543; AAB65743.1; --
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 EMBL; AF011549; AAB65749.1; --
 EMBL; AF011550; AAB65750.1; --
 EMBL; AF011551; AAB65751.1; --
 EMBL; AF011552; AAB65752.1; --
 EMBL; AF011553; AAB65753.1; --
 EMBL; AF011554; AAB65754.1; --
 EMBL; AF011555; AAB65755.1; --
 EMBL; AF011556; AAB65756.1; --
 EMBL; AF011557; AAB65757.1; --
 EMBL; AF011558; AAB65758.1; --
 EMBL; AF011559; AAB65759.1; --
 EMBL; AF011560; AAB65760.1; --
 EMBL; AF011561; AAB65761.1; --
 EMBL; AF011562; AAB65762.1; --
 EMBL; AF011563; AAB65763.1; --
 EMBL; AF011564; AAB65764.1; --
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 EMBL; AF011566; AAB65766.1; --
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 EMBL; AF011575; AAB65775.1; --
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 EMBL; AF011577; AAB65777.1; --
 EMBL; AF011578; AAB65778.1; --
 EMBL; AF011579; AAB65779.1; --
 EMBL; AF011580; AAB65780.1; --
 EMBL; AF011581; AAB65781.1; --
 EMBL; AF011582; AAB65782.1; --
 EMBL; AF011583; AAB65783.1; --
 EMBL; AF011584; AAB65784.1; --
 EMBL; AF011585; AAB65785.1; --
 EMBL; AF011586; AAB65786.1; --
 EMBL; AF011587; AAB65787.1; --
 EMBL; AF011588; AAB65788.1; --
 EMBL; AF011589; AAB65789.1; --
 EMBL; AF011590; AAB65790.1; --
 EMBL; AF011591; AAB65791.1; --
 EMBL; AF011592; AAB65792.1; --
 EMBL; AF011593; AAB65793.1; --
 EMBL; AF011594; AAB65794.1; --
 EMBL; AF011595; AAB65795.1; --
 EMBL; AF011596; AAB65796.1; --
 EMBL; AF011597; AAB65797.1; --
 EMBL; AF011598; AAB65798.1; --
 EMBL; AF011599; AAB65799.1; --
 EMBL; AF011600; AAB65800.1; --
 EMBL; AF011601; AAB65801.1; --
 EMBL; AF011602; AAB65802.1; --
 EMBL; AF011603; AAB65803.1; --
 EMBL; AF011604; AAB65804.1; --
 EMBL; AF011605; AAB65805.1; --
 EMBL; AF011606; AAB65806.1; --
 EMBL; AF011607; AAB65807.1; --
 EMBL; AF011608; AAB65808.1; --
 EMBL; AF011609; AAB65809.1; --
 EMBL; AF011610; AAB65810.1; --
 EMBL; AF011611; AAB65811.1; --
 EMBL; AF011612; AAB65812.1; --
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 EMBL; AF011617; AAB65817.1; --
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 EMBL; AF011619; AAB65819.1; --
 EMBL; AF011620; AAB65820.1; --
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 EMBL; AF011622; AAB65822.1; --
 EMBL; AF011623; AAB65823.1; --
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 EMBL; AF011625; AAB65825.1; --
 EMBL; AF011626; AAB65826.1; --
 EMBL; AF011627; AAB65827.1; --
 EMBL; AF011628; AAB65828.1; --
 EMBL; AF011629; AAB65829.1; --
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 EMBL; AF011631; AAB65831.1; --
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 EMBL; AF011635; AAB65835.1; --
 EMBL; AF011636; AAB65836.1; --
 EMBL; AF011637; AAB65837.1; --
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 EMBL; AF011640; AAB65840.1; --
 EMBL; AF011641; AAB65841.1; --
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 EMBL; AF011643; AAB65843.1; --
 EMBL; AF011644; AAB65844.1; --
 EMBL; AF011645; AAB65845.1; --
 EMBL; AF011646; AAB65846.1; --
 EMBL; AF011647; AAB65847.1; --
 EMBL; AF011648; AAB65848.1; --
 EMBL; AF011649; AAB65849.1; --
 EMBL; AF011650; AAB65850.1; --
 EMBL; AF011651; AAB65851.1; --
 EMBL; AF011652; AAB65852.1; --
 EMBL; AF011653; AAB65853.1; --
 EMBL; AF011654; AAB65854.1; --
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 EMBL; AF011656; AAB65856.1; --
 EMBL; AF011657; AAB65857.1; --
 EMBL; AF011658; AAB65858.1; --
 EMBL; AF011659; AAB65859.1; --
 EMBL; AF011660; AAB65860.1; --
 EMBL; AF011661; AAB65861.1; --
 EMBL; AF011662; AAB65862.1; --
 EMBL; AF011663; AAB65863.1; --
 EMBL; AF011664; AAB65864.1; --
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 EMBL; AF011666; AAB65866.1; --
 EMBL; AF011667; AAB65867.1; --
 EMBL; AF011668; AAB65868.1; --
 EMBL; AF011669; AAB65869.1; --
 EMBL; AF011670; AAB65870.1; --
 EMBL; AF011671; AAB65871.1; --
 EMBL; AF011672; AAB65872.1; --
 EMBL; AF011673; AAB65873.1; --<

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EMBL; AF177899; AAK43382.1; -	DR
InterPro; IPR000275; GPCR_Rhodopsn.	DR
Ffam; PF00001; 7tm1; 1.	DR
PRINTS; PR00237; GPCRHHODOPSN.	DR
PROSITE; PS00237; G PROTEIN RECP FL_1; 1.	DR
PROSITE; PS0262; G PROTEIN RECP FL_2; 1.	DR
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.	DR
DOMAIN 30 FT	DR
TRANSMEM 1	DR
FT 31	DR
FT 58	DR
DOMAIN 59	DR
FT 68	DR
FT TRANSMEM 69	DR
FT TRANSMEM 90	DR
FT TRANSMEM 103	DR
FT TRANSMEM 125	DR
FT TRANSMEM 141	DR
FT TRANSMEM 142	DR
FT TRANSMEM 167	DR
FT TRANSMEM 199	DR
FT TRANSMEM 219	DR
FT TRANSMEM 235	DR
FT TRANSMEM 236	DR
FT TRANSMEM 260	DR
FT TRANSMEM 261	DR
FT TRANSMEM 277	DR
FT TRANSMEM 301	DR
FT TRANSMEM 302	DR
FT TRANSMEM 352	DR
FT TRANSMEM 101	DR
FT TRANSMEM 178	DR
FT TRANSMEM 3	DR
FT TRANSMEM 3	DR
FT TRANSMEM 10	DR
FT TRANSMEM 10	DR
FT TRANSMEM 14	DR
FT TRANSMEM 14	DR
FT TRANSMEM 352 AA; 40436 MW; 9623CA98340CF274 CRC64;	DR
SEQUENCE	DR

```

RESULT 8
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CKR5_HVLSY
ID CKR5_HVLSY STANDARD; PRT; 352 AA.
Q95NC5;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
CKR5 OR CWRK5.
Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
NCBI_TaxID=9590;
[1]
SEQUENCE FROM N.A.
MEDLINE=95416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-----
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EMBL; AF17884; AAX43367.1; --	
InterPro; IPR000276; GPCR_Rhodpsn.	
Pfam; PF00001; 7tm 1; 1.	
PRINTS; PR00237; GPCRHHODPSN.	
PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; 1.	
PROSITE; PS00237; G PROTEIN RECEPTOR F1.2; 1.	
PROSITE; PS0262; G PROTEIN RECEPTOR; Transmembrane; Glycoprotein; Sulfation.	
G-protein coupled receptor; Extracellular (POTENTIAL).	
DOMAIN 1 30	
FT FT	1. (POTENTIAL).
TRANSMEM 31 58	1. (POTENTIAL).
FT FT	CYTOPLASMIC (POTENTIAL).
DOMAIN 59 68	2. (POTENTIAL).
FT FT	EXTRACELLULAR (POTENTIAL).
TRANSMEM 69 89	3. (POTENTIAL).
FT FT	CYTOPLASMIC (POTENTIAL).
DOMAIN 90 102	4. (POTENTIAL).
FT FT	EXTRACELLULAR (POTENTIAL).
TRANSMEM 103 124	5. (POTENTIAL).
FT FT	CYTOPLASMIC (POTENTIAL).
DOMAIN 125 141	6. (POTENTIAL).
FT FT	EXTRACELLULAR (POTENTIAL).
TRANSMEM 142 166	7. (POTENTIAL).
FT FT	CYTOPLASMIC (POTENTIAL).
DOMAIN 167 198	8. (POTENTIAL).
FT FT	EXTRACELLULAR (POTENTIAL).
TRANSMEM 199 218	9. (POTENTIAL).
FT FT	CYTOPLASMIC (POTENTIAL).
DOMAIN 219 235	10. (POTENTIAL).
FT FT	EXTRACELLULAR (POTENTIAL).
TRANSMEM 236 260	11. (POTENTIAL).
FT FT	CYTOPLASMIC (POTENTIAL).
DOMAIN 261 277	12. (POTENTIAL).
FT FT	EXTRACELLULAR (POTENTIAL).
TRANSMEM 278 301	13. (POTENTIAL).
FT FT	CYTOPLASMIC (POTENTIAL).
DOMAIN 302 352	14. (POTENTIAL).
FT FT	BY SIMILARITY.
DISULFID 101 176	15. (POTENTIAL).
FT FT	SULFATION (BY SIMILARITY).
MOD RES 3 3	SULFATION (BY SIMILARITY).
FT FT	SULFATION (BY SIMILARITY).
MOD RES 10 10	SULFATION (BY SIMILARITY).
FT FT	SULFATION (BY SIMILARITY).
MOD RES 14 14	SULFATION (BY SIMILARITY).
FT FT	SULFATION (BY SIMILARITY).
SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF659A CRC64;	

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RESULT 9
ID CCR5 MACMU STANDARD; PRT; 352 AA.
P79436; 002746;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
CCR5 OR CCKR5.
Macaca mulatta (Rhesus macaque),
Macaca fascicularis (Crab eating macaque), and
Macaca nemestrina (Pig-tailed macaque).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
NCBI_TaxID=9544, 9541, 9545;
[1] _RN
SEQUENCE FROM N.A.
SPECIES=M.mulatta;
MEDLINE=97194592; PubMed=9032394;
Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
Newman W., Gerard N., Gerard C., Sodroski J.;
"Utilization of C-C chemokine receptor 5 by the envelope
glycoproteins of a pathogenic simian immunodeficiency virus,
SIVmac239."
J. Virol. 71:2522-2527(1997).
[2] _RN
SEQUENCE FROM N.A.
SPECIES=M.mulatta; STRAIN=Indian macaque;
MEDLINE=97213934; PubMed=9060623;
Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;

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RT "Genetically divergent strains of simian immunodeficiency virus use
 RL CCR5 as a coreceptor for entry.";
 RN J. Virol. 71:2705-2714(1997).
 RP [3]
 RC SPECIES=M.mullatti; PubMed=11461684;
 RX MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 receptors.";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mullatti, M.fascicularis, and M.nemestrina;
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC -----
 DR EMBL; U77672; AAC51109.1; -
 DR EMBL; U73739; AAC51158.1; -
 DR EMBL; U96762; AAC34132.1; -
 DR EMBL; AF005660; AB62554.1; -
 DR EMBL; AF005661; AB62555.1; -
 DR EMBL; AF005662; AB62556.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00282; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 FT CARBOHYD 266 268
 FT CONFLICT 241 241 M -> I (IN REF. 3).
 FT CONFLICT 292 292 I -> M (IN REF. 3).
 SQ SEQUENCE 352 AA; 58936C85909FACB2 CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 |||||
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
 |||||
 RESULT 10
 CCR5_PANTR
 ID CCR5_PANTR STANDARD; PRT; 352 AA.
 AC P56440; O02778;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
 GN CCR5 OR CMKBR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=95598;
 RN [1]_TaxID=95598;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC Zimmerman P.A., Buckler-White A., Alkhatib G.;
 CC Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC [3]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=98022612; PubMed=9359654;
 CC Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 CC Ho D.D.;
 CC "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
 CC AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 CC [4]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=97426118; PubMed=9282822;
 CC Zacharova V., Zachar V., Goustin A.S.;
 CC "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
 CC HIV type 1 host.";
 CC AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
 CC [5]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=98090115; PubMed=9430250;
 CC Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Buter C.;
 CC "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
 CC AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
 CC [6]
 CC SEQUENCE FROM N.A.
 CC Zhang Y., Ryder O.A., Zhang Y.;
 CC "Sequence comparison of the CCR5 gene in primates and primate
 CC phylogeny.";
 CC Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC ENBL; AF003663; AAB62557.1; -
DR ENBL; U94329; AAB58446.1; -
DR ENBL; AF011542; AAB65742.1; -
DR ENBL; U97666; AAC51670.1; -
DR ENBL; AF01540; AAB65740.1; -
DR ENBL; U97979; AAC03717.1; -
DR ENBL; AF177894; AAK43377.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 322
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT CARBOHYD 268 268
FT CONFLICT 123 123
FT SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;
T -> S (IN REF. 1).
Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCOLLTGLYFIFGFFS 114
RESULT 11
ID CKR5_PAPHA STANDARD; PRT; 352 AA.
AC P56441;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CXCR5.
OS Papio hamadryas (Hamadryas baboon), and
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557, 9558;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;

RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."; (1997).
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RX MEDLINE=99210133; PubMed=10195758;
RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
RT "Species-specific changes in the CCR5 gene from African and Asian
RT nonhuman primates."; (1999).
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=P.anubis;
RA Bentou P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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DR EMEL; AF005658; AAB62552.1; -
DR EMEL; AF105287; AAD20556.1; -
DR EMEL; AF105288; AAD20557.1; -
DR EMEL; AF105289; AAD20558.1; -
DR EMEL; AF105290; AAD20559.1; -
DR EMEL; AF023452; AAC63830.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
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FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT CARBOHYD 268 268
FT SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1FE882 CRC64;
Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFFS 22
|||||
Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db      93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 12
CKR5_PONPY
ID CKR5_PONPY STANDARD; PRT; 352 AA.
AC 097881;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075446; AAD19858.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
CC PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58 1 (POTENTIAL).
CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 69 89 2 (POTENTIAL).
CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 103 124 3 (POTENTIAL).
CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 142 166 4 (POTENTIAL).
CC DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 199 218 5 (POTENTIAL).
CC DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 236 260 6 (POTENTIAL).
CC DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 278 301 7 (POTENTIAL).
CC DOMAIN 302 352 BY SIMILARITY.
CC DISULFID 101 178 SULFATION (BY SIMILARITY).
CC MOD_RES 3 3 SULFATION (BY SIMILARITY).
CC MOD_RES 10 10 SULFATION (BY SIMILARITY).
CC MOD_RES 14 14 SULFATION (BY SIMILARITY).
CC MOD_RES 15 15 SULFATION (BY SIMILARITY).
CC SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QWDFGNTMCQLLTGLYFIGFFS 22
|||||

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Db      93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 13
CKR5_PYGBI
ID CKR5_PYGBI STANDARD; PRT; 352 AA.
AC 097880;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075445; AAD19857.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
CC PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58 1 (POTENTIAL).
CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 69 89 2 (POTENTIAL).
CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 103 124 3 (POTENTIAL).
CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 142 166 4 (POTENTIAL).
CC DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 199 218 5 (POTENTIAL).
CC DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 236 260 6 (POTENTIAL).
CC DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 278 301 7 (POTENTIAL).
CC DOMAIN 302 352 BY SIMILARITY.
CC DISULFID 101 178 SULFATION (BY SIMILARITY).
CC MOD_RES 3 3 SULFATION (BY SIMILARITY).
CC MOD_RES 10 10 SULFATION (BY SIMILARITY).
CC MOD_RES 14 14 SULFATION (BY SIMILARITY).
CC MOD_RES 15 15 SULFATION (BY SIMILARITY).
CC SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QWDFGNTMCQLLTGLYFIGFFS 22
|||||

```

Db 93 QWDFGNTMCQLLTGLYFIGFFS 114
|||||

RESULT 14
CKRS PYGNE STANDARD; PRT; 352 AA.
AC Q97882: 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF075448; AAD19860.1;
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm1.1.
CC PRINTS: PR00237; GPCRHHODOPSN.
CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
CC PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 31 58 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 69 89 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 103 124 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 142 166 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 199 218 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 236 260 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 278 301 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 302 352 BY SIMILARITY.
FT DISULFID 101 178 SULFATION (BY SIMILARITY).
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B3E861 CRC64;
Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
|||||
DB 93 QWDFGNTMCQLLTGLYFIGFFS 114
|||||

RESULT 15
CKRS TRAPR STANDARD; PRT; 352 AA.
AC Q97878: 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKR5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: AF075442; AAD19854.1;
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm1.1.
CC PRINTS: PR00237; GPCRHHODOPSN.
CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
CC PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 31 58 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 69 89 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 103 124 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 142 166 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 199 218 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 236 260 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 278 301 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 302 352 BY SIMILARITY.
FT DISULFID 101 178 SULFATION (BY SIMILARITY).
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;
Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Qy 1 QWDFGNTMCQLLTGLYFIQFFS 22
Db 93 QWDFGNTMCQLLTGLYFIQFFS 114

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 16
CKR5_TRAPH STANDARD; PRT; 352 AA.
ID CKR5_MOUSE
AC P56484;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CKR5.
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154 (1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF0075443; AAD19855.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00242; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938F CRC64;
Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIQFFS 22
Db 93 QWDFGNTMCQLLTGLYFIQFFS 114

RESULT 17
CKR8_MOUSE STANDARD; PRT; 353 AA.
ID CKR8_MOUSE
AC P56484;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 8 (C-C CKR-8) (CCR-8) (CCR-8).
GN CKR8 OR CKR8R OR TER1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98334001; PubMed=9670926;
RA Zingoni A., Soto H., Hedrick J.A., Stoppacciaro A., Storlazzi C.T.,
RA Sinigaglia F., D'Ambrosio D., O'Garra A., Robinson D., Rocchi M.,
RA Santoni A., Zlotnik A., Napolitano M.;
RT "The chemokine receptor CKR8 is preferentially expressed in Th2 but
RT not Th1 cells.";
RL J. Immunol. 161:547-551 (1998).
CC -1- FUNCTION: Receptor for the TCA-3 chemokine.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; Z98206; CAB10896.1; -
CC EMBL; Z98205; CAB10895.1; -
CC MGD; AF001277; AAC97598.1; -
CC MGD; MGI:1201402; Ccr8.
CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0006935; P:chemotaxis; IDA.
CC InterPro; IPR004068; CC_8_receptor.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR01530; CHEMOKINER8.
CC PROSITE; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00242; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 61 1 (POTENTIAL).
FT DOMAIN 62 71 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 72 91 2 (POTENTIAL).
FT DOMAIN 92 105 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 106 127 3 (POTENTIAL).
FT DOMAIN 128 144 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 145 169 4 (POTENTIAL).
FT DOMAIN 170 200 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 201 220 5 (POTENTIAL).
FT DOMAIN 221 236 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 237 261 6 (POTENTIAL).
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FT DOMAIN 262 278 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 279 302 7 (POTENTIAL).
FT DOMAIN 303 353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 104 181 BY SIMILARITY.
FT CARBOHYD 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 353 AA; 40045 MW; 31EC4B642CDB9AE5 CRC64;
Query Match 70.6%; Score 89; DB 1; Length 353;
Best local similarity 63.6%; Pred. No. 4e-06; 3; Indels 0; Gaps. 0;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps. 0;
QY 1 QWDFGNTMCCQLGLYFIFGFFS 22
Db 96 QWVFGTAMCKVSGLYYIGFFS 117
RESULT 18
ID_CK2 HUMAN STANDARD; PRT; 374 AA.
AC P41597;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
GN CCR2 OR CCKBR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=94195821; PubMed=8146186;
RA Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,
RA Coughlin S.R.;
RT "Molecular cloning and functional expression of two monocyte
RT chemoattractant protein 1 receptors reveals alternative splicing of
RT the carboxyl-terminal tails."
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94324942; PubMed=8048929;
RA Yanagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
RT "cDNA cloning and functional expression of a human monocyte
RT chemoattractant protein 1 receptor."
RL Biochem. Biophys. Res. Commun. 202:1156-1162 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97150864; PubMed=8995400;
RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
RT chemoattractant protein 1 receptor gene. Evidence for the role of the
RT carboxyl-terminal tail in receptor trafficking."
RL J. Biol. Chem. 272:1038-1045 (1997).
RN [4]
RP SEQUENCE FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nham M., Farnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., Ia Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.
RA Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kulanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SULFATION OF TYR-26, AND N-GLYCOSYLATION.
RX MEDLINE=20501139; PubMed=11046064;
RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,

RA Chakravarty L., Kolattukudy P.E.;
RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
RT has tyrosine sulfation in a conserved extracellular N-terminal
RT region."
RL J. Immunol. 165:5295-5303 (2000).
CC FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
CC level. Alternative coreceptor with CD4 for HIV-1 infection.
CC SUBCELLULAR LOCATION: Integral membrane protein.
CC ALTERNATIVE PRODUCTS:
CC Events=Alternative splicing; Named isoforms=2;
CC Name=A; IsoId=P41597-1; Sequence=Displayed;
CC Name=B; IsoId=P41597-2; Sequence=VSP_001893;
CC PTM: N-glycosylated.
CC SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC EMBL; U03882; AAA19119.1; -
CC EMBL; U03905; AAA19120.1; -
CC EMBL; D29984; BAA06253.1; -
CC EMBL; U80924; AAC51637.1; -
CC EMBL; U80924; AAC51636.1; -
CC EMBL; U95626; AAB57791.1; -
CC EMBL; U95626; AAB57792.1; -
CC EMBL; AF545480; AAN16400.1; -
CC PIR; I38450; I38450.
CC PIR; JC2443; JC2443.
CC PDB; 1KAD; 14-AUG-02.
CC PDB; 1KE1; 23-JAN-02.
CC Genew; HGNC:1603; CCR2.
CC MIM; 601267; -
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005625; C: soluble fraction; TAS.
CC GO; GO:0004950; F: chemokine receptor activity; TAS.
CC GO; GO:0006960; F: antimicrobial humoral response (sensu Inver. . .); TAS.
CC GO; GO:0006968; P: cellular defense response; TAS.
CC GO; GO:0006935; P: chemotaxis; TAS.
CC GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
CC GO; GO:0006954; P: inflammatory response; TAS.
CC GO; GO:0007125; P: invasive growth; TAS.
CC GO; GO:0007259; P: JAK-STAT cascade; TAS.
CC GO; GO:0007194; P: negative regulation of adenylate cyclase ac. . .; TAS.
CC InterPro; IPR000376; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1
CC PRINTS; PR00237; GPCR_Rhodopsin.
CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW Polymorphism; Alternative splicing; 3D-structure.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 70 1 (POTENTIAL).
FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 100 2 (POTENTIAL).
FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 115 136 3 (POTENTIAL).
FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 178 4 (POTENTIAL).
FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 374 CYTOPLASMIC (POTENTIAL).


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FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD RES 26 26 SULFATION.
FT FT 113 190 BY SIMILARITY.
FT VARSPLIC 314 374 SLPHIALGCEIAPLOKPCVGGVGRKGNKVTQGLDGR
FT FT QKCVFGRPEASLDKGA -> RYLVSFFRKHITKRFCK
FT FT GCPVFYRETVDGVSTNTSTGEOEVSAGL (in
FT FT isoform B).
FT FT /FTID=VSP_001893.
FT FT V -> I (in dbSNP:1799864).
FT FT /FTID=VAR_014339.
FT FT G -> E.
FT VARIANT 355 355 /FTID=VAR_014340.
FT VARIANT 374 AA; 41914 MW; F865E0D39E74CF0F CR064;
SQ SEQUENCE 374 AA; 41914 MW; F865E0D39E74CF0F CR064;

Query Match 69.0%; Score 87; DB 1; Length 374;
Best Local Similarity 66.7%; Pred. No. 8.4e-06;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNMCKLTLGLYFIFGF 21
: ||||| ||||| ||||| |||||
DB 105 EWVFGNCKLFTGLYHYGF 125

RESULT 19
ID_CKR2_RAT STANDARD; PRT; 373 AA.
AC C5193;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2).
GN CKR2 OR CMKR2
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RA "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis.";
RL J. Neuroimmunol. 86:1-12(1998).
CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level (by similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
CC macrophages.
CC -!- INDUCTION: In animals in which experimental allergic
CC encephalomyelitis (EAE) has been induced.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U77349; AAC03242.1;
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1.1
CC PRINTS; PR00237; GPCR_RHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 61 81 POTENTIAL.
FT DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).
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FT TRANSMEM 92 112 POTENTIAL.
FT DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 129 149 POTENTIAL.
FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 POTENTIAL.
FT DOMAIN 192 220 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 221 241 POTENTIAL.
FT DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 277 POTENTIAL.
FT DOMAIN 278 301 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 302 322 POTENTIAL.
FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 203 BY SIMILARITY.
SQ SEQUENCE 373 AA; 42763 MW; 2E7B013F5D6F09 CRC64;

Query Match 68.3%; Score 86; DB 1; Length 373;
Best Local Similarity 66.7%; Pred. No. 1.2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNMCKLTLGLYFIFGF 21
: ||||| ||||| ||||| |||||
DB 118 EWVFGNCKLFTGLYHYGF 138

RESULT 20
ID_CKR5_RAT STANDARD; PRT; 354 AA.
AC O08556;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
DE alpha receptor).
GN CKR5 OR CMKR5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=98334064; PubMed=9670989;
RA Spleiss O., Gourmal N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
RA Berger M., Gebicke-Haerter P.J.;
RA "Cloning of rat HIV-1 chemokine coreceptor CKR5 from microglia and
RT upregulation of its mRNA in ischemic and endotoxemic rat brain.";
RL J. Neurosci. Res. 53:16-28(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RA "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis.";
RL J. Neuroimmunol. 86:1-12(1998).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y12009; CAA72737.1;
CC EMBL; U77350; AAC03243.1;
CC InterPro; IPR000276; GPCR_Rhodpsn.
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us-10-084-813-12.rsp

Tue Sep 28 15:49:56 2004

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DR PFAM: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 33 60 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 91 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 105 126 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 127 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 168 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 169 200 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 201 220 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 238 262 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 280 303 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 304 354 BY SIMILARITY.
FT DISULFID 103 180 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 270 270
SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

Query Match 66.7%; Score 84; DB 1; Length 354;
Best Local Similarity 61.9%; Pred. No. 2.3e-05;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCKLGLYFIFGF 21
DB 95 EWVFGNTMCKLFTGIYHGVF 115

RESULT 21
VC03 SPVKA STANDARD; PRT; 269 AA.
AC P32229;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE G-protein coupled receptor homolog C3.
GN C3L.
OS Swinepox virus (strain Kasza) (SPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Suipoxvirus.
NCBI_TaxID=10277;
DR EMBL; L22013; AAC37868.1;
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR PFAM; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 61 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 62 82 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 83 94 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 95 115 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 116 131 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 132 152 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 153 171 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 172 192 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 193 223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 224 244 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 245 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 286 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 287 301 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 302 321 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 322 370 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 370 AA; 43171 MW; 76D08613327B0CC0 CRC64;

Query Match 65.9%; Score 83; DB 1; Length 370;
Best Local Similarity 54.5%; Pred. No. 3.3e-05;

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GO	GO:0006954; P:inflammatory response; IMP.
GO	GO:0030334; P:regulation of cell migration; IMP.
InterPro	IPR000276; GPCR_Rhodpsn.
Pfam	PF00001; 7tm 1; 1.
PRINTS	PR00237; GPCRHOOPSN
PROSITE	PS00337; G_PROTEIN_RECEP_F1_1; 1.
PROSITE	PS00462; G_PROTEIN_RECEP_F1_2; 1.
KW	G-protein coupled receptor; Transmembrane.
FT DOMAIN	1 55 EXTRACELLULAR (POTENTIAL).
FT FT	TRANSMEM 56 83 1 (POTENTIAL).
FT FT	DOMAIN 84 93 CYTOPLASMIC (POTENTIAL).
FT FT	TRANSMEM 94 114 2 (POTENTIAL).
FT FT	DOMAIN 115 127 EXTRACELLULAR (POTENTIAL).
FT FT	TRANSMEM 128 149 3 (POTENTIAL).
FT FT	DOMAIN 150 166 CYTOPLASMIC (POTENTIAL).
FT FT	TRANSMEM 167 191 4 (POTENTIAL).
FT FT	DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT FT	TRANSMEM 220 239 5 (POTENTIAL).
FT FT	DOMAIN 240 256 CYTOPLASMIC (POTENTIAL).
FT FT	TRANSMEM 257 281 6 (POTENTIAL).
FT FT	DOMAIN 282 298 EXTRACELLULAR (POTENTIAL).
FT FT	TRANSMEM 299 322 7 (POTENTIAL).
FT FT	DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
FT FT	DISULFID 126 203 BY SIMILARITY.
FT FT	CONFLICT 39 39 Y -> H (IN REF. 1).
FT FT	CONFLICT 184 184 A -> G (IN REF. 1).
FT FT	CONFLICT 264 264 V -> G (IN REF. 1).
SQ	SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 65.9%; Score 83; DB 1; Length 373;
 Best Local Similarity 61.9%; Pred. No. 3.4e-05;
 Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY	1 QWDFGNTWCQLLTGLGYFIQGF 21
DB	118 EWVFGNIMKVFTGLYHIGYF 138
	: : :

RESULT 24

ID	CKR8_HUMAN	STANDARD;	PRT;	355 AA.
AC	P51685;			
DT	01-OCT-1996 (Rel. 34, Created)			
DD	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	C-C chemokine receptor type 8 (C-C CKR-8) (CCR-8) (GPR-CY6)			
DE	(GPCYC6) (Chemokine receptor-like 1) (CKR-L1) (TERL) (CMKRL2) (CC-			
DE	chemokine receptor CHEMK1).			
GN	CKR8 OR CMKBR8 OR CKRL1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
NCBI	[TaxID=9606;			
RN	[1]__OX			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=97351133; PubMed=9207005;			
RR	Tiffany H.L., Lautens L.L., Gao J.-L., Pease J., Locati M.,			
RA	Combadiere C., Modi W., Bonner T.I., Murphy P.M.;			
RA	"Identification of CCR8: a human monocyte and thymus receptor for the			
ET	CC chemokine I-309";			
EL	J. Exp. Med. 186:165-170 (1997).			
RN	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=98129363; PubMed=9469461;			
RR	Goya I., Gutierrez J., Varona R., Kremer L., Zaballos A., Marquez G.;			
RA	"Identification of CCR8 as the specific receptor for the human beta-			
RA	chemokine I-309: cloning and molecular characterization of murine			
RT	CCR8 as the receptor for ICA-3.";			
RT	J. Immunol. 160:1975-1981 (1998).			
RN	[3]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=97040707; PubMed=8886020;			
RR	Zaballos A., Varona R., Gutierrez J., Lind P., Maymone G.;			


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FT TRANSMEM 204 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 356 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 184 BY SIMILARITY.
SQ SEQUENCE 356 AA; 41210 MW; 1979628DEE4845B CRC64;

Query Match
Best Local Similarity 54.5%; Score 82; DB 1; Length 356;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 1 QWDFGNTMCCOLLGLYFIFGS 22
DB 98 QWVFGVNCVKSQVSGFYIIGFYS 119

RESULT 26
CKR2 MACMU STANDARD; PRT; 360 AA.
ID CKR2 MACMU STANDARD; PRT; 360 AA.
AC O18793;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
DE CCR2 OR CMKBR2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461584;
RA Margulies B.J., Haver D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
CC level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=B;
CC IsoId=O18793-1; Sequence=Displayed;
CC Name=A;
CC IsoId=O18793-2; Sequence=Not described;
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
CC EMBL; AF013958; AAD11572.1;
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1.1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PSC0237; G-PROTEIN RECP F1.1; 1.
CC PROSITE; PSS0262; G-PROTEIN RECP F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
CC Alternative splicing.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 70 1 (POTENTIAL).
FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 100 2 (POTENTIAL).
FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
```

```
FT TRANSMEM 115 136 3 (POTENTIAL).
FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 178 4 (POTENTIAL).
FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 243 6 (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC... ) (POTENTIAL).
FT MOD_RES 26 26 SULFATION (BY SIMILARITY).
FT DISULFID 113 190 BY SIMILARITY.
SQ SEQUENCE 360 AA; 41139 MW; 4B2552BC913FE9F CRC64;

Query Match
Best Local Similarity 64.3%; Score 81; DB 1; Length 360;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 QWDFGNTMCCOLLGLYFIFG 20
DB 105 EWVFGNACVCKLFTGLYHIGY 124

RESULT 27
CKR5 MOUSE STANDARD; PRT; 354 AA.
ID CKR5 MOUSE STANDARD; PRT; 354 AA.
AC P51682; O35313; O35891; P97308; P97405; Q61867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
DE alpha receptor).
DE CCR5 OR CMKBR5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SVJ; TISSUE=Spleen;
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9."
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96278910; PubMed=862890;
RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Cloning and characterization of a novel murine macrophage
RT inflammatory protein-1 alpha receptor."
RL J. Biol. Chem. 271:14445-14451(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=129/Ola;
RX Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
RX MEDLINE=98001397; PubMed=9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses."
RL J. Virol. 71:8642-8656(1997).
RN [5]
RP SEQUENCE FROM N.A.
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SQ SEQUENCE 358 AA; 41623 MW; 7B73FAB7A3BC3670 CRC64;
Query Match 62.7%; Score 79; DB 1; Length 358;
Best Local Similarity 50.0%; Pred. No. 0.00013;
Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCCOLLGLYFIFGFFS 22
Db 102 KWFVGHFMCKIISGLYVGLFS 123

RESULT 29
CKR1 MOUSE
ID CKR1_MOUSE STANDARD; PRT; 355 AA.
AC P51675; Q91VP9;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)
DE Macrophage inflammatory protein-1 alpha receptor (MIP-1alpha-R)
DE (RANTES-R)
DE GN
DE CCR1 OR CMKBR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=129/SvJ; TISSUE=Peritoneal macrophage;
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA "Molecular characterization of two murine eosinophil beta chemokine
RT receptors.";
RL J. Immunol. 155:5299-5305(1995).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=129/SvJ;
RX MEDLINE=95340546; PubMed=7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
RT beta chemokine receptor-like genes, including the gene for a
RT functional macrophage inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 270:17494-17501(1995).
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE=Breast;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC RANTES, AND LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
CC PROLIFERATION.

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CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in the heart, spleen, lung,
CC peritoneal exudate cells and leukocytes.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC -----
CC EMBL; U29678; AAA86119.1; -
CC EMBL; U28404; AAA89153.1; -
CC EMBL; BC011092; AAH11092.1; -
CC PIR; I49339; I49339
CC MGD; MGI:104618; Ccr1.
CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0030595; P:immune cell chemotaxis; IDA.
CC GO; GO:0006954; P:inflammatory response; IMP.
CC GO; GO:0030099; P:myeloid blood cell differentiation; IMP.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane.
CC DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 35 60 1 (POTENTIAL).
CC DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 65 91 2 (POTENTIAL).
CC DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 108 129 3 (POTENTIAL).
CC DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 147 171 4 (POTENTIAL).
CC DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 198 223 5 (POTENTIAL).
CC DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 240 264 6 (POTENTIAL).
CC DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 282 305 7 (POTENTIAL).
CC DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
CC DISULFID 106 183 BY SIMILARITY.
CC CONFLICT 55 55 M -> V (IN REF. 2 AND 3).
CC CONFLICT 149 149 L -> F (IN REF. 3).
CC CONFLICT 278 278 H -> Q (IN REF. 3).
CC SEQUENCE 355 AA; 40901 MW; FCE9FFF70E6F38B1 CRC64;
Query Match 60.1%; Score 76; DB 1; Length 355;
Best Local Similarity 52.4%; Pred. No. 0.00037;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
Qy 2 WDFGNTMCCOLLGLYFIFGFFS 22
Db 99 WIFGDAMCKLLSGFYVGLYS 119
RESULT 30
CKR3_MOUSE
ID CKR3_MOUSE STANDARD; PRT; 359 AA.
AC O54814; O55169;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
DE (CCR3).
DE GN CCR3 OR CMKBR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

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RN RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=Wistar; TISSUE=Spleen;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Peng L., Sonntag M.K.,
RA Defiebre C.M., Pannell N.A., Streif W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RL allergic encephalomyelitis";
RL J. Neuroimmunol. 86:1-12(1998).
RN [2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RA Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in spleen but not in astrocytes or
CC microglia.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF003954; AAC03337.1; -.
CC EMBL; U13400; CAAT73830.1;
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN RECP Fl_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECP Fl_2; 1.
CC G-protein coupled receptor; Transmembrane.
CC KW DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 44 64 POTENTIAL.
CC FT DOMAIN 45 74 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 75 95 POTENTIAL.
CC FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 113 133 POTENTIAL.
CC FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 155 175 POTENTIAL.
CC FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 207 227 POTENTIAL.
CC FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 244 264 POTENTIAL.
CC FT DOMAIN 265 288 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 289 309 POTENTIAL.
CC FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
CC FT CONFLICT 164 164 F -> L (IN REF. 2).
CC SEQUENCE 359 AA; 41643 MW; 880F682984F501DA CRC64;
RN RP Query Match 59.5%; Score 75; DB 1; Length 359;
RN RP Best Local Similarity 45.5%; Pred. No. 0.00052;
RN RP Matches 10; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
RN QY 1 QWFGNTMCCOLLTGLTYFIFGFS 22
RN DB 102 EWFGHCKMCKMGLSGLYLYALS 123
RN RESULT 31
RN ID CKRV_MOUSE STANDARD; PRT; 356 AA.
RN AC P51676;
RN DT 01-OCT-1996 (Rel. 34, Created)
RN DT 01-OCT-1996 (Rel. 34, Last sequence update)
RN DT 28-FEB-2003 (Rel. 41, Last annotation update)
RN DE C-C chemokine receptor 1-like protein 1 (Macrophage inflammatory

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DE GN protein-1 alpha receptor-like 1).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RN RP SEQUENCE FROM N.A.
RN RC STRAIN=129/SWJ;
RN RX MEDLINE=95340546; PubMed=7542241;
RN RA Gao J.-L., Murphy P.M.;
RN RT "Cloning and differential tissue-specific expression of three mouse
RN RT beta chemokine receptor-like genes, including the gene for a
RN RT functional macrophage inflammatory protein-1 alpha receptor.";
RN RL J. Biol. Chem. 270:17494-17501(1995).
CC -!- FUNCTION: Probable receptor for a C-C type chemokine.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in the spleen, liver and leukocytes.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U28405; AAA89154.1; -.
CC PIR; I49340; I49340.
CC MGID; MGI:104617; Cor11.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN RECP Fl_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECP Fl_2; 1.
CC G-protein coupled receptor; Transmembrane.
CC KW DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 33 60 1 (POTENTIAL).
CC FT DOMAIN 61 67 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 68 92 2 (POTENTIAL).
CC FT DOMAIN 93 108 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 109 130 3 (POTENTIAL).
CC FT DOMAIN 131 147 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 148 172 4 (POTENTIAL).
CC FT DOMAIN 173 198 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 199 224 5 (POTENTIAL).
CC FT DOMAIN 225 240 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 241 265 6 (POTENTIAL).
CC FT DOMAIN 266 282 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 283 306 7 (POTENTIAL).
CC FT DOMAIN 307 356 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 107 184 BY SIMILARITY.
CC SEQUENCE 356 AA; 40934 MW; 58C01ABA8D7D4B06 CRC64;
RN RP Query Match 58.7%; Score 74; DB 1; Length 356;
RN RP Best Local Similarity 47.8%; Pred. No. 0.00073;
RN RP Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
RN QY 2 WDFGNTMCCOLLTGLTYFIFGFS 22
RN DB 100 WIFGNMCKFVSGFYLYGLYS 120
RN RESULT 32
RN ID CKRI_HUMAN STANDARD; PRT; 355 AA.
RN AC P32246;
RN DT 01-OCT-1993 (Rel. 27, Created)
RN DT 01-OCT-1993 (Rel. 27, Last sequence update)
RN DT 15-MAR-2004 (Rel. 43, Last annotation update)
RN DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)
RN DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)

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DE (RANTES-R) (HM145) (LD78 receptor).
GN CCR1 OR CMK1R OR CMK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93161416; PubMed=7679328;
RA Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
RT "Molecular cloning, functional expression, and signaling
RT characteristics of a C-C chemokine receptor.";
RL Cell 72:415-425 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93240122; PubMed=7683036;
RA Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
RT "Structure and functional expression of the human macrophage
RT inflammatory protein 1 alpha/RANTES receptor.";
RL J. Exp. Med. 177:1421-1427 (1993).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Monocytes;
RX MEDLINE=94092629; PubMed=7505609;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
RT leukocyte chemotactic peptide receptors.";
RL Int. Immunol. 5:1239-1249 (1993).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-
CC beta or MCP-1 and subsequently transduces a signal by increasing
CC the intracellular calcium ions level. Responsible for affecting
CC stem cell proliferation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed in different hematopoietic
CC cells.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; L09230; AAA58408.1; -;
CC EMBL; L10918; AAA36543.1; -;
CC EMBL; D10925; BA01723.1; -;
CC F01; A45177; A45177.
CC Genew; HGNC:1602; CCR1.
CC MIM; 601159; -;
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004950; P:chemokine receptor activity; TAS.
CC GO; GO:0007155; P:cell adhesion; TAS.
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
CC GO; GO:0007265; P:cell-cell signaling; TAS.
CC GO; GO:0006935; P:chemotaxis; TAS.
CC GO; GO:0007204; P:cyclosolic calcium ion concentration elevation; TAS.
CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
CC GO; GO:0006955; P:immune response; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC GO; GO:0007125; P:invasive growth; TAS.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
CC PROSITE; PS00262; G PROTEIN RECP F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT CONFLICT 337 337 E -> D (IN REF. 3).
SQ SEQUENCE 355 AA; 41172 MW; 52C100FFED75985 CRC64;
Query Match 56.3%; Score 71; DB 1; Length 355;
Best Local Similarity 47.6%; Pred. No. 0.0021;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
Oy 2 WDRGNTMCQLLTGLYPTGFPS 22
Db 99 WFGDAMCKILSGFYTGGLYS 119
||||:||||:|:|:|
RESULT 33
ID_CCR1_MACMU STANDARD; PRT; 355 AA.
AC PS6482;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 1 (C-CR-1) (CCR-1) (CCR1).
GN CCR1 OR CMK1R.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors.";
RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC RANTES, MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
CC PROLIFERATION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF017282; AAB70526.1; -;
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
CC PROSITE; PS00262; G PROTEIN RECP F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 65 91 2 (POTENTIAL).
 FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 198 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 SQ SEQUENCE 355 AA; 41198 MW; 41CAEA7CC19D23D4 CRC64;
 Query Match 56.3%; Score 71; DB 1; Length 355;
 Best Local Similarity 47.6%; Pred. No. 0.0021;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 2 WDFGNMTCOLLTGLYFIGPFS 22
 Db 99 WIFGDAMCKILSGFYTGDIYS 119
 RESULT 34
 ID_CK3_MOUSE STANDARD; PRT; 359 AA.
 AC PS1678;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3)
 DE (CCR3) (CCR3) (Macrophage inflammatory protein-1 alpha receptor-like
 2) (MIP-1 alpha RL2).
 GN CCR3 OR CMKBR3 OR CMKBR112.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=96072806; PubMed=7594543;
 RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
 Gerard C.;
 RA "Molecular characterization of two murine eosinophil beta chemokine
 receptors";
 RT J. Immunol. 155:5299-5305(1995).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=95340546; PubMed=7542241;
 RA Gao J.-L., Murphy P.M.;
 RA "Cloning and differential tissue-specific expression of three mouse
 beta chemokine receptor-like genes, including the gene for a
 functional macrophage inflammatory protein-1 alpha receptor.";
 RT J. Biol. Chem. 270:17494-17501(1995).
 CC -/- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
 MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level.
 CC -/- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -/- TISSUE SPECIFICITY: Detected in skeletal muscle and in trace
 amounts in leukocytes.
 CC -/- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 or send an email to license@isb-sib.ch).

CC EMBL; U29677; AAA86118.1; --
 DR EMBL; U28406; AAA89155.1; --
 DR MGI; 104616; CCR3.
 DR GO; GO:0016493; F1C-C chemokine receptor activity; IDA.
 DR GO; GO:0005915; P:protein binding; IPI.
 DR GO; GO:0006935; P:chemotaxis; IDA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 39 64 1 (POTENTIAL).
 FT DOMAIN 65 68 1 (POTENTIAL).
 FT TRANSMEM 69 95 2 (POTENTIAL).
 FT DOMAIN 96 111 3 (POTENTIAL).
 FT TRANSMEM 112 133 3 (POTENTIAL).
 FT DOMAIN 134 150 4 (POTENTIAL).
 FT TRANSMEM 151 175 4 (POTENTIAL).
 FT DOMAIN 176 201 5 (POTENTIAL).
 FT TRANSMEM 202 227 5 (POTENTIAL).
 FT DOMAIN 228 243 6 (POTENTIAL).
 FT TRANSMEM 244 268 6 (POTENTIAL).
 FT DOMAIN 269 285 7 (POTENTIAL).
 FT TRANSMEM 286 309 7 (POTENTIAL).
 FT DOMAIN 310 359 7 (POTENTIAL).
 FT DISULFID 110 187 BY SIMILARITY.
 FT CONFLICT 270 270 R -> S (IN REF. 2).
 SQ SEQUENCE 359 AA; 41825 MW; AC1ED66283CEAF CRC64;
 Query Match 55.6%; Score 70; DB 1; Length 359;
 Best Local Similarity 40.9%; Pred. No. 0.003;
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
 QY 1 QWDFGNMTCOLLTGLYFIGPFS 22
 Db 102 EWGFGHYMCKSLSGFYLYALYS 123
 RESULT 35
 ID_CK3_HUMAN STANDARD; PRT; 355 AA.
 AC PS1677; Q15748; Q85WD2; Q9ULY8;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
 DE (CCR3) (Eosinophil eotaxin receptor).
 GN CCR3 OR CMKBR3
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Monocytes;
 RX MEDLINE=95348056; PubMed=7622448;
 RA Combadiere C., Ahuja S.K., Murphy P.M.;
 RA "Cloning and functional expression of a human eosinophil CC chemokine
 receptor.";
 RT J. Biol. Chem. 270:16491-16494(1995).
 RL [2]
 RN ERZATUM.
 RA Combadiere C., Ahuja S.K., Murphy P.M.;
 RL J. Biol. Chem. 270:30235-30235(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96235044; PubMed=8642344;
 RA Daugherty B.L., Siciliano S.J., Demartino J.A., Malkowitz L.,
 RA Sirotina A., Springer M.S.;
 RA "Cloning, expression, and characterization of the human eosinophil
 CC

RT eotaxin receptor.";
RL J. Exp. Med. 183:2349-2354 (1996).
RN [4].
RP SEQUENCE FROM N.A.
RX MEDLINE=96281895; PubMed=8676064;
RA Ponath P.D., Qin S., Post T.W., Wang J., Wu L., Gerard N.P.,
RA Newman W., Gerard C., Mackay C.R.;
RT "Molecular cloning and characterization of a human eotaxin receptor
RT expressed selectively on eosinophils.";
RL J. Exp. Med. 183:2737-2748 (1996).
RN [5].
RP SEQUENCE FROM N.A.
RA Xiao L., Weiss S., Oari S., Rudolph D., Hodge T., Lal R.;
RT "Partial resistance to infection by syncytium-inducing primary HIV-1
RT in exposed uninfected individuals homozygous for CCR5 32bp deletion.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [6].
RP SEQUENCE FROM N.A., AND VARIANT SER-218.
RX MEDLINE=21040311; PubMed=11196669;
RA Kato H., Teuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104 (1999).
RN [7].
RP SEQUENCE FROM N.A.
RX MEDLINE=22074933; PubMed=12079287;
RA Vijh S., Dayhoff D.E., Wang C.E., Imam Z., Ehrenberg P.K.,
RA Michael N.L.;
RT "Transcription regulation of human chemokine receptor CCR3: evidence
RT for a rare TATA-less promoter structure conserved between Drosophila
RT and humans.";
RL Genomics 80:86-95 (2002).
RN [8].
RP SEQUENCE FROM N.A.
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [9].
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, Lung, and Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.N., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lomellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rutherford Y.S.N., Krzywinski M.T., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maizumi M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC eotaxin-3, MCP-3, MCP-4, RANTES, and MIP-1 delta. Subsequently
CC transduces a signal by increasing the intracellular calcium ions
CC level. Alternative coreceptor with CD4 for HIV-1 infection.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: In eosinophils as well as trace amounts in
CC neutrophils and monocytes.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U28694; AAC50469.1; -;
CC EMBL; U51241; AAB1831.1; -;
CC EMBL; U49727; AAB09726.1; -;
CC EMBL; AF026535; AAB82589.1; -;
CC EMBL; AB023887; AAB86964.1; -;
CC EMBL; AF247361; AAL85154.1; -;
CC EMBL; AY221092; AA065970.2; -;
CC EMBL; BC033514; AAH33514.1; -;
CC PIR; G02436; G02436;
CC Genew; HGNC:1604; CCR3.
CC MIM; 601268; -;
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004950; F:chemokine receptor activity; TAS.
CC GO; GO:0007155; P:cell adhesion; TAS.
CC GO; GO:0006968; P:cellular defense response; TAS.
CC GO; GO:0006935; P:chemotaxis; TAS.
CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
CC GO; GO:0007188; P:G-protein signaling, coupled to camp nucleo. .; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC GO; GO:0007125; P:invasive growth; TAS.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR0237; GPCRHOOPS.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
CC KW G-protein coupled receptor; Transmembrane; Polymorphism.
CC FT DOMAIN 1 34
CC FT TRANSMEM 35 62
CC FT DOMAIN 63 72
CC FT TRANSMEM 73 93
CC FT DOMAIN 94 107
CC FT TRANSMEM 108 129
CC FT DOMAIN 130 146
CC FT TRANSMEM 147 171
CC FT DOMAIN 172 203
CC FT TRANSMEM 204 223
CC FT DOMAIN 224 239
CC FT TRANSMEM 240 264
CC FT DOMAIN 265 281
CC FT TRANSMEM 282 305
CC FT DOMAIN 306 355
CC FT DISULFID 106 183
CC FT VARIANT 218 218
CC FT C->S (polymorphism found in about 7% of
CC the population; may show reduced
CC activity).
CC FTID=VAR 010668.
CC FTID=VAR 010668.
CC S->T (IN REF. 4 AND 5).
CC CONFLICT 276 276
CC SEQUENCE 355 AA; 41043 MW; B95DCD7A6C643874 CRC64;
Query Match 53.2%; Score 67; DB 1; Length 355;
Best Local Similarity 52.4%; Pred. No. 0.0083;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 2 WDFGNTMQLLTGLYFIFGFFS 22
DB 99 WYFGHCKLLSGFYHTGLYS 119
RESULT 36
CC CCR6_CERAE
ID CCR6_CERAE STANDARD; PRT; 342 AA.
AC Q18983;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled
DE receptor bonzo).

GN CXCR6 OR BONZO.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97373958; PubMed=9230441;
RX Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
RL immunodeficiency viruses.";
RL Nature 388:296-300(1997).
CC -1- FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a
CC coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF007859; AAB64225.1; --
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
DR PROSITE; PS00237; G PROTEIN RECP FL 2; 1.
DR PROSITE; PS0262; G PROTEIN RECP FL 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT TRANSMEM 33 59
FT DOMAIN 60 68
FT TRANSMEM 69 89
FT DOMAIN 90 103
FT TRANSMEM 104 125
FT DOMAIN 126 143
FT TRANSMEM 144 164
FT DOMAIN 165 187
FT TRANSMEM 188 215
FT DOMAIN 216 231
FT TRANSMEM 232 259
FT DOMAIN 260 275
FT TRANSMEM 276 293
FT DOMAIN 294 342
FT DISULFID 102 180
FT CARBOHYD 16 16
SQ SEQUENCE 342 AA; 39226 MW; 6CBFE389C6E5919E CRC64;
Query Match 52.4%; Score 66; DB 1; Length 342;
Best Local Similarity 45.5%; Pred. No. 0.011; Mismatches 0; Gaps 0;
Matches 10; Conservative 5; Indels 7; Lengths 0;
Oy 1 QWDFGNTMCQLLTGLYIFGIFS 22
Db 94 EWIFQVCKTLLGIYINFTY 115
RESULT 37
ID CKR4 HUMAN STANDARD; PRT; 360 AA.
AC P51679; Q9ULY6; Q9ULY7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 4 (C-C CKR-4) (CCR-4) (CCR4)
DE (K5-5).
GN CKR4 OR CMKBR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Spleen;
RX MEDLINE=95370289; PubMed=7642634;
RA Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,
RA Proudfoot A.E.I., Wells T.N.C.;
RA "Molecular cloning and functional expression of a novel CC chemokine
RT receptor cDNA from a human basophilic cell line.";
RL J. Biol. Chem. 270:19495-19500(1995).
RN [2]
RP SEQUENCE FROM N.A. AND VARIANTS VAL-130 AND SER-178.
RA MEDLINE=21040311; PubMed=11196669;
RA Kato H., Tsuchiya N., Izumi S., Miyamae M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RA "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RA "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP FUNCTION.
RX MEDLINE=973133486; PubMed=9169480;
RA Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;
RA "The T cell-directed CC chemokine TARC is a highly specific
RT biological ligand for CC chemokine receptor 4.";
RL J. Biol. Chem. 272:15036-15042(1997).
RN [5]
RP FUNCTION.
RX MEDLINE=98104168; PubMed=9430724;
RA Imai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska R.,
RA Yoshie O., Gray P.W.;
RA "Macrophage-derived chemokine is a functional ligand for the CC
RT chemokine receptor 4.";
RL J. Biol. Chem. 273:1764-1768(1998).
RN [6]
RP FUNCTION.
RX MEDLINE=99394604; PubMed=10466728;
RA Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Ponath P.,
RA Andrew D.P., Wanke R., Ruffing N., Kassam N., Wu L., Butcher E.C.;
RA "The chemokine receptor CCR4 in vascular recognition by cutaneous but
RT not intestinal memory T cells.";
RL Nature 400:776-780(1999).
RN [7]
RP FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.
RX MEDLINE=20219238; PubMed=10754297;
RA Immgjerdigen M., Damaj B., Maghazachi A.A.;
RA "Human NK cells express CC chemokine receptors 4 and 8 and respond to
RT thymus and activation-regulated chemokine, macrophage-derived
RL chemokine, and I-309.";
RL J. Immunol. 164:4048-4054(2000).
CC -1- FUNCTION: High affinity receptor for the C-C type chemokines
CC TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is
CC mediated by G(i) proteins which activate a phosphatidylinositol-
CC calcium second messenger system. Can function as a chemoattractant
CC homing receptor on circulating memory lymphocytes and as a
CC coreceptor for some primary HIV-2 isolates. In the CNS, could
CC mediate hippocampal-neuron survival.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Predominantly expressed in the thymus, in
CC peripheral blood leukocytes, including T cells, mostly cd4+ cells,
CC and in monocytes. Detected also in macrophages, IL-2-activated
CC natural killer cells and skin-homing memory T cells, mostly the
CC ones expressing the cutaneous lymphocyte antigen (CLA). Expressed
CC in brain microvascular and coronary artery endothelial cells.
CC -1- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
CC PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
CC BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.

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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:56:16 ; Search time 35.2 Seconds
(without alignments)
197.199 Million cell updates/sec

Title: US-10-084-813-12
Perfect score: 126
Sequence: 1 QWDFGNTMCQLLTGLYFIFGRFS 22

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: SP_ARCHEA:*
 - 2: SP_BACTERIA:*
 - 3: SP_FUNGI:*
 - 4: SP_HUMAN:*
 - 5: SP_INVERTEBRATE:*
 - 6: SP_MAMMAL:*
 - 7: SP_MBC:*
 - 8: SP_ORGANELLE:*
 - 9: SP_PHAGE:*
 - 10: SP_PLANT:*
 - 11: SP_RODENT:*
 - 12: SP_VIRUS:*
 - 13: SP_VIRTEBRATE:*
 - 14: SP_UNCLASSIFIED:*
 - 15: SP_VIRUS:*
 - 16: SP_BACTERIAP:*
 - 17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	100.0	215	4	075303
2	126	100.0	333	4	014694
3	126	100.0	339	4	Q8UN24
4	126	100.0	339	4	Q8UN23
5	126	100.0	339	4	Q8UN27
6	126	100.0	339	4	Q8UN25
7	126	100.0	339	4	Q8UN27
8	126	100.0	339	4	Q8UN29
9	126	100.0	339	4	Q8UN28
10	126	100.0	339	6	Q8TQW4
11	126	100.0	339	6	Q8TUX1
12	126	100.0	339	6	Q8TUX8
13	126	100.0	339	6	Q8TUT4
14	126	100.0	339	6	Q8TUT9
15	126	100.0	339	6	Q8TUX8
16	126	100.0	339	6	Q8TQW4

ALIGNMENTS

RESULT 1

075303	PRELIMINARY;	PRT;	215 AA.
AC	075303		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	CC-chemokine receptor.		
GN	CCR-5.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Tse L., Ehrenberg P.K., Chang G., Michael N.L.;		
RT	"Genomic Organization and Functional Characterization of the Complete Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-Receptor for HIV-1."		
RT	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF009962; AAC23944.1; -.		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.		
DR	InterPro; IPR000276; GPCR_Rhodopsn.		
DR	Efam; PF00001; 7tm1; 1.		
DR	PRINTS; PR00237; GPCRHHODOPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.		
DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.		
KW	Receptor.		
SQ	SEQUENCE 215 AA; 23946 MW; 3C9146C768A416F7 CRC64;		
Query Match 100.0%; Score 126; DB 4; Length 215;			
Best Local Similarity 100.0%; Pred.No.1.9e-11;			
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 QWDFGNTMCQLLTGLYFIFGRFS 22		

Q9TUW4 pan troglod
Q9TUW7 cercopithec
Q9TUU3 macaca mula
Q9TUR9 saguinus sp
Q9TQT0 macaca fasc
Q9TUT9 macaca mula
Q9TSN2 macaca fasc
Q9TUR6 cercopithec
Q9TQV6 colobus gue
Q9TUW6 pan troglod
Q9TUR9 cercopithec
Q9TSN3 macaca fasc
Q9TUU7 macaca fasc
Q9TQV0 papio papio
Q9TQV5 cercopithec
Q9TUS7 papio papio
Q9TUW7 pan troglod
Q9TUW3 pongo pygma
Q9TUS5 papio papio
Q9TUU0 macaca mula
Q9TQV2 papio papio
Q9TQV3 cercopithec
Q9TUQ8 cercopithec
Q9TQW2 pongo pygma
Q9TUU1 macaca mula
Q9TUT6 macaca neme
Q9TSQ4 cercopithec
Q9TUT3 macaca neme
Q9TUT0 macaca neme

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Db      93 QWDFGNTMCOLLTGLYFIFGFFS 114
RESULT 2
O14694 PRELIMINARY; PRT; 333 AA.
AC O14694
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011504; AAB5704.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 333 333
SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

Query Match 100.0%; Score 126; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFFS 22
Db 74 QWDFGNTMCOLLTGLYFIFGFFS 95

RESULT 3
Q9UN24 PRELIMINARY; PRT; 339 AA.
AC Q9UN24
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161919; AAD4767.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFFS 22
Db 86 QWDFGNTMCOLLTGLYFIFGFFS 107

RESULT 5
Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161919; AAD4767.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.

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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFFS 22
Db 86 QWDFGNTMCOLLTGLYFIFGFFS 107

RESULT 4
Q9UN23 PRELIMINARY; PRT; 339 AA.
AC Q9UN23
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD4767.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFFS 22
Db 86 QWDFGNTMCOLLTGLYFIFGFFS 107

RESULT 5
Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD4767.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFFS 22
Db 86 QWDFGNTMCOLLTGLYFIFGFFS 107

RESULT 5
Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD4767.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.

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Db 86 QWDFGNTWCQLLTGLTYFGFFS 107

RESULT 7
Q9UN27
ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
DE CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RRL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RRL EMBL; AF161914; AAD47671.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHHODPSN.
DR PROSITE; PS0237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SEQUENCE 339 AA; 39086 MW; 86AD8B44E2CB4EC2 CRC64;
Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps

OY 1 QWDFGNTWCQLLTGLTYFGFFS 22
|||||
Db 86 QWDFGNTWCQLLTGLTYFGFFS 107
|||||

RESULT 8
Q9UN27
ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
DE CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RRL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RRL EMBL; AF161915; AAD47672.1; -
DR EMBL; AF161909; AAD47666.1; -
DR EMBL; AF161910; AAD47667.1; -
DR EMBL; AF161911; AAD47668.1; -
DR EMBL; AF161912; AAD47669.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.

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DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F47 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFGFFS 107

RESULT 9
Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AADA7670.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFGFFS 107

RESULT 10
Q9TQW0 PRELIMINARY; PRT; 339 AA.
AC Q9TQW0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
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DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AADA7779.1; -.
DR EMBL; AF161889; AADA7646.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAF2614D35C CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFGFFS 107

RESULT 11
Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AADA7644.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39075 MW; 09257F8B834C4AE CRC64;
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Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
|||
Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

RESULT 12
Q9TUT8 PRELIMINARY; PRT; 339 AA.
ID Q9TUT8
AC Q9TUT8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47651.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39079 MW; 44A79753DA2F7AAF CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
|||
Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

RESULT 13
Q9TUT4 PRELIMINARY; PRT; 339 AA.
ID Q9TUT4
AC Q9TUT4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47734.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39092 MW; 84B51B9548E0703C CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
|||
Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

RESULT 14
Q9TUT9 PRELIMINARY; PRT; 339 AA.
ID Q9TUT9
AC Q9TUT9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161890; AAD47647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39024 MW; EC4CE48DEEF107E CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
|||
Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

RESULT 15
Q9TUT8 PRELIMINARY; PRT; 339 AA.
ID Q9TUT8
AC Q9TUT8

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Cercopithecus diana (Diana monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=36224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161949; AAD47705.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 339
 FT NON_TER 339 AA; 39049 MW; 6DIA93F6270F3ED CRC64;
 SQ SEQUENCE 339 AA; 39049 MW; 6DIA93F6270F3ED CRC64;
 Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCOLLTGLYFIIGFFS 22
 Db 86 QWDFGNTMCOLLTGLYFIIGFFS 107
 [1]
 RESULT 16
 Q9TQW4 PRELIMINARY; PRT; 339 AA.
 AC Q9TQW4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161903; AAD47660.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 339
 FT NON_TER 339 AA; 39159 MW; 8E699E882BAC0E84 CRC64;
 SQ SEQUENCE 339 AA; 39159 MW; 8E699E882BAC0E84 CRC64;
 Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCOLLTGLYFIIGFFS 22
 Db 86 QWDFGNTMCOLLTGLYFIIGFFS 107
 [1]
 RESULT 17
 Q9TQW4 PRELIMINARY; PRT; 339 AA.
 AC Q9TQW4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161903; AAD47660.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 339
 FT NON_TER 339 AA; 39159 MW; 8E699E882BAC0E84 CRC64;
 SQ SEQUENCE 339 AA; 39159 MW; 8E699E882BAC0E84 CRC64;
 Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCOLLTGLYFIIGFFS 22
 Db 86 QWDFGNTMCOLLTGLYFIIGFFS 107
 [1]
 RESULT 18
 Q9TQW4 PRELIMINARY; PRT; 339 AA.
 AC Q9TQW4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Cercopithecus nictitans (white-nosed guenon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=36228;
 RN [1]

[1]
SEQUENCE FROM N.A.
RP Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -
DR EMBL; AF162042; AAD47797.1; -
DR EMBL; AF162044; AAD47799.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39150 MW; 847592B03E5E2 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107
|||||
[1]
SEQUENCE FROM N.A.
RP Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -
DR EMBL; AF162042; AAD47797.1; -
DR EMBL; AF162044; AAD47799.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39150 MW; 847592B03E5E2 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107
|||||
[1]
SEQUENCE FROM N.A.
RP Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -
DR EMBL; AF162042; AAD47797.1; -
DR EMBL; AF162044; AAD47799.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39121 MW; AFB6E3EE4D6D3484 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107
|||||
[1]
SEQUENCE FROM N.A.
RP Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162015; AAD47770.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39063 MW; 78BCE7A84B877085 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107
|||||
[1]
SEQUENCE FROM N.A.
RP Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162015; AAD47770.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39063 MW; 78BCE7A84B877085 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107
|||||
[1]
SEQUENCE FROM N.A.
RP Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162015; AAD47770.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39063 MW; 78BCE7A84B877085 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107
|||||
[1]
SEQUENCE FROM N.A.
RP Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162015; AAD47770.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39063 MW; 78BCE7A84B877085 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IP0000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39097 MW; C576B7AA92D7080 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 22
Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF161972; AAD4727.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IP0000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39067 MW; 5BFCB5BA96C2F9E CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 23
Q9TSN2 PRELIMINARY; PRT; 339 AA.
AC Q9TSN2
DT 01-MAY-2000 (TRENBLrel. 13, Created)

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DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF161953; AAD4709.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IP0000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39137 MW; 9E626ED3288607C1 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 24
Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopitheidae.
OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF162026; AAD4781.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IP0000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 1

```


	Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Pan.
OC	NCSI_TaxID=9598;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agly M.,
RA	Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT	"Sequences of the CCR5 genes from diverse simian and prosimian
RT	species.";
RL	Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF161900; AAC47657.1; -
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin.. . ; IEA.
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRRHODPSN.
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW	Receptor.
FT	NON_TER
FT	NON_TER
SQ	SEQUENCE 339 AA; 39103 MW; 4038C13D024CSA4 CRC64;
	Query Match 100.0%; Score 126; DB 6; Length 339;
	Best Local Similarity 100.0%; Pred. No. 3.1e-11;
	Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 QWDFGNMTCOLLTGLTYFGFFS 22
Db	86 QWDFGNMTCOLLTGLTYFGFFS 107
RESULT 27	
QSTUO9	PRELIMINARY; PRT; 339 AA.
ID	Q9TUO9
AC	Q9TUO9;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	C-C chemokine receptor 5 (Fragment).
CN	CCR5.
OS	Cercopithecus mona.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciae;
OC	Cercopitheciae; Cercopitheciae.
OX	NCSI_TaxID=36226;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agly M.,
RA	Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT	"Sequences of the CCR5 genes from diverse simian and prosimian
RT	species.";
RL	Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF162041; AAC47796.1; -
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin.. . ; IEA.
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRRHODPSN.
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW	Receptor.
FT	NON_TER
FT	NON_TER
SQ	SEQUENCE 339 AA; 39168 MW; 6A4BF72FBF566F CRC64;
	Query Match 100.0%; Score 126; DB 6; Length 339;
	Best Local Similarity 100.0%; Pred. No. 3.1e-11;
	Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 QWDFGNMTCOLLTGLTYFGFFS 22
Db	86 QWDFGNMTCOLLTGLTYFGFFS 107
RESULT 26	
Q9TUW6	PRELIMINARY; PRT; 339 AA.
ID	Q9TUW6
AC	Q9TUW6;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	C-C chemokine receptor 5 (fragment).
CN	CCR5.
OS	Fan troglodytes (Chimpanzee).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 28

Q9TSN3 PRELIMINARY; PRT; 339 AA.
 AC Q9TSN3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161951; AAD47707.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PS00237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39098 MW; F01328B0C44EF829 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 29

Q9TUU7 PRELIMINARY; PRT; 339 AA.
 AC Q9TUU7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Macaca fuscata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161955; AAD47711.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PS00237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 30

Q9TVQV PRELIMINARY; PRT; 339 AA.
 AC Q9TVQV;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Papio papio (Guinea baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OX NCBI_TaxID=100937;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161989; AAD47744.1; -.
 DR EMBL; AF161988; AAD47743.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PS00237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39113 MW; 7F9803EAO50AF9ED CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 31

Q9TOU5 PRELIMINARY; PRT; 339 AA.
 ID Q9TOU5
 AC Q9TOU5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162046; AAD47801.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39178 MW; 847F8F936B00E6E2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 126; DB 6; Length 339;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTWCQLLTGLYFIFGFS 22
Db 86 QWDFGNTWCQLLTGLYFIFGFS 107

RESULT 32
Q9TUS7 PRELIMINARY; PRT; 339 AA.
ID Q9TUS7
AC Q9TUS7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161935; AAD47750.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39178 MW; 847F8F936B00E6E2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 126; DB 6; Length 339;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTWCQLLTGLYFIFGFS 22
Db 86 QWDFGNTWCQLLTGLYFIFGFS 107

RESULT 33
Q9TUS7 PRELIMINARY; PRT; 339 AA.
ID Q9TUS7
AC Q9TUS7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161899; AAD47656.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39157 MW; 4A9EBAD183E8E72D CRC64;

Query Match
Best Local Similarity 100.0%; Score 126; DB 6; Length 339;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTWCQLLTGLYFIFGFS 22
Db 86 QWDFGNTWCQLLTGLYFIFGFS 107

RESULT 34
Q9TUS7 PRELIMINARY; PRT; 339 AA.
ID Q9TUS7
AC Q9TUS7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
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RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161908; AAD47665.1; -.
 DR GO; GO:0015021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39103 MW; 4350C4625FB0657C CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
 |||||
 DB 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 35

ID Q9TUS5 PRELIMINARY; PRT; 339 AA.
 AC Q9TUS5;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Papio papio (Guinea baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Papio.
 OC NCBI_TaxID=100937;
 RN [1]
 SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RA "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161997; AAD47752.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39028 MW; 8C9C978FD80B936 CRC64;

Query Match. 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
 |||||
 DB 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 36

ID Q9TUU0 PRELIMINARY; PRT; 339 AA.
 AC Q9TUU0;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OC NCBI_TaxID=9544;
 RN [1]
 SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RA "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161970; AAD47725.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39155 MW; 3D1B5039B9E24C82 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
 |||||
 DB 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 37
 Q9TQV2 PRELIMINARY; PRT; 339 AA.
 AC Q9TQV2;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Papio papio (Guinea baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Papio.
 OC NCBI_TaxID=100937;
 RN [1]
 SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RA "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161993; AAD47748.1; -.
 DR EMBL; AF161987; AAD47742.1; -.
 DR EMBL; AF161990; AAD47745.1; -.
 DR EMBL; AF161991; AAD47746.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
 |||||
 DB 86 QWDFGNTMCQLLTGLYFIFGFS 107

```
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39079 MW; 7176E3EA0E00F3ED CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIIGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIIGFFS 107

RESULT 38
Q9TUQ3 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus mona.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
CX NCBI_TaxID=36226;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162040; AAD47795.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39079 MW; 7176E3EA0E00F3ED CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIIGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIIGFFS 107

RESULT 39
Q9TUQ8 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
CX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162045; AAD47800.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39148 MW; 0CA289CDDDEDE831 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIIGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIIGFFS 107

RESULT 40
Q9TUW2 PRELIMINARY; PRT; 339 AA.
AC Q9TUW2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pongo.
CX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161907; AAD47664.1; -.
DR EMBL; AF161906; AAD47663.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39117 MW; 4C4E35625BDS4E9C CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
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Best Local Similarity 100.0%; Pred. No. 3.le-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

Search completed: September 28, 2004, 09:06:18
Job time : 36.2 secs

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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:51:21 ; Search time 42.975 Seconds
(without alignments)
118.345 Million cell updates/sec

Title: US-10-084-813-13

Perfect score: 96

Sequence: 1 SQYQFWKQFQTLKIVILG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: Geneseqp29Jan04:*
 - 2: Geneseqp1980s:*
 - 3: Geneseqp1990s:*
 - 4: Geneseqp2000s:*
 - 5: Geneseqp2001s:*
 - 6: Geneseqp2002s:*
 - 7: Geneseqp2003as:*
 - 8: Geneseqp2003bs:*
 - 9: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	4	AAB88954
2	96	100.0	18	4	AAB88954
3	96	100.0	352	2	AAW27407 Human CCR
4	96	100.0	352	2	AAW27123 Human che
5	96	100.0	352	2	AAW07602 Human G-P
6	96	100.0	352	2	AAW23835 Human CC
7	96	100.0	352	2	AAW88232 HIV-1 co-
8	96	100.0	352	3	AAW80128 Human G-P
9	96	100.0	352	4	AAW79089 Amino aci
10	96	100.0	352	4	AAE07045 Human G-P
11	96	100.0	352	4	AAE07048 Human G-P
12	96	100.0	352	4	AAW80111 Human CCR
13	96	100.0	352	4	AAE04321 Human che
14	96	100.0	352	4	AAE07037 Human G-P
15	96	100.0	352	4	AAE07039 Human G-P
16	96	100.0	352	4	AAW46858 Human HDG
17	96	100.0	352	4	ABW56342 Non-endog
18	96	100.0	352	4	AAW83354 Human CCR
19	96	100.0	352	4	AAW82948 Human HIV
20	96	100.0	352	5	AAU97150 Human G-P
21	96	100.0	352	5	AAU97152 Human CCR
22	96	100.0	352	5	AAW52829 Human CCR
23	96	100.0	352	5	AAW52828 Human CC
24	96	100.0	352	5	ABG70597 Human G-P
25	96	100.0	352	5	ABG92883 Human imm

ALIGNMENTS

RESULT 1

AAE88954

ID AAB88954 standard; peptide; 18 AA.

XX AAB88954;

XX DT 23-MAY-2001 (first entry)

XX DE HIV gp120 protein binding peptide #47.

XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Homo sapiens.
XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US023505.
XX PR 27-AUG-1999; 99US-0151270P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PA Saxinger C;
XX PI WPI; 2001-244398/25.
XX DR Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions.
XX PS Example 1; Page 37; 114pp; English.
XX CC The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus.
XX CC The present sequence is an example of a peptide of the invention

SQ Sequence 18 AA;

Query Match 100.0%; Score 96; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKQFQTLKIVILG 18

```

Db      1  SOYQFWKMFQTLKIVILG 18
|||||
RESULT 2
ID      AAB88995
XX      AAB88995 standard; peptide; 18 AA.
AC      AAB88995;
XX      23-MAY-2001 (first entry)
XX      HIV gp120 protein binding peptide #88.
DE      Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW      replication; CCR5; CXCR4; CD4; STRL33.
XX      OS Homo sapiens.
XX      WO200116182-A2.
FN      08-MAR-2001.
XX      25-AUG-2000; 2000WO-US023505.
XX      27-AUG-1999; 99US-0151270P.
XX      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA      Saxinger C;
PI      WPI; 2001-244398/25.
XX      Novel polypeptides useful for treating HIV infection, have homology to
PT      regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT      and binds to HIV gp120 under physiological conditions.
XX      Claim 21; Page 38; 114pp; English.
XX      The present invention describes a number of peptides which are able to
CC      bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC      chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC      useful in the treatment of HIV, as they prevent replication of the virus.
CC      The present sequence is an example of a peptide of the invention
XX      Sequence 18 AA;
SQ      Query Match 100.0%; Score 96; DB 4; Length 18;
        Best Local Similarity 100.0%; Pred. No. 4.2e-08;
        Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SOYQFWKMFQTLKIVILG 18
Db      1  SOYQFWKMFQTLKIVILG 18
|||||
RESULT 3
ID      AAW27407
XX      AAW27407 standard; protein; 352 AA.
AC      AAW27407;
XX      14-APR-1998 (first entry)
XX      Human CCR5.
DE      Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
KW      type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
KW      inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
KW      idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
KW      atherosclerosis; autoimmune disorder.
XX      OS Homo sapiens.

Db      1  SOYQFWKMFQTLKIVILG 18
|||||
RESULT 4
ID      AAW27123
XX      AAW27123 standard; protein; 352 AA.
AC      AAW27123;
XX      14-DEC-1997 (first entry)
XX      Human chemokine receptor 88C.
DE      Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
KW      asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
KW      diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
KW      modulator; antibody; human.
XX      OS Homo sapiens.
XX      Key Location/Qualifiers
FH      Domain 1..32
FT      /label= Extracellular_domain
FT      Domain 56..67
FT      /label= Intracellular_domain
FT      Domain 89..112
FT      /label= Extracellular_domain
FT      Domain 125..145
FT      /label= Extracellular_domain
FT      Domain 166..191
FT      /label= Extracellular_domain

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XX      WO9732019-A2.
XX      04-SEP-1997.
XX      28-FEB-1997; 97WO-BE0000023.
XX      01-MAR-1996; 96EP-00870021.
XX      06-AUG-1996; 96EP-00870102.
XX      (EURO-) EUROSCREEN SA.
XX      Samson M, Parmentier M, Vassart G, Libert F;
PI      WPI; 1997-479829/44.
DR      N-PSDB; AAT90117.
XX      Active and inactive forms of human CC chemokine receptor CCR-5 - useful
PT      to diagnose, prevent and/or treat inflammatory disorders, autoimmune
PT      disease and viral infection.
XX      Claim 4; Fig 1b-c; 94pp; English.
XX      The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
CC      which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but
CC      not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,
CC      interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
CC      chemokines. Active CCR-5 is also a receptor of human immunodeficiency
CC      virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its CDNA can be used to
CC      diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
CC      arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
CC      psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
CC      atherosclerosis and autoimmune disorders
XX      Sequence 352 AA;
SQ      Query Match 100.0%; Score 96; DB 2; Length 352;
        Best Local Similarity 100.0%; Pred. No. 8.9e-07;
        Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SOYQFWKMFQTLKIVILG 18
Db      185  SOYQFWKMFQTLKIVILG 202
|||||
RESULT 4
ID      AAW27123
XX      AAW27123 standard; protein; 352 AA.
AC      AAW27123;
XX      14-DEC-1997 (first entry)
XX      Human chemokine receptor 88C.
DE      Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
KW      asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
KW      diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
KW      modulator; antibody; human.
XX      OS Homo sapiens.
XX      Key Location/Qualifiers
FH      Domain 1..32
FT      /label= Extracellular_domain
FT      Domain 56..67
FT      /label= Intracellular_domain
FT      Domain 89..112
FT      /label= Extracellular_domain
FT      Domain 125..145
FT      /label= Extracellular_domain
FT      Domain 166..191
FT      /label= Extracellular_domain

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FT	Domain	213..235	
FT	FT	/label= Intracellular_domain	
FT	Domain	259..280	
FT	FT	/label= Extracellular_domain	
FT	Domain	301..352	
FT	FT	/label= Intracellular_domain	
XX	WO9722698-A2.		
XX	XX		
XX	26-JUN-1997.		
XX	XX		
XX	20-DEC-1996;	96WO-US020759.	
XX	XX		
XX	20-DEC-1995;	95US-00575967.	
PR	07-JUN-1996;	96US-00661393.	
XX	XX		
XX	(ICOS-) ICOS CORP.		
XX	XX		
PI	Gray PW, Schweickart VL, Raport CJ;		
XX	XX		
DR	WPI; 1997-341689/31.		
DR	N-PSDB; AAT85161.		
XX	XX		
PT	New nucleic acid encoding chemokine receptors 88-2B and 88C - used to		
PT	modulate leukocyte trafficking, e.g. for treatment of inflammation,		
PT	tumours, viral infections, auto-immune diseases, etc.		
XX	XX		
PS	Claim 16; Page 47-48; 65pp; English.		
XX	XX		
CC	This polypeptide sequence comprises novel human chemokine receptor 88C, a		
CC	G protein coupled receptor that is involved in leukocyte trafficking. Its		
CC	amino sequence was deduced from a cDNA clone (AAT85161) isolated from a		
CC	macrophage library. It shows 62% identity to CCKAR1. Chemokine receptor		
CC	88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors		
CC	and their polypeptide fragments can be produced in transformed host		
CC	cells. The receptors, peptides comprising one or more of the		
CC	extracellular or intracellular domains, and anti-receptor antibodies can		
CC	be used to modulate receptor activities, particularly ligand and G		
CC	protein binding, and are potentially potentially useful in the treatment		
CC	of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral		
CC	infection, AIDS, inflammatory conditions, pathological immune response,		
XX	abnormal haematopoietic processes etc		
XX	XX		
SQ	Sequence 352 AA;		
	Query Match	100.0%; Score 96; DB 2; Length 352;	
	Best Local Similarity	100.0%; Pred. No. 8.9e-07;	
	Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 SQYQFWKNFQTLKIVILG 18		
Db	185 SQYQFWKNFQTLKIVILG 202		
RESULT 5			
AAW07602			
ID	AAW07602 standard; protein; 352 AA.		
XX	XX		
AC	AAW07602;		
XX	XX		
DT	26-FEB-1997 (first entry)		
XX	XX		
DE	Human G-protein chemokine receptor HDGNR10.		
XX	XX		
KW	G-protein chemokine receptor; HDGNR10; signal transduction;		
KW	haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;		
KW	therapy.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
FN	WO9639437-A1.		
XX	XX		
PD	12-DEC-1996.		

XX	06-JUN-1995;	95WO-US007173.	
PF			
XX	06-JUN-1995;	95WO-US007173.	
PR			
XX			
XX	(HUMA-) HUMAN GENOME SCI INC.		
PA			
XX			
XX	Li Y, Ruben SM;		
PI			
XX			
DR	WPI; 1997-043072/04.		
XX	N-PSDB; AAT44042.		
XX			
PT	Human G-protein chemokine receptor, HDGNR10 - useful to identify		
PT	(ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and		
PT	acute inflammation, rheumatoid arthritis, etc.		
XX			
XX	Claim 1; Page 44-46; 61pp; English.		
PS			
XX			
CC	Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7		
CC	transmembrane protein involved in signal transduction. Its amino acid		
CC	sequence was deduced from a cDNA clone (AA744042) isolated from a human		
CC	monocyte library. Isolation of the cDNA allows prodn. of recombinant		
CC	HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant		
CC	receptor can be used to identify agonists or antagonists of the receptor;		
CC	such cpds. can be used to treat conditions related to the under- and over		
CC	-expression of G-protein chemokine receptors		
XX			
XX	Sequence 352 AA;		
SQ			

XX
PF 06-JUN-1995; 95WO-US007173.

XX
PF 06-JUN-1995; 95WO-US007173.

FT Region 261..276
 FT /note= "extracellular loop-3 (Claim 19)"
 FT Domain 277..300
 FT /label= VII
 FT /note= "transmembrane domain"
 XX
 PN WO9745543-A2.
 XX
 PD 04-DEC-1997.
 XX
 XX 28-MAY-1997; 97WO-US009586.
 PF 28-MAY-1996; 96US-0018508P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
 PI Broder CC, Kennedy PE;
 XX WPI; 1998-032650/03.
 DR N-PSDB; AAT76920.
 XX
 XX CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
 PT between HIV and a target cell.
 XX Claim 68; Fig 1C; 70pp; English.
 PS
 XX This protein sequence comprises of a novel human macrophage-selective CC
 CC chemokine receptor that has been designated CCR5. The sequence was
 CC deduced from an isolated cDNA clone (see AAT76920). An Alai27Leu variant
 CC (see W238340 of CCR5 was also identified. The susceptibility of human
 CC macrophages to HIV infection depends on cell surface expression of CD4
 CC and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
 CC protein coupled cell surface molecules. It plays an essential role in the
 CC membrane fusion step of infection by some HIV isolates. The establishment
 CC of stable, non-human cell lines and transgenic mammals having cells that
 CC coexpress human CD4 and CCR5 provides valuable tools for research of HIV
 CC infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
 CC agents capable of blocking membrane fusion between HIV and target cells
 CC represent potential anti-HIV therapeutics for macrophage tropic strains
 CC of HIV
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No; 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SOYQFWKMFQTLKIVILG 18
 |||||
 Db 185 SOYQFWKMFQTLKIVILG 202
 RESULT 7
 AAW88232
 ID AAW88232 standard; protein; 352 AA.
 XX
 AC AAW88232;
 XX
 XX 15-MAR-1999 (first entry)
 DT
 XX HIV-1 co-receptor CCR5.
 DE
 XX HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
 KW gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 32..56
 FT /note= "transmembrane domain 1"
 FT Domain 67..87
 FT /note= "transmembrane domain 2"
 FT

FT Misc-difference 101
 FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA
 FT (Stop) in CCR5m303"
 FT Domain 103..124
 FT /note= "transmembrane domain 3"
 FT Domain 142..167
 FT /note= "transmembrane domain 4"
 FT Domain 200..223
 FT /note= "transmembrane domain 5"
 FT Domain 236..260
 FT /note= "transmembrane domain 6"
 FT Domain 275..301
 FT /note= "transmembrane domain 7"
 XX
 PN WO9854317-A1.
 XX
 XX 03-DEC-1998.
 PD
 XX 29-MAY-1998; 98WO-EP003437.
 PF
 XX 30-MAY-1997; 97US-0048057P.
 PR
 XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
 PA Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
 PI WPI; 1999-059835/05.
 DR N-PSDB; AAW84126.
 XX
 XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 PT resistance of CCR5-expressing cells to HIV-1 infection.
 XX Disclosure; Page 34-35; 55pp; English.
 PS
 XX This is the amino acid sequence of wild-type human CCR5, which serves as
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of
 CC HIV-1. The invention relates to the identification of a CCR5 variant (see
 CC AAW8231), designated CCR5m303, comprising the first two transmembrane
 CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
 CC presence of the CCR5m303 variant with the wild type CCR5 allele shows a
 CC positive correlation with resistance to infection with M-tropic HIV-1
 CC strains, and may indicate slower progression of the disease. The
 CC detection of CCR5 variants may be used to identify individuals at lower
 CC risk of infection relative to the general population who, if infected,
 CC may exhibit slower progression to AIDS. Probes and primers (see AAW8412-
 CC 36) are provided for use in diagnostic methods for detecting the presence
 CC of such variants. A method is provided for inhibiting HIV-1 infection of
 CC a cell expressing the CCR5 receptor. This involves introducing a nucleic
 CC acid encoding a CCR5 variant into the cell, thereby reducing the number
 CC of functional CCR5 molecules present on the cell surface
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No; 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SOYQFWKMFQTLKIVILG 18
 |||||
 Db 185 SOYQFWKMFQTLKIVILG 202
 RESULT 8
 AAY80128
 ID AAY80128 standard; protein; 352 AA.
 XX
 AC AAY80128;
 XX
 XX 19-MAY-2000 (first entry)
 DT
 XX Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
 DE
 XX Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;
 KW

KW diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
 KW tumour; infection; leukaemia; psoriasis; allergy;
 KW T-cell mediated autoimmune disease; atherogenesis; anaphylaxis;
 KW inflammation; allergic reaction; silicosis; sarcoidosis;
 KW rheumatoid arthritis; hyper-eosinophilia syndrome.
 XX
 OS Homo sapiens.
 XX
 PN US6025154-A.
 XX
 XX 15-FEB-2000.
 XX
 XX 06-JUN-1995; 95US-00466343.
 XX
 XX 06-JUN-1995; 95US-00466343.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Li Y, Ruben SM;
 XX WPI; 2000-181807/16.
 XX N-PSDB; AAZ91481.
 XX
 XX Isolated nucleic acid encoding human G-protein chemokine receptor useful
 XX for diagnostic assays, scientific research and screening for compounds
 XX which bind to and activate or inhibit activation of the receptor
 XX polypeptides.
 XX
 XX Claim 1; Fig 1; 22pp; English.
 XX
 XX The present sequence represents a human G-protein chemokine receptor
 XX designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
 XX screening for compounds which bind to and either: (1) activate the
 XX HDGNR10 polypeptides causing stimulation of haematopoiesis, wound
 XX healing, coagulation, and angiogenesis; treatment of solid tumours,
 XX chronic infections, leukaemia, T-cell mediated autoimmune diseases,
 XX parasitic infections, psoriasis, and to stimulate growth factor activity;
 XX or (2) inhibit activation of the HDGNR10 polypeptides which is useful for
 XX preventing and/or treating allergy, atherogenesis, anaphylaxis,
 XX malignancy, chronic and acute inflammation, histamine and immunoglobulin
 XX E-mediated allergic reactions, prostaglandin-independent fever, bone
 XX marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
 XX hyper-eosinophilia syndrome. The polynucleotides are also useful for
 XX diagnostic assays for detecting diseases related to mutations in the
 XX nucleic acid sequences encoding the polypeptides and for detecting an
 XX altered level of the soluble form of the receptor polypeptides. The
 XX polynucleotides are also useful for in vitro purposes related to
 XX scientific research, synthesis of DNA and manufacture of DNA vectors
 XX
 XX Sequence 352 AA;
 XX
 XX Query Match 100.0%; Score 96; DB 3; Length 352;
 XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 SQYQFWKNFQTLKIVILG 18
 XX |||||
 XX 185 SQYQFWKNFQTLKIVILG 202
 XX
 XX
 XX RESULT 9
 XX AAG79089
 XX ID AAG79089 standard; protein; 352 AA.
 XX AC AAG79089;
 XX 10-DEC-2001 (first entry)
 XX
 XX Amino acid sequence of human CCR5 protein.
 XX
 XX Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
 KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
 XX

OS Homo sapiens.
 XX WO200164752-A2.
 XX
 XX 07-SEP-2001.
 XX
 XX 28-FEB-2001; 2001WO-US006322.
 XX
 XX 02-MAR-2000; 2000US-00517605.
 XX
 XX (UYNY) UNIV NEW YORK STATE.
 XX (UYNI-) UNIV NIJMEGEN.
 XX
 XX Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
 XX WPI; 2001-602565/68.
 XX
 XX An antibody for the treatment or prevention of HIV-infection comprises a
 XX gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of
 XX DC-SIGN due to concomitant conformational change.
 XX
 XX Disclosure; Page 118-119; 131pp; English.
 XX
 XX The specification describes an antibody which is specific for an
 XX antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
 XX is exposed upon gp120 binding of DC-SIGN due to concomitant
 XX conformational change. DC-SIGN is a receptor that is specifically
 XX expressed on dendritic cells and facilitates infection of T lymphocytes
 XX with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
 XX -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
 XX with high affinity. The antibody of the invention inhibits the trans
 XX enhancement of HIV entry into a T cell or macrophage facilitated by
 XX dendritic cells. The antibody is useful to treat or prevent HIV
 XX infection. The present sequence represents a human CCR5 protein, which is
 XX a translocation promoting agent that interacts with CD4. This receptor
 XX functions in HIV-1 entry into cells
 XX
 XX Sequence 352 AA;
 XX
 XX Query Match 100.0%; Score 96; DB 4; Length 352;
 XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 SQYQFWKNFQTLKIVILG 18
 XX |||||
 XX 185 SQYQFWKNFQTLKIVILG 202
 XX
 XX
 XX RESULT 10
 XX AAE07046
 XX ID AAE07046 standard; protein; 352 AA.
 XX AC AAE07046;
 XX 16-OCT-2001 (first entry)
 XX
 XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
 XX
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 XX Homo sapiens.
 XX
 XX OS
 XX
 XX FH Key Location/Qualifiers
 XX Domain 1..36
 XX FT /label= Extracellular_domain

Domain 37..305
/label= Transmembrane_domain
Domain 37..58
/label= Transmembrane_domain
/note= "Segment 1"
Domain 59..67
/label= Intracellular_loop_1
Domain 68..88
/label= Transmembrane_domain
/note= "Segment 2"
Domain 89..102
/label= Extracellular_loop_1
Domain 103..124
/label= Transmembrane_domain
/note= "Segment 3"
Domain 125..141
/label= Intracellular_loop_2
Domain 142..166
/label= Transmembrane_domain
/note= "Segment 4"
Domain 167..195
/label= Extracellular_loop_2
Domain 196..223
/label= Transmembrane_domain
/note= "Segment 5"
Domain 224..235
/label= Intracellular_loop_3
Domain 236..260
/label= Transmembrane_domain
/note= "Segment 6"
Domain 261..274
/label= Extracellular_loop_3
Domain 287..305
/label= Transmembrane_domain
/note= "Segment 7"
Domain 306..352
/label= Intracellular_domain

WO200158916-A2.
16-AUG-2001.
09-FEB-2001; 2001WO-US004153.
09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Roschke V, Li Y, Ruben SM;
WPI; 2001-488966/53.
N-PSDB; AAD13282.

Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

Claim 102; Fig 1; 518pp; English.
The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack

of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemias) and wound healing. The present sequence is human CCR5 HDGNR10 protein

XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKMFQTLKIVILG 18
DB 185 SOYQFWKMFQTLKIVILG 202

RESULT 11

AAE07048
ID AAE07048 standard; protein; 352 AA.

XX AAE07048;

XX 16-OCT-2001 (first entry)

XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
XX human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
XX cytostatic; immunosuppressive; neutropenic; neuroprotective; gene therapy;
XX neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
XX rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
XX gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
XX haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
XX multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
XX cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX WO200158916-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004153.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;
XX WPI; 2001-488966/53.
XX N-PSDB; AAD13299.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

XX Example 40; Page 504-505; 518pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder

CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC disease or disorder may be associated with aberrant CCR5 expression, lack
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGMR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGMR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGMR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The
 CC present sequence is human CCR5 HDGMR10 protein
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
 DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 12
 AAG80111
 ID AAG80111 standard; protein; 352 AA.

AC AAG80111;

DT 17-JAN-2002 (first entry)

DE Human CCR5 protein.

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.

OS Homo sapiens.

PN WO200172830-A2.

XX 04-OCT-2001.

XX 02-APR-2001; 2001WO-EP003708.

XX 31-MAR-2000; 2000DE-01016013.

XX (IFPP-) IPF PHARM GMBH.

XX (FORS/) FORSMANN U.

PI Forssmann W, Adermann K, Heitland A, Spodsborg N;

XX WPI; 2001-626256/72.

XX Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.

PS Disclosure; Page 10; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in

CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation) or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
 DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 13

AAG804321
 ID AAG804321 standard; protein; 352 AA.

XX AAG804321;

XX 04-SEP-2001 (first entry)

DE Human chemokine receptor (CKR), CC-CKR-5 related protein #2.

XX Human; transformed mammalian cell; CD4; reporter gene; translocation;
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
 KW chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor;
 KW CC-CKR-5; envelope glycoprotein; anti-HIV.

OS Homo sapiens.

PN US6258527-B1.

XX 10-JUL-2001.

XX 21-MAY-1997; 97US-00861105.

XX 20-MAY-1996; 96US-0017157P.

XX 19-JUN-1996; 96US-0020043P.

XX 19-MAY-1997; 97US-00858660.

XX (AARO-) AARON DIAMOND AIDS RES CENT.

XX (UANY) UNIV NEW YORK STATE.

XX Littman DR, Deng H, Elmeier W, Landau NR, Liu R;

XX WPI; 2001-417127/44.

XX DR N-PSDB; AAD08577.

XX Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
 PT and HIV LTR for identification of drugs and antibodies for treatment of
 PT HIV.

PS Disclosure; Col 47-50; 37pp; English.

XX The present invention relates to a transformed mammalian cell that
 CC contains a gene encoding CD4, a construct encoding a reporter gene under
 CC the regulation of an human immuno deficiency virus (HIV) long terminal
 CC repeat (LTR) and that has been transduced with a vector encoding a human
 CC chemokine receptor (CKR) where the CD4 and the CKR are present on the
 CC cell surface of transformed mammalian cell. The invention is useful for

CC identifying drugs or antibodies that interfere with the translocation of
 CC HIV into transformed mammalian cell or for identifying a human chemokine
 CC receptor that facilitates the infection of a particular HIV strain into
 CC the transformed mammalian cell. Compounds identified can be used to treat
 CC cellular dysfunction and to prevent or combat HIV infection. The present
 CC sequence is a human chemokine receptor (CCR), CC-CCR-5 related protein.
 CC CC-CCR-5 is the principal cofactor for entry, mediated by the envelope
 CC glycoproteins of primary macrophage-tropic strains of HIV-1
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
 |||||
 Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 14
 ID AAE07037 standard; protein; 352 AA.
 AC AAE07037;

DT 16-OCT-2001 (first entry)
 XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
 DE
 XX

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 OS Homo sapiens.

EH Key Location/Qualifiers
 FT Domain 1..36 /label= Extracellular_domain
 FT Domain 37..305 /label= Transmembrane_domain
 FT Domain 37..58 /label= Transmembrane_domain
 FT /label= Transmembrane_domain
 FT /note= "Segment 1"
 FT Domain 59..67 /label= Intracellular_loop_1
 FT Domain 68..88 /label= Transmembrane_domain
 FT /label= Transmembrane_domain
 FT /note= "Segment 2"
 FT Domain 89..102 /label= Intracellular_loop_1
 FT Domain 103..124 /label= Transmembrane_domain
 FT /label= Transmembrane_domain
 FT /note= "Segment 3"
 FT Domain 125..141 /label= Intracellular_loop_2
 FT Domain 142..166 /label= Transmembrane_domain
 FT /label= Transmembrane_domain
 FT /note= "Segment 4"
 FT Domain 167..195 /label= Extracellular_loop_2
 FT Domain 196..223 /label= Transmembrane_domain
 FT /label= Transmembrane_domain
 FT /note= "Segment 5"
 FT Domain 224..235 /label= Intracellular_loop_3
 FT Domain 236..260

FT /label= Transmembrane_domain
 FT /note= "Segment 6"
 FT 261..274 /label= Extracellular_loop_3
 FT 287..305 /label= Transmembrane_domain
 FT /label= Transmembrane_domain
 FT /note= "Segment 7"
 FT 306..352 /label= Intracellular_domain
 FT

XX WO200158915-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004152.

XX 09-FEB-2000; 2000US-0181258P.

PR 09-MAR-2000; 2000US-0187999P.

PR 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

DR WPI; 2001-488965/53.

DR N-PSDB; AAD13181.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX
 XX Claim 102; Fig 1; 495pp; English.

XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5
 CC HDGNR10 antibodies are useful for treating, preventing or ameliorating a
 CC disease or disorder associated with inflammation, defective or aberrant
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen
 CC presenting cell interaction. The disease or disorder may also be an
 CC infectious disease (e.g. a viral infection such as an early stage HIV
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative
 CC disorder. The disease or disorder may be associated with aberrant CCR5
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or
 CC lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food
 CC additive or preservative to increase or decrease storage capabilities.
 CC CCR5 HDGNR10 DNA are useful for chromosome identification and in gene
 CC therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists
 CC are also useful in the diagnosis, treatment and prevention of cancer
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,
 CC liver, lung, urogenital); immune disorders (Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis); cardiovascular disorders (myocardial ischaemia) and wound
 CC healing
 XX

SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
 |||||
 Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 15
 AAE07039 standard; protein; 352 AA.
 ID AAE07039
 XX

AC AAE07039;
XX
DT 16-OCT-2001. (first entry)
XX
DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
XX
KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
KW cytosolic; immunosuppressive; nontropic; neuroprotective; gene therapy;
KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
KW cardiovascular disorder; myocardial ischaemia.
XX
OS Homo sapiens.
XX
FN WO200158915-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004152.
XX
PR 09-FEB-2000; 2000US-0181258P.
XX
PR 09-MAR-2000; 2000US-0187999P.
XX
PR 22-SEP-2000; 2000US-0234336P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Roschke V, Li Y, Ruben SM;
XX
XX WPI; 2001-488965/53.
XX
DR N-PSDB; AAD13198.
XX
XX Isolated nucleic acid encoding a human G-protein chemokine receptor
XX (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
XX diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
XX neurodegenerative disorders.
XX
XX Example 40; Page 486-487; 495pp; English.
XX
XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
XX protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or
XX ameliorating a disease or disorder associated with inflammation,
XX defective or aberrant chemotaxis of immune cells, HIV infection (such as
XX Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
XX aberrant T-cell antigen presenting cell interaction. The disease or
XX disorder may also be an infectious disease (e.g. a viral infection such
XX as an early stage HIV infection, a cytomegalovirus infection, or a
XX poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
XX a neurodegenerative disorder. The disease or disorder may be associated
XX with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
XX ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
XX is used as a food additive or preservative to increase or decrease
XX storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
XX identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
XX antibodies, agonists and antagonists are also useful in the diagnosis,
XX treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
XX bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
XX disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
XX autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
XX sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular
XX disorders (myocardial ischaemias) and wound healing

Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWNFQTLKIVILG 18
|||||

Db 185 SQYQFWNFQTLKIVILG 202
RESULT 16
AAB46858
ID AAB46858 standard; protein; 352 AA.
XX
AC AAB46858;
XX
XX 16-AUG-2001 (revised)
DT 02-AUG-2001 (revised)
DT 04-MAY-2001 (first entry)
XX
DE Human HDGNR10 protein.
XX
XX HDGNR10; human; G-protein chemokine receptor; antiinflammatory;
KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
KW cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;
KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
KW anaphylaxis; malignancy; inflammation; histamine; IGE; silicosis; shock;
KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
KW hyper-eosinophilic syndrome; vulnery.
XX
OS Homo sapiens.
XX
XX US2001000241-A1.
XX
XX 12-APR-2001.
XX
XX 29-NOV-2000; 2000US-00725285.
XX
XX 06-JUN-1995; 95US-00466343.
XX
XX 18-NOV-1998; 98US-00195662.
XX
XX 25-JUN-1999; 99US-00339912.
XX
XX (LIVY/) LI Y.
XX
XX (RUBE/) RUBEN S M.
XX
XX Li Y, Ruben SM;
XX
XX WPI; 2001-226317/23.
XX
XX N-PSDB; AAF26390.
XX
XX New human G-protein chemokine receptor polypeptides and polynucleotides,
XX useful for identifying (ant)agonists to the G-protein chemokine receptor.
XX
XX Claim 1a; Page 15; 22pp; English.
XX
XX This invention describes a novel receptor polypeptide (I) selected from
XX (i) a fully defined 329 amino acid sequence (ii) fully disclosed in the
XX specification; and (ii) a polypeptide encoded by the cDNA contained in a
XX plasmid, and fragments, analogs and derivatives of the polypeptide. The
XX products of the invention have antiinflammatory, immunomodulatory,
XX anticoagulant, antiallergic, immunosuppressive, vulnery, cytostatic,
XX antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic
XX activity and can be used for gene therapy. The G-protein chemokine
XX receptors, HDGNR10, (I) are useful for screening for compounds which
XX activate or inhibit activation of (I). The products of the invention can
XX also be used for stimulating haematopoiesis, wound healing, coagulation,
XX angiogenesis, treating solid tumours, chronic infections, leukemia, T-
XX cell mediated autoimmune diseases, parasitic infections, psoriasis, and
XX stimulating growth factor activity. HDGNR10 is useful for treating
XX allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
XX inflammation, histamine and immunoglobulin E (IGE)-mediated allergic
XX reactions, prostaglandin-independent fever, bone marrow failure,
XX silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
XX eosinophilic syndrome. (N.B. this record was resubmitted to correct
XX errors in the keyword formatting)
XX
XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
 |||||
 DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 17
 ABB56342
 ID ABB56342 standard; protein; 352 AA.
 AC ABB56342;
 XX
 DT 18-FEB-2002 (first entry)
 XX Non-endogenous human GPCR protein, SEQ ID NO: 477.
 DE Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 KW constitutively activated GPCR; agonist; disease.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200177172-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 05-APR-2001; 2001WO-US011098.
 XX
 PR 07-APR-2000; 2000US-0195747P.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Lehmann-Bruinsma K, Liaw CW, Lin I;
 XX
 DR WPI; 2001-648759/74.
 DR N-PSDB; ABI97978.
 XX
 PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with versions
 PT of GPCRs.
 PS Claim 1; Page 277-278; 394pp; English.
 XX
 CC The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous constitutively
 CC activated versions of known GPCRs are used in the invention for the
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists. Such agonists are useful as
 CC therapeutic agents for diseases or disorders associated with GPCRs. The
 CC present sequence is a non-endogenous version of a known human GPCR
 XX
 XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
 |||||
 DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 18
 AAB83354
 ID AAB83354 standard; protein; 352 AA.
 XX
 AC AAB83354;
 XX
 DT 09-OCT-2001 (first entry)

XX Human CCR5 protein sequence.
 DE
 XX Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
 KW human immunodeficiency virus; anti-inflammatory disease; human.
 XX
 OS Homo sapiens.
 XX
 PN EP1118858-A2.
 XX
 PD 25-JUL-2001.
 XX
 PF 03-JAN-2001; 2001EP-00300020.
 XX
 PR 12-JAN-2000; 2000GB-00000659.
 PR 12-JAN-2000; 2000GB-00000661.
 PR 12-JAN-2000; 2000GB-00000663.
 XX
 PA (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX
 PI Dobbs S, Perros M, Rickett GA;
 XX
 DR WPI; 2001-477088/52.
 DR N-PSDB; AAF87099.
 XX
 PT Determining if an agent can modulate CCR5-gp120 interaction, comprises
 PT incubating the agent with CCR5 and gp120 and determining if the agent
 PT modulates the interaction.
 XX
 XX Claim 1; Page 110; 113pp; English.
 XX
 CC This sequence represents the human CCR5 protein sequence. The invention
 CC relates to a method for determining whether an agent is capable of
 CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
 CC with gp120, comprising incubating the agent with CCR5 and gp120 and
 CC determining whether the agent modulates the interaction, where gp120 is
 CC associated with CD4, and where the interaction is a low affinity binding.
 CC The method is used to identify an agent capable of modulating the
 CC interaction of CCR5 with gp120. An agent identified by the method is used
 CC to prepare a pharmaceutical composition for the treatment of a disease or
 CC condition associated with CCR5 and gp120 interaction, to treat a subject
 CC with a disease or condition associated with CCR5 and gp120 interaction,
 CC and for preparing a pharmaceutical for treating human immunodeficiency
 CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
 CC is commercially useful, amenable to high throughput screening, and
 CC detects interaction of gp120 with cells expressing only CCR5
 XX
 XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
 |||||
 DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 19
 AAB82948
 ID AAB82948 standard; protein; 352 AA.
 XX
 AC AAB82948;
 XX
 DT 21-DEC-2001 (first entry)
 XX
 DE Human HIV-1 co-receptor CCR5.
 XX CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
 KW infection; therapy; vaccine; anti-HIV-1.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
FT Binding-site 2..18
FT /note= "binds to HIV-1 gp120"
XX
XX WO200164710-A2.
XX
XX 07-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US006699.
XX
XX 29-FEB-2000; 2000US-0185667P.
PR 19-MAY-2000; 2000US-0205839P.
PR 07-FEB-2001; 2001US-0267231P.
XX
XX (PROG-) PROGENICS PHARM INC.
XX (AARO-) AARON DIAMOND AIDS RES CENT.
XX
XX Dragic T, Olson WC;
XX WPI; 2001-611273/70.
DR N-PSDB; AAH26903.
XX
XX Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-
PT receptor) amino terminal domain including negatively charged and two
PT sulfated tyrosine residues is useful for treating HIV infection in
PT humans.
XX
XX Claim 1; Page 30; 163pp; English.
XX
XX The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids
CC 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding
CC site that determines the specificity of the interaction between CCR5 and
CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the
CC CCR5 N-terminus is required for gp120 binding and may critically modulate
CC the susceptibility of target cells to HIV-1 infection in vivo. The
CC invention provides claimed sulfated peptides (see AAB2347) that are
CC based on the CCR5 N-terminal region and which are effective for
CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed
CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+
CC cells from becoming infected with HIV, of treating a subject whose CD4+
CC cells are infected with HIV, and of identifying an agent which inhibits
CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried
CC out in a subject, especially a human, infected (therapeutic method), not
CC infected with HIV (prophylactic method), or in a subject who is not
CC infected with, but has been exposed to, HIV
XX
XX Sequence 352 AA;
SQ
Query Match 100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202
RESULT 20
AAU97150
ID AAU97150 standard; protein; 352 AA.
XX
XX AAU97150;
XX
XX 13-AUG-2002 (first entry)
XX
XX Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
XX
XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
XX immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
XX neurodegeneration; viral infection; Kaposi sarcoma; cancer;
XX hyperproliferative disease; neurological disease; receptor.
XX

OS Homo sapiens.
XX
XX US2002048786-A1.
XX
XX 25-APR-2002.
XX
XX 09-FEB-2001; 2001US-00779879.
XX
XX 09-FEB-2000; 2000US-0181258P.
PR 09-MAR-2000; 2000US-0187999P.
PR 22-SEP-2000; 2000US-0234336P.
XX
XX (ROSE/) ROSEN C A.
PA (ROSC/) ROSCHKE V.
PA (LIYY/) LI Y.
PA (RUBE/) RUBEN S M.
XX
XX Rosen CA, Roschke V, Li Y, Ruben SM;
PI WPI; 2002-434754/46.
XX N-PSDB; ABK51853.
DR
XX
XX New nucleic acid encoding an antibody specific for the G-protein
PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
PT inflammation.
XX
XX Claim 61; Fig 1; 180pp; English.
XX
XX The present invention relates to the isolation of a novel human G-protein
CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
CC sequences encoding it. The invention also describes antibodies that bind
CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide
CC sequences encoding the antibodies. The antibodies are useful for treating
CC or preventing inflammation, defective or aberrant chemotaxis of immune
CC cells and T-cell/antigen-presenting cell interactions, infections and
CC autoimmune diseases, Rheumatoid arthritis, neurodegeneration, viral
CC infections (especially early-stage human immune deficiency virus (HIV),
CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
CC associated with aberrant or deficient expression of the CCR5 receptor or
CC its ligands. The antibodies are also useful to determine CCR5 expression,
CC e.g. for diagnosis, prognosis and monitoring of cancer and other
CC hyperproliferative diseases. The polynucleotide sequences encoding human
CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
CC recombinant receptor, and in the treatment of a wide range of diseases
CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
CC present sequence represents human G-protein chemokine receptor (CCR5)
CC HDGNR10 #1
XX
XX Sequence 352 AA;
SQ
Query Match 100.0%; Score 96; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202
RESULT 21
AAU97152
ID AAU97152 standard; protein; 352 AA.
XX
XX AAU97152;
XX
XX 13-AUG-2002 (first entry)
XX
XX Human G-protein chemokine receptor (CCR5) HDGNR10 #2.
XX
XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
XX immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
XX neurodegeneration; viral infection; Kaposi sarcoma; cancer;
XX

XX hyperproliferative disease; neurological disease; receptor.
XX Homo sapiens.
XX US2002048786-A1.
XX 25-APR-2002.
XX 09-FEB-2001; 2001US-00779879.
XX 09-FEB-2000; 2000US-0181258P.
XX 09-MAR-2000; 2000US-0187999P.
XX 22-SEP-2000; 2000US-0234336P.
XX (ROSE/) ROSEN C A.
XX (ROSC/) ROSCHKE V.
XX (LIYU/) LI Y.
XX (RUBE/) RUBEN S M.
XX Rosen CA, Roschke V, Li Y, Ruben SM;
XX WPI; 2002-434754/46.
XX N-PSDB; ABK51870.
XX New nucleic acid encoding an antibody specific for the G-protein
XX chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
XX inflammation.
XX Disclosure; Page 165-166; 180pp; English.
XX The present invention relates to the isolation of a novel human G-protein
XX chemokine receptor (CCR5) designated HDGMR10, and polynucleotide
XX sequences encoding it. The invention also describes antibodies that bind
XX human G-protein chemokine receptor (CCR5) HDGMR10 and polynucleotide
XX sequences encoding the antibodies. The antibodies are useful for treating
XX cells and T-cell/antigen-presenting cell interactions, infections and
XX autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
XX infections (especially early-stage human immune deficiency virus (HIV),
XX cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
XX associated with aberrant or deficient expression of the CCR5 receptor or
XX its ligands. The antibodies are also useful to determine CCR5 expression,
XX e.g. for diagnosis, prognosis and monitoring of cancer and other
XX hyperproliferative diseases. The polynucleotide sequences encoding human
XX G-protein chemokine receptor (CCR5) HDGMR10 can be used to produce the
XX recombinant receptor, and in the treatment of a wide range of diseases
XX such as infectious diseases (e.g. influenza), neurological diseases (e.g.
XX Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
XX present sequence represents human G-protein chemokine receptor (CCR5)
XX HDGMR10 #2
XX Sequence 352 AA;
XX Query Match 100.0%; Score 96; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 SQYQFWKFNQTLKIVILG 18
XX 185 SQYQFWKFNQTLKIVILG 202
XX RESULT 22
XX AAM52829
XX ID AAM52829 standard; protein; 352 AA.
XX AC AAM52829;
XX DT 22-FEB-2002 (first entry)
XX DE Human CCR5 Gln 55 variant.
XX XX CCR5; CC chemokine receptor 5; human; HIV infection;
KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
KW drug screening; identification; variant.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Misc-difference 55 /note= "Glu replaces wild-type Leu; encoded by CTG"
XX Misc-difference 58 /note= "Encoded by AGC"
XX WO200171346-A2.
XX 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009155.
XX 21-MAR-2000; 2000US-0190946P.
XX 21-MAR-2000; 2000US-0190966P.
XX 21-MAR-2000; 2000US-0191299P.
XX 20-MAR-2001; 2001US-00813448.
XX 20-MAR-2001; 2001US-00813651.
XX 20-MAR-2001; 2001US-00813653.
XX (CONS-) CONSENSUS PHARM INC.
XX Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX WPI; 2002-010610/01.
XX N-PSDB; ABA02318.
XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,
XX comprises binding a molecule from library to a molecule having binding
XX property corresponding to CCR5 and identifying bound molecule.
XX Example 3; Fig 4B; 50pp; English.
XX The invention relates to a method for identifying a binding compound for
XX CC chemokine receptor 5 (CCR5). The method involves screening a library
XX of test molecules (particularly peptides) with immobilised CCR5, and then
XX identifying those molecules which bind. The invention also relates to
XX CCR5-binding molecules identified using the method of the invention, a
XX methods for identifying consensus motifs for CCR5-binding peptides, a
XX transfer vector encoding tagged CCR5, a computer-aided methods for
XX determining the relative binding affinity of a test molecule to CCR5 and
XX a computer aided drug screening assay that utilises the three-dimensional
XX structure of CCR5. Compounds identified using the methods of the
XX invention are useful for treating or preventing HIV (human
XX immunodeficiency virus) infection or AIDS (acquired immunodeficiency
XX syndrome) in a patient. The methods of the invention may also be used to
XX identify agonists or antagonists of the interaction of CCR5 with its
XX natural ligand, and to determine a binding motif for CCR5. The present
XX sequence represents a naturally occurring variant of human CCR5 in which
XX there is a glutamine, rather than a leucine, at position 55
XX Sequence 352 AA;
XX Query Match 100.0%; Score 96; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 SQYQFWKFNQTLKIVILG 18
XX 185 SQYQFWKFNQTLKIVILG 202
XX RESULT 23
XX AAM52828
XX ID AAM52828 standard; protein; 352 AA.
XX AC AAM52828;
XX DT 22-FEB-2002 (first entry)

```

XX DE Human CC chemokine receptor 5 (CCR5).
XX DE CCR5; CC chemokine receptor 5; human; HIV infection;
KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
KW drug screening; identification.
XX OS Homo sapiens.
XX PN WO200171346-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009155.
XX PR 21-MAR-2000; 2000US-0190946P.
XX PR 21-MAR-2000; 2000US-0190966P.
XX PR 21-MAR-2000; 2000US-0191299P.
XX PR 20-MAR-2001; 2001US-00813448.
XX PR 20-MAR-2001; 2001US-00813451.
XX PR 20-MAR-2001; 2001US-00813653.
XX PA (CONS-) CONSENSUS PHARM INC.
XX PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX WPI; 2002-010610/01.
XX N-PSDB; ABA02317.
XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,
XX comprises binding a molecule from library to a molecule having binding
XX property corresponding to CCR5 and identifying bound molecule.
XX Example 3; Fig 4A; 50pp; English.
XX The invention relates to a method for identifying a binding compound for
XX CC chemokine receptor 5 (CCR5). The method involves screening a library
XX of test molecules (particularly peptides) with immobilised CCR5, and then
XX identifying those molecules which bind. The invention also relates to
XX CCR5-binding molecules identified using the method of the invention,
XX methods for identifying consensus motifs for CCR5-binding peptides, a
XX transfer vector encoding tagged CCR5, a computer-aided methods for
XX determining the relative binding affinity of a test molecule to CCR5 and
XX a computer aided drug screening assay that utilises the three-dimensional
XX structure of CCR5. Compounds identified using the methods of the
XX invention are useful for treating or preventing HIV (human
XX immunodeficiency virus) infection or AIDS (acquired immunodeficiency
XX syndrome) in a patient. The methods of the invention may also be used to
XX identify agonists or antagonists of the interaction of CCR5 with its
XX natural ligand, and to determine a binding motif for CCR5. The present
XX sequence represents human CCR5
XX SQ Sequence 352 AA;
XX Query Match 100.0%; Score 96; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 SOYQFWKNFQTLKIVILG 18
XX Db 185 SOYQFWKNFQTLKIVILG 202
XX RESULT 24
XX ABG70597
XX ID ABG70597 standard; protein; 352 AA.
XX AC ABG70597;
XX XX
XX DT 03-DEC-2002 (first entry)
XX DE Human G-protein chemokine receptor, HDGNR10.
XX

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```

KW Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;
KW hematopoiesis; wound healing; coagulation; angiogenesis; solid tumour;
KW chronic infection; leukaemia; T-cell mediated autoimmune disease;
KW parasitic infection; psoriasis; growth factor activity; allergy;
KW atherogenesis; anaphylaxis; malignancy; inflammation; histamine;
KW immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis;
KW prostaglandin-independent fever; bone marrow failure; shock;
KW rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic;
KW immunosuppressive; antiparasitic; antipsoriatic; antiallergic;
KW antiarteriosclerotic; antiinflammatory; antirheumatic; antiarthritic;
KW antipyretic; receptor.
XX OS Homo sapiens.
XX PN US2002099176-A1.
XX PD 25-JUL-2002.
XX PF 25-JUN-1999; 99US-00339912.
XX PR 06-JUN-1995; 95US-00466343.
XX (LIYY/) LI Y.
XX (RUBS/) RUBEN S M.
XX PI Li Y, Ruben SM;
XX WPI; 2002-690494/74.
XX N-PSDB; ABS54272.
XX Novel human G-protein chemokine receptor polypeptide useful for
XX identifying modulators for stimulating hematopoiesis, wound healing,
XX leukemia, for treating allergy, rheumatoid arthritis, shock and as
XX research agents.
XX Claim 7; Fig 1; 22pp; English.
XX The present invention relates to the isolation of human G-protein
XX chemokine receptor, HDGNR10 (CCR5 receptor), and the polynucleotide
XX sequence encoding it. HDGNR10 polypeptide and polynucleotide sequences
XX are useful for diagnosing a disease or a susceptibility to a disease
XX related to underexpression of HDGNR10. They are useful for identifying
XX modulators for stimulating haematopoiesis, wound healing, coagulation,
XX angiogenesis, to treat solid tumours, chronic infections, leukaemia, T-
XX cell mediated autoimmune diseases, parasitic infections, psoriasis, or
XX for stimulating growth factor activity. The sequences are also useful for
XX preventing and/or treating allergy, atherogenesis, anaphylaxis,
XX malignancy, chronic and acute inflammation, histamine and immunoglobulin
XX E (IgE)-mediated allergic reactions, prostaglandin-independent fever,
XX bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-
XX eosinophilic syndrome. Polynucleotide sequences encoding HDGNR10 can be
XX used in gene therapy to treat conditions related to underexpression of
XX HDGNR10. The present sequence represents human G-protein chemokine
XX receptor, HDGNR10
XX SQ Sequence 352 AA;
XX Query Match 100.0%; Score 96; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 SOYQFWKNFQTLKIVILG 18
XX Db 185 SOYQFWKNFQTLKIVILG 202
XX RESULT 25
XX ABG92883
XX ID ABG92883 standard; protein; 352 AA.
XX AC ABG92883;
XX XX
XX DT 19-NOV-2002 (first entry)

```

XX DE Human immunoglobulin variable heavy domain #1.

XX XX Immunoglobulin; variable heavy chain; variable light chain; human;

KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;

KW immunologic deficiency syndrome; blood protein disorder; nephritis;

KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;

KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;

KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;

KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;

KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;

KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;

KW lymphocytopenia.

XX OS Homo sapiens.

XX XX WO200264612-A2.

XX PD 22-AUG-2002.

XX PF 08-FEB-2002; 2002WO-US003634.

XX PR 09-FEB-2001; 2001US-00779880.

PR 09-FEB-2001; 2001WO-US004153.

PR 12-JUN-2001; 2001US-0297257P.

PR 08-AUG-2001; 2001US-0310458P.

PR 12-OCT-2001; 2001US-0328447P.

PR 21-DEC-2001; 2001US-0341725P.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX PA Roschke V, Rosen CA, Ruben SM;

XX PI WPI; 2002-643455/69.

XX DR N-PSDB; ABS68606.

XX DR New human G-protein Chemokine Receptor gene (HDGNR10) useful for

PT treating, preventing, ameliorating or monitoring diseases or disorders

PT associated with aberrant expression of HDGNR10 e.g. cancer.

XX XX Example 55; Fig 4; 562pp; English.

XX CC The invention describes an isolated polynucleotide encoding a first

CC antibody at least 95-100% identical to a second antibody consisting of an

CC amino acid sequence comprising at least one, two or three CDR regions of

CC a variable heavy (VH) or variable light (VL) domain of the antibody

CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,

CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.18B5,

CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody

CC is useful treating, preventing, ameliorating, prognosing or monitoring

CC cancers or other diseases or disorders e.g. immunologic deficiency

CC syndromes such as blood protein disorders and ataxia telangiectasia,

CC inflammation associated disorders such as endotoxin lethality, nephritis

CC and inflammatory bowel disease, conditions associated with an increase in

CC certain haematopoietic cells such as histiocytosis, defective or aberrant

CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,

CC an infectious disease, an autoimmune disease such as Addison's disease,

CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative

CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or

CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,

CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a

CC disease or disorder associated with aberrant expression of novel human G-

CC protein chemokine receptor (CCR5).HDGNR10. This is the amino acid

CC sequence of human immunoglobulin sequence associated with the antibodies

CC against HDGNR10

XX XX Sequence 352 AA;

SQ Query Match 100.0%; Score 96; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWNFQTLKIVILG 18

Db 185 SQYQFWNFQTLKIVILG 202

RESULT 26

ABG92880

ID ABG92880 standard; protein; 352 AA.

XX ABG92880;

XX 19-NOV-2002 (first entry)

DT Human G-protein chemokine receptor (CCR5) HDGNR10 #1.

XX DE Immunoglobulin; variable heavy chain; variable light chain; human;

XX KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;

KW immunologic deficiency syndrome; blood protein disorder; nephritis;

KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;

KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;

KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;

KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;

KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;

KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;

KW lymphocytopenia.

XX OS Homo sapiens.

XX XX WO200264612-A2.

XX PD 22-AUG-2002.

XX PF 08-FEB-2002; 2002WO-US003634.

XX PR 09-FEB-2001; 2001US-00779880.

PR 09-FEB-2001; 2001WO-US004153.

PR 12-JUN-2001; 2001US-0297257P.

PR 08-AUG-2001; 2001US-0310458P.

PR 12-OCT-2001; 2001US-0328447P.

PR 21-DEC-2001; 2001US-0341725P.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX PA Roschke V, Rosen CA, Ruben SM;

XX PI WPI; 2002-643455/69.

XX DR N-PSDB; ABS68653.

XX DR New human G-protein Chemokine Receptor gene (HDGNR10) useful for

PT treating, preventing, ameliorating or monitoring diseases or disorders

PT associated with aberrant expression of HDGNR10 e.g. cancer.

XX XX Disclosure; Fig 1A-B; 562pp; English.

XX CC The invention describes an isolated polynucleotide encoding a first

CC antibody at least 95-100% identical to a second antibody consisting of an

CC amino acid sequence comprising at least one, two or three CDR regions of

CC a variable heavy (VH) or variable light (VL) domain of the antibody

CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,

CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.18B5,

CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody

CC is useful treating, preventing, ameliorating, prognosing or monitoring

CC cancers or other diseases or disorders e.g. immunologic deficiency

CC syndromes such as blood protein disorders and ataxia telangiectasia,

CC inflammation associated disorders such as endotoxin lethality, nephritis

CC and inflammatory bowel disease, conditions associated with an increase in

CC certain haematopoietic cells such as histiocytosis, defective or aberrant

CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,

CC an infectious disease, an autoimmune disease such as Addison's disease,

CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative

CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or

CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,

CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a

CC disease or disorder associated with aberrant expression of novel human G-

CC protein chemokine receptor (CCR5).HDGNR10. This is the amino acid

CC sequence of human immunoglobulin sequence associated with the antibodies

CC against HDGNR10

CC protein chemokine receptor (CCR5) HDGNR10. This is an amino acid sequence
CC of Human G-protein chemokine receptor (CCR5) HDGNR10 #1
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
|||
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 27
AAE25808
ID AAE25808 standard; protein; 352 AA.
XX
AC AAE25808;

DT 24-FEB-2003 (first entry)

DE Human G-protein chemokine receptor (CCR5), HDGNR10 #1.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
KW inflammation; viral infection; autoimmune disease; neurodegeneration;
KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
KW hyperproliferative disease; receptor.

XX Homo sapiens.

XX US2002061834-A1.

XX 23-MAY-2002.

XX 09-FEB-2001; 2001US-00779880.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (ROSE/) ROSEN C A.

XX (ROSC/) ROSCHKE V.

XX (LIYY/) LI Y.

XX (RUBE/) RUBEN S M.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2002-499674/53.

XX N-PSDB; AAD42409.

XX New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,

XX useful for treatment, prevention and diagnosis of e.g. cancer, also

XX related antibodies.

XX Claim 61; Page 163-164; 186pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5), CCR5
CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
CC antibodies are used for the treatment or prevention of inflammation,
CC defective or aberrant chemotaxis of immune cells or T cell antigen-
CC presenting cell interaction, viral infections (specifically human immune
CC deficiency (including its early stages), cytomegalo or pox viruses),
CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
CC carinii infection, Kaposi's sarcoma or any condition associated with
CC aberrant expression of CCR5 or their ligands. They are also used for the
CC detection, diagnosis, prognosis and monitoring of cancers or other
CC hyperproliferative diseases. The present sequence is human G-protein
CC chemokine receptor (CCR5), HDGNR10 DNA

XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
|||
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 28

AAE25811
ID AAE25811 standard; protein; 352 AA.

XX AAE25811;

XX 24-FEB-2003 (first entry)

DE Human G-protein chemokine receptor (CCR5), HDGNR10 #2.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
KW inflammation; viral infection; autoimmune disease; neurodegeneration;
KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
KW hyperproliferative disease; receptor.

XX Homo sapiens.

XX US2002061834-A1.

XX 23-MAY-2002.

XX 09-FEB-2001; 2001US-00779880.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (ROSE/) ROSEN C A.

XX (ROSC/) ROSCHKE V.

XX (LIYY/) LI Y.

XX (RUBE/) RUBEN S M.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2002-499674/53.

XX N-PSDB; AAD42426.

XX New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,

XX useful for treatment, prevention and diagnosis of e.g. cancer, also

XX related antibodies.

XX Disclosure; Page 170; 186pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5), CCR5
CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
CC antibodies are used for the treatment or prevention of inflammation,
CC defective or aberrant chemotaxis of immune cells or T cell antigen-
CC presenting cell interaction, viral infections (specifically human immune
CC deficiency (including its early stages), cytomegalo or pox viruses),
CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
CC carinii infection, Kaposi's sarcoma or any condition associated with
CC aberrant expression of CCR5 or their ligands. They are also used for the
CC detection, diagnosis, prognosis and monitoring of cancers or other
CC hyperproliferative diseases. The present sequence is human G-protein
CC chemokine receptor (CCR5), HDGNR10 DNA

XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
|||
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 29
 ABB81054
 ID ABB81054 standard; protein; 352 AA.
 XX AC ABB81054;
 XX DT 05-NOV-2002 (first entry)
 XX DE G-protein chemokine receptor, HDGNR10.
 XX KW 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10;
 KW G-protein chemokine receptor; haematopoietic; immunosuppressant;
 KW antiparasitic; antiparasitic; antiallergic; antiinflammatory; cytostatic;
 KW antirheumatic; antiarthritic; gene therapy; human; receptor.
 XX OS Homo sapiens.
 XX PN US2002076745-A1.
 XX PD 20-JUN-2002.
 XX PF 18-NOV-1998; 98US-00195662.
 XX PR 06-JUN-1995; 95US-00466343.
 XX PA (LIVY/) LI Y.
 XX PA (RUBE/) RUBEN S M.
 XX PI Li Y, Ruben SM;
 XX WPI; 2002-598724/64.
 DR N-PSDB; ABB86542.
 PT New polynucleotide encoding a human G protein chemokine receptor HDGNR10,
 PT useful e.g. for treating tumors.
 PS Claim 7; Fig 1; 22pp; English.
 CC The invention relates to a novel human 7-transmembrane receptor, HDGNR10,
 CC which has been identified as a G-protein chemokine receptor. The GPCR
 CC HDGNR10 polypeptide can be expressed by standard recombinant methodology.
 CC Compounds that activate or inhibit the receptor polypeptide, optionally
 CC expressed from DNA in gene therapy vectors, are used to treat diseases
 CC that require: (a) activation of the receptor (e.g. stimulation of
 CC haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune
 CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the
 CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis
 CC etc). The present sequence represents the human HDGNR10 receptor
 CC polypeptide
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFOTLKIVILG 18
 DB 185 SQYQFWKNFOTLKIVILG 202
 RESULT 30
 ABB08343
 ID ABB08343 standard; protein; 352 AA.
 XX AC ABB08343;
 XX DT 18-JUN-2002 (first entry)
 XX DE Human chemokine (C-C motif) receptor 5 polypeptide.
 XX

KW Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;
 KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;
 KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;
 KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;
 KW chromosome 3p21.
 XX OS Homo sapiens.
 XX XX
 XX Key Location/Qualifiers
 FH Misc-difference 55
 FT /label= Leu, Gln
 FT Misc-difference 182
 FT /label= Phe, Leu
 FT Misc-difference 223
 FT /label= Arg, Gln
 XX WO200177125-A2.
 XX 18-OCT-2001.
 XX 04-APR-2001; 2001WO-US010708.
 XX 05-APR-2000; 2000US-0194361P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Choi JY, Kliehm SE, Koshy B;
 PI WPI; 2002-041282/05.
 DR N-PSDB; ABA97318, ABA97319.
 XX New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful
 PT to diagnose and treat diseases associated with its abnormal expression or
 PT function, including human immunodeficiency virus-1 infection.
 XX Claim 29; Fig 3; 61pp; English.
 CC The present sequence is that of a polypeptide encoded by the human
 CC chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see
 CC ABA97318, ABA97319). The specification describes haplotyping the CCR5
 CC gene of an individual by determining if the individual has one of the
 CC CCR5 haplotypes or haplotype pairs fully defined in the specification.
 CC The specification also describes an isolated polynucleotide comprising a
 CC nucleotide sequence which is a polymorphic variant of the reference CCR5
 CC gene sequence and comprises an isogene defined by a haplotype described
 CC in the specification and its encoded polypeptide. The methods of the
 CC invention are useful to diagnose and develop treatment for diseases
 CC associated with abnormal expression or function of the gene. The CCR5
 CC isogenes and the screened compounds are useful for treating human
 CC immunodeficiency virus (HIV)-1 infection and the progression to acquired
 CC immunodeficiency syndrome (AIDS). The invention has antiviral
 CC applications. The specification describes genotyping the CCR5 gene of an
 CC individual; predicting a haplotype pair for the CCR5 gene of an
 CC haplotype pair of the CCR5 gene. The specification describes a
 CC composition comprising a genotyping oligonucleotide for detecting a CCR5
 CC polymorphism; a recombinant non-human organism transformed with CCR5
 CC polynucleotide expressing a CCR5 protein encoded by the variant sequence;
 CC an isolated antibody specific for the CCR5 polypeptide and a method for
 CC screening drugs targeting the CCR5 polypeptide
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFOTLKIVILG 18
 DB 185 SQYQFWKNFOTLKIVILG 202
 RESULT 31

ABG75540
ID ABG75540 standard; protein; 352 AA.
XX
XX AC ABG75540;
XX
XX DT 16-APR-2003 (first entry)
XX
XX DE Human G-protein chemokine receptor, HDGMR10, protein.
XX
XX KW Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor;
XX HDGMR10; signal transduction; gene therapy; haematopoiesis;
XX wound healing; coagulation; angiogenesis; tumour; chronic infection;
XX leukaemia; T-cell mediated auto-immune disease; parasitic infection;
XX psoriasis; growth factor; allergy; atherogenesis; anaphylaxis;
XX malignancy; inflammation; histamine; IgE-mediated;
XX prostaglandin-independent fever; bone marrow failure; silicosis;
XX sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.
XX
XX OS Homo sapiens.
XX
XX PN US2002132269-A1.
XX
XX PD 19-SEP-2002.
XX
XX PF 11-FEB-2000; 2000US-00502783.
XX
XX PR 06-JUN-1995; 95US-00466343.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Li Y, Ruben SM;
XX
XX DR WPI; 2003-208944/20.
XX N-PSDB; ABX10635.
XX
XX PT Novel human G-protein chemokine receptor polypeptide useful for
XX diagnostic purposes and for identifying modulators of the polypeptide
XX useful for treating leukemia, autoimmune diseases, psoriasis and allergic
XX reactions.
XX
XX PS Claim 7; Fig 1; 22pp; English.
XX
XX CC The invention discloses a G-protein chemokine receptor (sometimes
XX referred to as a 7-transmembrane receptor) polypeptide, HDGMR10, and the
XX polynucleotide encoding it. G-protein chemokine receptors are involved in
XX signal transduction pathways. The polynucleotide and polypeptide can be
XX used to identify compounds which activate or inhibit activation of the
XX protein and these compounds are useful for treating a patient having need
XX to activate or inhibit a G-protein chemokine receptor. The compound is
XX administered by providing to the patient DNA encoding the agonist or
XX antagonist and expressing them in vivo (gene therapy). The
XX polynucleotides and polypeptide are also useful for diagnosing a
XX disease or susceptibility to a disease related to an under-expression of
XX the protein, for chromosome identification or as immunogens for producing
XX antibodies. Agonists are useful in stimulating haematopoiesis, wound
XX healing, coagulation, angiogenesis, to treat solid tumours, chronic
XX infections, leukaemia, T-cell mediated auto-immune diseases, parasitic
XX infections, psoriasis and to stimulate growth factor activity.
XX Antagonists are useful in the prevention and treatment of allergy,
XX atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation,
XX histamine and IgE-mediated allergic reactions, prostaglandin-independent
XX fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis,
XX shock and hyper-eosinophilic syndrome. The sequence presented is the
XX human HDGMR10 protein
XX
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 96; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0

Db 185 SQYQFWKFNQTLKIVILG 202
RESULT 32
ABR58602
ID ABR58602 standard; protein; 352 AA.
XX
XX AC ABR58602;
XX
XX DT 09-JUL-2003 (first entry)
XX
XX DE Human cancer related protein SEQ ID NO:259.
XX
XX KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
XX heart disease; atherosclerosis; endometriosis.
XX
XX OS Homo sapiens.
XX
XX PN WO2003025138-A2.
XX
XX PD 27-MAR-2003.
XX
XX PF 17-SEP-2002; 2002WO-US0295560.
XX
XX PR 17-SEP-2001; 2001US-0323469P.
XX
XX PR 20-SEP-2001; 2001US-0323887P.
XX
XX PR 13-NOV-2001; 2001US-0350666P.
XX
XX PR 08-FEB-2002; 2002US-0355145P.
XX
XX PR 08-FEB-2002; 2002US-0355257P.
XX
XX PR 12-APR-2002; 2002US-0372246P.
XX
XX (EOSE-) EOS BIOTECHNOLOGY INC.
XX
XX PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
XX Zlotnik A;
XX
XX DR WPI; 2003-354600/33.
XX N-PSDB; ACC72740.
XX
XX PT New genes that are up-regulated or down-regulated in cancers, useful as
XX markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX therapeutic targets for screening drugs for treating these diseases.
XX
XX PS Claim 12; Page 745; 767pp; English.
XX
XX CC The present invention describes an isolated nucleic acid molecule, which
XX comprises the sequence of any of the genes that are up-regulated or down-
XX regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX related gene nucleotide sequences which encode the proteins given in
XX ABR58521 to ABR58709. Also described: (1) determining the presence or
XX absence of a pathological cell in a patient; (2) an expression vector
XX comprising a nucleic acid molecule described above; (3) a host cell
XX comprising the vector; (4) an isolated polypeptide, which is encoded by
XX the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX of (4); (6) specifically targeting a compound to a pathological cell in a
XX patient by administering to the patient the antibody above; and (7) a
XX drug screening assay. The nucleic acid is useful as diagnostic markers or
XX therapeutic targets. In particular, the nucleic acid is useful for
XX diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
XX atherosclerosis and endometriosis. The nucleic acid is also useful in
XX drug screening, particularly for identifying agents for treating these
XX pathologies
XX
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 96; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0

Db 185 SQYQFWKNFQTLKIVILG 202
|||||

RESULT 33

AAO29514
ID AAO29514 standard; protein; 352 AA.

XX AC AAO29514;

XX DT 27-AUG-2003 (first entry)

XX DE Human C-C chemokine receptor type 5 (333) protein.

XX KW Human; urological disorder; stress urinary incontinence; prostate cancer;
KW benign prostatic hyperplasia; overactive bladder; oversensitive bladder;
KW overflow urinary incontinence; gene therapy; nephrotropic; prostatitis;
KW kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.

XX OS Homo sapiens.

XX PN WO2003039475-A2.

XX PD 15-MAY-2003.

XX PF 07-NOV-2002; 2002WO-US035824.

XX PR 07-NOV-2001; 2001US-0344552P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Silos-Santiago I;

XX DR WPI; 2003-449396/42.

XX DR N-PSDB; AAL59912.

XX PT Identifying a compound, capable of treating urological disorder e.g.,
PT benign prostatic hyperplasia, by assaying the ability of the compound to
PT modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or
PT polypeptide activity.

XX PS Disclosure; Page 81; 87pp; English.

XX CC The invention relates to a method for treating a urological disorder
CC which comprises assaying the ability of the compound to modulate 313,
CC 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide
CC activity. The method is useful for identifying a compound for treating an
CC urological disorder comprising urinary incontinence e.g., overactive/
CC oversensitive bladder, overflow urinary incontinence, stress urinary
CC incontinence caused by dysfunction of the bladder, urethra or central/
CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,
CC prostate cancer or kidney disorders. It is also used in gene therapy. The
CC present sequence is human C-C chemokine receptor type 5 (CCR5; 333)
CC protein. This sequence is used to illustrate the method of the invention

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 6; Length 352;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18

DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 34

ABU61654
ID ABU61654 standard; protein; 352 AA.

XX AC ABU61654;

XX DT 08-AUG-2003 (first entry)

XX DE Human G-protein chemokine receptor (HDGNR10) polypeptide.
XX KW Human; G-protein chemokine receptor; receptor; HDGNR10;
KW 7-transmembrane receptor.

XX OS Homo sapiens.

XX PN US2003023044-A1.

XX PD 30-JAN-2003.

XX PF 03-SEP-2002; 2002US-00232686.

XX PR 06-JUN-1995; 95US-00466343.

XX PR 18-NOV-1998; 98US-00195662.

XX PR 25-JUN-1999; 99US-00339912.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Li Y, Ruben SM;

XX DR WPI; 2003-456307/43.

XX DR N-PSDB; ACA61721.

XX PT Producing an antibody, involves immunizing an animal with a polypeptide
PT or with a polypeptide encoded by the human G-protein chemokine receptor
PT clone in ATCC 97183, and recovering the antibody.

XX PS Claim 1; Fig 1; 23pp; English.

XX CC The invention relates to a method of producing an antibody, involving
CC immunising an animal with a human G-protein chemokine receptor (HDGNR10)
CC polypeptide (also referred to as a human 7-transmembrane receptor) and
CC recovering an antibody which binds the polypeptide. The method is useful
CC for producing an antibody which binds specifically to the human G-protein
CC chemokine receptor polypeptide. This sequence represents the HDGNR10
CC polypeptide of the invention

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 6; Length 352;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18

DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 35

ABP97728

ID ABP97728 standard; protein; 352 AA.

XX AC ABP97728;

XX DT 28-MAY-2003 (first entry)

XX DE Amino acid sequence of human chemokine receptor CCR5.

XX KW Human; chemokine receptor; CCR5; viral infection; surface protein;
KW respiratory virus infection; respiratory syncytial virus infection;
KW RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.

XX OS Homo sapiens.

XX PN WO2003014153-A2.

XX PD 20-FEB-2003.

XX PF 12-AUG-2002; 2002WO-CA001248.

XX PR 10-AUG-2001; 2001US-0311088P.

XX (TOPI-) TOPIGEN PHARM INC.
XX Renzi P, Zemzoumi K;
XX WPI; 2003-256541/25.
XX N-PSDB; ABZ68881.
XX
XX Modulating viral infection of a cell, for treating or preventing
XX respiratory virus infections, bronchitis, pneumonia or asthma, by
XX modulating a binding interaction between a cell chemokine-receptor and a
XX surface protein of the virus.
XX
XX Disclosure; Page 96-98; 120pp; English.
XX
XX The present sequence represents human chemokine receptor CCR5. The
XX specification describes a method for modulating viral infection of a
XX cell. The method comprises modulating a binding interaction between a
XX cell chemokine-receptor and a surface protein of the virus. The proviso
XX is that the cell chemokine-receptor is not CXCR1 and that the virus is
XX not HIV. The method is useful for treating or preventing respiratory
XX virus infection in vertebrates, more particularly respiratory syncytial
XX virus (RSV) infections, and related diseases, e.g. bronchiolitis,
XX bronchitis, pneumonia or asthma
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 96; DB 6; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SQYQFWKNFQTLKIVILG 18
XX |||||
XX Db 185 SQYQFWKNFQTLKIVILG 202
XX
XX RESULT 36
XX ABP81933
XX ID ABP81933 standard; protein; 352 AA.
XX
XX AC ABP81933;
XX
XX DT 04-MAR-2003. (first entry)
XX
XX DE Human C-C chemokine receptor 5 protein SEQ ID NO:352.
XX
XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX G protein-coupled receptor modulator; antibody; immune-related disease;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related cell proliferative disease; autoimmune disease;
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer.
XX
XX OS Homo sapiens.
XX
XX PN WO200261087-A2.
XX
XX PD 08-AUG-2002.
XX
XX PF 19-DEC-2001; 2001WO-US050107.
XX
XX PR 19-DEC-2000; 2000US-0257144P.
XX
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
XX FI Burmer GC, Roush CL, Brown JP;
XX WPI; 2003-046718/04.
XX

DR N-PSDB; ABZ42781.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
XX
XX Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (I) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX exemplification of the present invention
XX
XX Sequence 352 AA;
XX

Query Match 100.0%; Score 96; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
|||||
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 37
ADC03341
ID ADC03341 standard; protein; 352 AA.

AC ADC03341;
DT 18-DEC-2003 (first entry)
DE Human chemokine receptor 88-C.

KW receptor; human; anti-HIV; virucide; HIV; SIV; 88-C; 88-2B;
KW chemokine receptor; envelope protein; protein; atherosclerosis;
KW rheumatoid arthritis; tumour growth suppression; asthma; viral infection;
KW AIDS; inflammatory condition.

OS Homo sapiens.

PN US2002150888-A1.

PD 17-OCT-2002.

PF 26-MAR-2002; 2002US-00106623.

PR 20-DEC-1995; 95US-00575967.

PR 07-JUN-1996; 96US-00661393.

PR 20-DEC-1996; 96US-00771276.

```

PA (GRAY/) GRAY P W.
PA (SCHW/) SCHWEICKART V L.
PA (RAPO/) RAPORT C J.
XX
PI Gray PW, Schweickart VL, Raport CJ;
XX
XX WPI; 2003-182491/18.
XX N-PSDB; ADC03340.
XX
XX Screening for a modulator of HIV and SIV infection utilizing
XX PT polynucleotides that encode the 88C or 88-2B chemokine receptors, useful
XX PT for diagnosing and treating disorders such as atherosclerosis, arthritis,
XX PT AIDS and asthma.
XX
XX Claim 2; Page 17-18; 29pp; English.
XX
XX The invention relates to screening for a modulator of human
XX CC immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV)
XX CC infection, comprising contacting a first composition having an human
XX CC (ADC03341) or macaque (ADC03359) 88C chemokine receptor polypeptide with
XX CC a second composition having an HIV or SIV envelope protein in the
XX CC presence or absence of a compound. Also included are screening for a
XX CC modulator of HIV infection, detecting HIV infection of cells (comprising
XX CC contacting a cell that has been recombinantly modified to express at
XX CC least one of human chemokine receptors 88C and 88-2B with HIV, and
XX CC detecting HIV infection in the cell) and inhibiting HIV infection of
XX CC cells (comprising contacting cells with an antibody to at least one of
XX CC human chemokine receptors 88C and 88-2B with HIV, and detecting HIV
XX CC infection of the cell after the contacting step). The methods and
XX CC compositions of the present invention are useful for the diagnosis and
XX CC treatment of disorders associated with the aberrant expression or
XX CC activity of 88C or 88-2B chemokine receptors, such as atherosclerosis,
XX CC rheumatoid arthritis, tumour growth suppression, asthma, viral infection,
XX CC AIDS and other inflammatory conditions. The genes for human 88-C and 88-
XX CC 2B are located on chromosome 3p21. The present sequence represents human
XX CC chemokine receptor 88-C.
XX
XX Sequence 352 AA;
SQ
Query Match 100.0%; Score 96; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNQTLKIVILG 18
Db 185 SQYQFWKFNQTLKIVILG 202
|||||
|

RESULT 38
AAW23834
ID AAW23834 standard; protein; 371 AA.
XX
XX AAW23834;
XX
XX 08-JUN-1998 (first entry)
XX
XX Human CC chemokine receptor 5 (CCR5) A127V variant.
XX
XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;
XX KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 48..74
XX /label= I
XX /note= "transmembrane domain"
XX Domain 123..145
XX /label= III
XX /note= "transmembrane domain"
XX Domain 162..190
XX /label= IV
XX /note= "transmembrane domain"
XX
Domain 213..238
/label= V
/note= "transmembrane domain"
Domain 257..277
/label= VI
/note= "transmembrane domain"
Domain 296..319
/label= VII
/note= "transmembrane domain"
XX
XX WO9745543-A2.
XX
XX 04-DEC-1997.
XX
XX 28-MAY-1997; 97WO-US009586.
XX
XX 28-MAY-1996; 96US-0018508P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
XX Broder CC, Kennedy PE;
XX
XX WPI; 1998-032650/03.
XX N-PSDB; AAT76919.
XX
XX CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
XX between HIV and a target cell.
XX
XX Example 1; Fig 1B; 70pp; English.
XX
XX This protein sequence comprises an Ala127Leu variant of a novel human
XX macrophage-selective CC chemokine receptor (see also AAW23835) that has
XX been designated CCR5. The sequence was deduced from an isolated cDNA
XX clone (see AAT76919). The conservative variation should not affect the
XX activity of CCR5. The susceptibility of human macrophages to HIV
XX infection depends on cell surface expression of CD4 and CCR5. CCR5 is a
XX member of the 7-transmembrane superfamily of G-protein coupled cell
XX surface molecules. It plays an essential role in the membrane fusion step
XX of infection by some HIV isolates. The establishment of stable, non-human
XX cell lines and transgenic mammals having cells that coexpress human CD4
XX and CCR5 provides valuable tools for research of HIV infection.
XX Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding agents
XX capable of blocking membrane fusion between HIV and target cells
XX represent potential anti-HIV therapeutics for macrophage tropic strains
XX of HIV
XX
XX Sequence 371 AA;
Query Match 100.0%; Score 96; DB 2; Length 371;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNQTLKIVILG 18
Db 204 SQYQFWKFNQTLKIVILG 221
|||||
|

RESULT 39
AAAY41280
ID AAAY41280 standard; protein; 439 AA.
XX
XX AAAY41280;
XX
XX 11-FEB-2000 (first entry)
XX
XX Fusion protein containing human chemokine receptor CCR-5.
XX
XX Prostaglandin; PG; E2EP3 receptor; E2EP2 receptor; CCR-5; human;
XX chemokine receptor; ss2 adrenergic receptor; small G-protein rho;
XX renal outer medullary potassium ion channel protein; ion-channel protein;
XX lambda phage repressor protein; G-protein coupled receptor; bacteria;
XX biochemical; vaccine; immunohistochemical; orphan receptor; HIV.
XX

```

XX	Synthetic.
OS	Homo sapiens.
XX	
XX	W09953033-A1.
XX	
PD	21-OCT-1999.
XX	
XX	
PF	16-APR-1999; 99WO-US008214.
XX	
XX	
PR	16-APR-1998; 98US-0081989P.
XX	
PA	(UYVA-) UNIV VANDERBILT.
PI	
PI	Breyer RM, Ma L, Kennedy C;
XX	
XX	WPI; 1999-620416/53.
DR	N-PSDB; AAZ24738.
XX	
XX	
PT	New nucleic acid constructs for high level expression of eukaryotic
PT	proteins in bacteria, for producing e.g. chemokine receptor CCR-5 for
PT	preventing HIV infection.
XX	
XX	
PS	Disclosure; Page 49-53; 81pp; English.
XX	
XX	The invention provides isolated nucleic acid sequences that encode rabbit
CC	prostaglandin (PG) E2EP3 receptor, human PG E2EP2 receptor, human
CC	chemokine receptor CCR-5, human ss2 adrenergic receptor, rat renal outer
CC	medullary potassium ion channel protein or human small G-protein rho,
CC	together with deduced protein sequences. Also provided is a method for
CC	the production of eukaryotic proteins by culturing bacteria transformed
CC	with vectors containing the above nucleic acid sequences or a nucleic
CC	acid (I) that comprises: (i) first sequence that encodes either a
CC	sequence comprising at least three positively charged amino acids, or a
CC	DNA-binding protein, or a lambda phage repressor protein, placed upstream
CC	of, and in frame with, (ii) a sequence encoding a protein. (I) are used
CC	for recombinant production of eukaryotic proteins, particularly membrane
CC	proteins, G-protein coupled receptors or ion-channel proteins, in
CC	bacteria. These proteins are useful for biochemical or structural studies
CC	; as therapeutic agents; in diagnostic and screening assays and as
CC	antigens for use in vaccines, and for raising antibodies that are useful
CC	as immunohistochemical markers, e.g. for orphan receptors or ion
CC	channels. Antibodies raised against the chemokine receptor CCR-5 can be
CC	used (when administered as antiserum or generated in vivo) to prevent
CC	entry of human immune deficiency virus (HIV) into cells
XX	
XX	
SQ	Sequence 439 AA;
	Query Match 100.0%; Score 96; DB 2; Length 439;
	Best Local Similarity 100.0%; Pred. NO. 1.1le-06;
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 SQYQWQNFQTLKIVILG 18
DB	263 SQYQWQNFQTLKIVILG 280
	RESULT 40
AAW27125	ID
XX	AAW27125 standard; protein; 352 AA.
XX	
AC	AAW27125;
XX	
DT	14-DSC-1997 (first entry)
DE	
XX	Macaque chemokine receptor 88C.
XX	
KW	Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
KW	asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
KW	diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
XX	modulator; antibody.
XX	
OS	Macaca sp.

```

XX PN WO9722698-A2.
XX
XX XX
XX PD 26-JUN-1997.
XX
XX PF 20-DEC-1996; 96WO-US020759.
XX
XX PF 20-DEC-1995; 95US-00575967.
XX
XX PF 07-JUN-1996; 96US-00661393.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray PW, Schweickart VL, Raport CJ;
XX
XX WPI; 1997-341689/31.
XX
XX N-PSDB; AAT85163.
XX
XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX PT tumours, viral infections, auto-immune diseases, etc.
XX
XX Claim 36; Page 57-58; 65pp; English.
XX
XX This polypeptide sequence comprises macaque chemokine receptor 88C, a G
XX CC protein coupled receptor that is involved in leukocyte trafficking. Its
XX CC amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR
XX CC amplification. It shows 97% identity to human 88C (AAW27123). 88C
XX CC receptors and their polypeptide fragments can be produced in transformed
XX CC host cells. The receptors, peptides comprising one or more of the
XX CC extracellular or intracellular domains, and anti-receptor antibodies can
XX CC be used to modulate receptor activities, particularly ligand and G
XX CC protein binding, and are potentially useful in the treatment
XX CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX CC infection, AIDS, inflammatory conditions, pathological immune response,
XX CC abnormal haematopoietic processes etc. A hybridoma that produces an
XX CC antibody that specifically binds to macaque 88C is claimed
XX
XX Sequence 352 AA;
XX
XX Query Match 96.9%; Score 93; DB 2; Length 352;
XX Best Local Similarity 94.4%; Pred. No. 2.6e-06;
XX Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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XX | | | | | | | | | | | | | | | | | |
XX Db 185 SQYQFWKNFQTLKIVILG 202
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XX Job time : 43.975 secs

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Job time : 43.975 secs

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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:06:23 ; Search time 59.625 Seconds
(without alignments)
97.074 Million cell updates/sec

Title: US-10-084-813-13

Perfect score: 96

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Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters: 1349238

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	96	100.0	18	14	US-10-084-813-13
2	96	100.0	18	14	Sequence 13, Appl
3	96	100.0	49	16	US-10-084-813-77
4	96	100.0	49	16	Sequence 77, Appl
5	96	100.0	54	9	US-10-661-798-11
6	96	100.0	54	9	Sequence 11, Appl
7	96	100.0	54	9	US-10-612-731-11
8	96	100.0	54	9	Sequence 11, Appl
9	96	100.0	352	9	US-09-938-703-11
10	96	100.0	352	9	Sequence 11, Appl
11	96	100.0	352	9	US-09-725-285-2
12	96	100.0	352	9	Sequence 2, Appl
13	96	100.0	352	9	US-09-841-2
14	96	100.0	352	9	Sequence 2, Appl
15	96	100.0	352	9	US-09-779-879A-2
					Sequence 22, Appl
					US-09-779-880A-2
					Sequence 22, Appl
					US-09-779-880A-2
					Sequence 15, Appl
					US-09-813-653-15
					Sequence 17, Appl

16	96	100.0	352	9	US-09-796-202-1	Sequence 1, Appl
17	96	100.0	352	9	US-09-195-662A-2	Sequence 2, Appl
18	96	100.0	352	9	US-09-339-912A-2	Sequence 2, Appl
19	96	100.0	352	9	US-09-938-719-5	Sequence 5, Appl
20	96	100.0	352	9	US-09-939-226-5	Sequence 5, Appl
21	96	100.0	352	9	US-09-938-703-5	Sequence 5, Appl
22	96	100.0	352	9	US-09-502-783A-2	Sequence 2, Appl
23	96	100.0	352	10	US-09-734-421A-14	Sequence 14, Appl
24	96	100.0	352	11	US-09-826-509-477	Sequence 477, App
25	96	100.0	352	12	US-10-151-274-5	Sequence 5, Appl
26	96	100.0	352	13	US-10-106-623-2	Sequence 2, Appl
27	96	100.0	352	14	US-10-232-686-2	Sequence 2, Appl
28	96	100.0	352	14	US-10-086-814-1	Sequence 1, Appl
29	96	100.0	352	14	US-10-067-800-2	Sequence 2, Appl
30	96	100.0	352	14	US-10-067-800-22	Sequence 2, Appl
31	96	100.0	352	14	US-10-290-058A-6	Sequence 6, Appl
32	96	100.0	352	14	US-10-225-567A-352	Sequence 352, App
33	96	100.0	352	14	US-10-323-314-1	Sequence 1, Appl
34	96	100.0	352	14	US-10-072-301-1	Sequence 1, Appl
35	96	100.0	352	14	US-10-164-649-52	Sequence 52, Appl
36	96	100.0	352	14	US-10-071-866-1	Sequence 1, Appl
37	96	100.0	352	14	US-10-135-839-2	Sequence 2, Appl
38	96	100.0	352	14	US-10-135-839-22	Sequence 22, Appl
39	96	100.0	352	14	US-10-239-423-67	Sequence 67, Appl
40	96	100.0	352	14	US-10-439-845-2	Sequence 2, Appl
41	96	100.0	352	14	US-10-439-845-4	Sequence 4, Appl
42	96	100.0	352	15	US-10-360-828-1	Sequence 1, Appl
43	96	100.0	352	16	US-10-661-798-5	Sequence 5, Appl
44	96	100.0	352	16	US-10-791-505-2	Sequence 2, Appl
45	96	100.0	352	16	US-10-612-791-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-10-084-813-13
; Sequence 13, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT FILING DATE: 2002-02-27
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-13

Query Match 100.0%; Score 96; DB 14; Length 18;
Best Local Similarity 100.0%; Pred.No. 3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVLG 18

Db 1 SQYQFWKNFQTLKIVLG 18

RESULT 2

US-10-084-813-77
; Sequence 77, Application US/10084813
; Publication No. US20030068615A1

GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084.813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-77

Query Match 100.0%; Score 96; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-10-661-798-11
; Sequence 11, Application US/10661798
; Publication No. US20040110127A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; APPLICANT: Frederic, Libert
; TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV En
; FILE REFERENCE: 9409/2023F
; CURRENT APPLICATION NUMBER: US/10/661,798
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: 09/938,703
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/626,939
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 08/833,752
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: 08/810,028
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: EP 96870021.1
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: EP 96870102.9
; PRIOR FILING DATE: 1996-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-798-11

Query Match 100.0%; Score 96; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4 SOYQFWKNFQTLKIVILG 21

RESULT 4

US-10-612-791-11
; Sequence 11, Application US/10612791
; Publication No. US20040161739A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; APPLICANT: Gilbert
; TITLE OF INVENTION: HIV Diagnostic Methods
; FILE REFERENCE: 9409/2023E
; CURRENT APPLICATION NUMBER: US/10/612,791
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/938,703
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/626,939
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 08/833,752
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: 08/810,028
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: EP 96870021.1
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: EP 96870102.9
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; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-791-11

Query Match 100.0%; Score 96; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
|||
DB 4 SOYQFWKNFQTLKIVILG 21

RESULT 5

US-09-938-719-11
; Sequence 11, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:

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; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 54 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 11:
;
US-09-938-719-11
Query Match      100.0%; Score 96; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 9 SQYQFWKNFQTLKIVILG 26

RESULT 6
US-09-939-226-11
; Sequence 11, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 54 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 11:
;
US-09-939-226-11
Query Match      100.0%; Score 96; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 9 SQYQFWKNFQTLKIVILG 26

RESULT 7
US-09-938-703-11
; Sequence 11, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 54 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 11:
;
US-09-938-703-11
Query Match      100.0%; Score 96; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 9 SQYQFWKNFQTLKIVILG 26

RESULT 8
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
;
US-09-725-285-2
Query Match      100.0%; Score 96; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 9 SQYQFWKNFQTLKIVILG 26
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

Query Match          100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SQYQFWKNFQTLKIVILG 18
Db      185 SQYQFWKNFQTLKIVILG 202

RESULT 9
US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Perros, Manoussos
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PC10348PME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-841-2

Query Match          100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SQYQFWKNFQTLKIVILG 18
Db      185 SQYQFWKNFQTLKIVILG 202

RESULT 10
US-09-779-879A-2
; Sequence 2, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
US-09-779-879A-2

Query Match          100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SQYQFWKNFQTLKIVILG 18
Db      185 SQYQFWKNFQTLKIVILG 202

RESULT 11
US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-22

Query Match          100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SQYQFWKNFQTLKIVILG 18
Db      185 SQYQFWKNFQTLKIVILG 202

RESULT 12
US-09-779-880A-2
; Sequence 2, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
US-09-779-880A-2
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; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-2

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 13

US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-22

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 14

US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 15

; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-15

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 15

US-09-813-653-17
; Sequence 17, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 17
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-17

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 16

US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US2002006813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SOYQFWKNFQTLKIVILG 18
Db      185 SOYQFWKNFQTLKIVILG 202

RESULT 17
US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2
Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SOYQFWKNFQTLKIVILG 18
Db      185 SOYQFWKNFQTLKIVILG 202

RESULT 18
US-09-339-912A-2
; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2
Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SOYQFWKNFQTLKIVILG 18
Db      185 SOYQFWKNFQTLKIVILG 202

RESULT 19
US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2
Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SOYQFWKNFQTLKIVILG 18
Db      185 SOYQFWKNFQTLKIVILG 202

RESULT 20
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5
Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SOYQFWKNFQTLKIVILG 18
Db      185 SOYQFWKNFQTLKIVILG 202

US-09-938-719-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-939-226-5

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 21
US-09-938-703-5
; Sequence 5, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 22
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. US20020132269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
; FILE REFERENCE: HDGRL10
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 23
US-09-734-221A-14
; Sequence 14, Application US/09734221A
; Publication No. US20030096221A1
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; DENG, HONGKUI
; ELLMEIER, WILFRIED
; LANDAU, NATHANIEL R.
; LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,221A
; FILING DATE: 11-Dec-2000

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;
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14

Query Match      100.0%; Score 96; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SOYQFWKNFQTLKIVILG 18
Db      185 SOYQFWKNFQTLKIVILG 202

RESULT 24
US-09-826-509-477
; Sequence 477, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 477
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-477

Query Match      100.0%; Score 96; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SOYQFWKNFQTLKIVILG 18
Db      185 SOYQFWKNFQTLKIVILG 202

RESULT 25
US-10-151-274-5
; Sequence 5, Application US/10151274
; Publication No. US20030064071A1
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Xwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
; TITLE OF INVENTION: INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/10/151,274
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US/09/517,605
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-274-5

Query Match      100.0%; Score 96; DB 12; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SOYQFWKNFQTLKIVILG 18
Db      185 SOYQFWKNFQTLKIVILG 202

RESULT 26
US-10-106-623-2
; Sequence 2, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
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; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2

Query Match 100.0%; Score 96; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 27
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 28
US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; PRIOR FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 29
US-10-067-800-2
; Sequence 2, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000I
; CURRENT APPLICATION NUMBER: US/10/067,800
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-2

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 30
US-10-067-800-22
; Sequence 22, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000I
; CURRENT APPLICATION NUMBER: US/10/067,800
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-067-800-22

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
   |||||
Db 185 SOYQFWKNFQTLKIVILG 202

RESULT 31
US-10-290-058A-6
; Sequence 6, Application US/10290058A
; Publication No. US20030104455A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and Compositions for Treating
; FILE REFERENCE: MP101-289P1RM
; CURRENT APPLICATION NUMBER: US/10/290,058A
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/344,552
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-290-058A-6

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
   |||||
Db 185 SOYQFWKNFQTLKIVILG 202

RESULT 32
US-10-225-567A-352
; Sequence 352, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-352

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
   |||||
Db 185 SOYQFWKNFQTLKIVILG 202
```

```
RESULT 33
US-10-323-314-1
; Sequence 1, Application US/10323314
; Publication No. US20030139571A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010-1/JPM/MAF/DJK
; CURRENT APPLICATION NUMBER: US/10/323,314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-10-323-314-1

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
   |||||
Db 185 SOYQFWKNFQTLKIVILG 202

RESULT 34
US-10-072-301-1
; Sequence 1, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-301-1

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
   |||||
Db 185 SOYQFWKNFQTLKIVILG 202

RESULT 35
US-10-164-649-52
; Sequence 52, Application US/10164649
; Publication No. US20030162943A1
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
```

; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/164,649
; FILING DATE: 07-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-164-649-52

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 36
US-10-071-866-1
; Sequence 1, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST P
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-866-1

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 37
US-10-135-839-2
; Sequence 2, Application US/10135839
; Publication No. US20030166024A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGHR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-03-09
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-2

; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGHR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-2

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 38
US-10-135-839-22
; Sequence 22, Application US/10135839
; Publication No. US20030166024A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGHR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-22

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 39
US-10-239-423-67
; Sequence 67, Application US/10239423
; Publication No. US2003018689A1
; GENERAL INFORMATION:

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; APPLICANT: FORSMANN, Wolf-Georg; FORSMANN, Ulf; ADERMAN, Knut;
; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikola
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
; FILE REFERENCE: 022217us
; CURRENT APPLICATION NUMBER: US/10/239,423
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: DE10016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-67

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Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SOYQFWKMFQTLKIVILG 18
DB 185 SOYQFWKMFQTLKIVILG 202

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RESULT 40
US-10-439-845-2
; Sequence 2, Application US/10439845
; Publication NO. US20030195348A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; TITLE OF INVENTION: AND THERAPEUTIC AGENTS FOR HIV INFECTION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-439-845-2
Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYQFWKMFQTLKIVILG 18
DB 185 SOYQFWKMFQTLKIVILG 202
Search completed: September 28, 2004, 09:44:41
Job time : 59.625 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:57:36 ; Search time 9.675 Seconds
(without alignments)
178.961 Million cell updates/sec

Title: US-10-084-813-13
Perfect score: 96
Sequence: 1 SQYQFWXNFQTLKIVILG 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	352	2 A43113	chemokine (C-C) re
2	47	49.0	355	2 I49339	macrophage inflam
3	46	47.9	196	2 T22609	hypothetical prote
4	45	46.9	177	2 S34499	hypothetical prote
5	45	46.9	302	2 G75203	2-phosphoglycerate
6	45	46.9	314	2 G85575	hypothetical prote
7	45	46.9	314	2 G90724	hypothetical prote
8	45	46.9	1289	2 S67200	hypothetical prote
9	44.5	46.4	301	2 C71236	probable 2-phospho
10	44	45.8	467	2 A81263	probable integral
11	44	45.8	616	1 I64056	secretion protein
12	43	44.8	237	2 C95199	nitrereductase fam
13	43	44.8	237	2 A98066	NADPH-flavin oxido
14	43	44.8	242	2 A86719	oxidoreductase yng
15	43	44.8	344	2 JCS942	chemokine receptor
16	43	44.8	475	2 G98183	periplasmic sorbit
17	43	44.8	3587	2 I40486	surfactin syntheta
18	42	43.8	241	2 S30843	UTR4 protein - yea
19	42	43.8	350	2 E81303	probable branched-
20	42	43.8	383	2 D90528	hypothetical prote
21	42	43.8	421	2 AB2315	PAD-dependent mono
22	42	43.8	421	2 E97889	hypothetical prote
23	42	43.8	496	2 C84678	hypothetical prote
24	41.5	43.2	159	2 H81442	hypothetical prote
25	41.5	43.2	334	2 S16296	hypothetical prote
26	41.5	43.2	334	2 A85558	ferric enterobacti
27	41.5	43.2	334	2 E90707	ferric enterobacti
28	41	42.7	46	2 I37047	NADH2 dehydrogenas
29	41	42.7	118	2 H83734	hypothetical prote

RESULT 1

A43113

Chemokine (C-C) receptor 5 - human

N/Alternate names: C-C CR-5; CCR5

C/Species: Homo sapiens (man)

C/Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000

C/Accession: A43113; S71808; A58834; A58832; G02653; A58833

R/Samson: M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

Biochemistry 35, 3362-3367, 1996

A/Title: Molecular cloning and functional expression of a new human CC-chemokine receptor

A/Reference number: A43113; MUID:96241590; PMID:8639485

A/Accession: A43113

A/Molecule type: mRNA

A/Residues: 1-352 <SAM1>

A/Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811

R/Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragost;

M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa;

Nature 382, 722-725, 1996

A/Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of

A/Reference number: S71808; MUID:96345670; PMID:8751444

A/Accession: S71808

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 182-206;207-230 <SAM2>

A/Accession: A58834

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-184,'IKDSHLGAGPARACHGHLILGNPKNSASYSK' <SAM3>

A/Cross-references: GB:X93939; NID:g1524062; PIDN:CAA67767.1; PID:g1524063

A/Note: This frameshift mutation results in a non-functional receptor but confers a degree

nd may have had a selective advantage by conferring resistance to Yersinia plague infect;

R/Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.

J. Leukoc. Biol. 60, 147-152, 1996

A/Title: Cloning and functional expression of CC CK35, a human monocyte CC chemokine rec

A/Reference number: A58832; MUID:96295970; PMID:8699119

A/Accession: A58832

A/Molecule type: mRNA

A/Residues: 1-352 <COM1>

A/Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409

A/Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes

R/Combadiere, C.

submitted to the EMBL Data Library, May 1996

A/Reference number: H01541

A/Accession: G02653

A/Status: translated from GB/EMBL/DBDJ

A/Molecule type: mRNA

A/Residues: 1-89,'I',91-352 <COM2>

A/Cross-references: EMBL:U57840

R/Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.

J. Biol. Chem. 271, 17161-17166, 1996

A/Title: Molecular cloning and functional characterization of a novel human CC chemokine

A/Reference number: A58833; MUID:96291862; PMID:8663314


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A:Gene: PAB2253
C:Superfamily: 2-phosphoglycerate kinase

Query Match          46.9%; Score 45; DB 2; Length 302;
Best Local Similarity 37.5%; Pred. No. 10;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 QYQFWKNFQTLKIVIL 17
    :|||:|:|:|:|
Db 77 RYLFWRFRKQKVPLL 92

RESULT 6
G85575
hypothetical protein Z0898 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: G85575
R:Ferna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.;
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, N.;
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11208551
A:Accession: G85575
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-314 <STO>
A:Cross-references: GB:AE005174; NID:g12513664; PIDN:AGS5067.1; GSPDB:GN00145; UWGP:Z0898
A:Experimental source: strain O157:H7, substrain EDL333
C:Genetics:
A:Gene: Z0898

Query Match          46.9%; Score 45; DB 2; Length 314;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVI 16
    |||:|:|:|:|
Db 289 SQYRFFKMTNLALVI 304

RESULT 7
G90724
hypothetical protein ECs0767 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: G90724
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: G90724
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-314 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA034190.1; PID:g13360226; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs0767

Query Match          46.9%; Score 45; DB 2; Length 314;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVI 16
    |||:|:|:|:|
Db 289 SQYRFFKMTNLALVI 304

RESULT 8
S67200
hypothetical protein YOR296w - yeast (Saccharomyces cerevisiae)

```

A;Cross-references: GB:AL139079; GB:AL111169; NID:G6968971; PIDN:CAB73647.1; PID:G696907
 A;Experimental source: serotype O2, strain NCTC 11168
 C;Genetics:
 A;Gene: Cj1660

Query Match 45.8%; Score 44; DB 2; Length 467;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 YQFWKFNQTLKIVILG 18

DB 77 FYFWKTEILNFILLG 92

RESULT 11

I64056

secretion protein secD - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman,
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
 A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: I64056

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-616 <TIGR>

A;Cross-references: GB:U22710; GB:I42023; NID:G1573200; PIDN:AAC21908.1; PID:G1573205; T

C;Genetics:

C;Superfamily: protein export membrane protein secD

C;Keywords: inner membrane; protein export; transmembrane protein

F;10-30/Domain: transmembrane #status predicted <TM1>

F;457-473/Domain: transmembrane #status predicted <TM2>

F;478-495/Domain: transmembrane #status predicted <TM3>

F;503-519/Domain: transmembrane #status predicted <TM4>

F;565-581/Domain: transmembrane #status predicted <TM5>

F;587-605/Domain: transmembrane #status predicted <TM6>

Query Match 45.8%; Score 44; DB 1; Length 616;
 Best Local Similarity 38.9%; Pred. No. 30;
 Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18

DB 3 NRYPLKMLWIFVIAIG 20

RESULT 12

C95199

nitroreductase family protein [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001

R;Fetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
 nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A;Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: C95199

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-237 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75788.1; PID:G14973205; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP1710

C;Superfamily: NADPH-flavin oxidoreductase homolog

Query Match 44.8%; Score 43; DB 2; Length 237;
 Best Local Similarity 41.7%; Pred. No. 17;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17

DB 40 WKNFQSYVIVV 51

RESULT 13

A98066

NADPH-flavin oxidoreductase (EC 1.6.99.-) homolog [imported] - Streptococcus pneumoniae

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Es
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: A98066

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-237 <KUR>

A;Cross-references: GB:AE007317; PIDN:AAL00358.1; PID:G15459219; GSPDB:GN00174

C;Genetics:

A;Gene: frp

C;Superfamily: NADPH-flavin oxidoreductase homolog

C;Keywords: oxidoreductase

Query Match 44.8%; Score 43; DB 2; Length 237;
 Best Local Similarity 41.7%; Pred. No. 17;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17

DB 40 WKNFQSYVIVV 51

RESULT 14

A86719

oxidoreductase yhgA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C;Accession: A86719

R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Mearns, K.; Weissenbach, J.; Ehrlic
 Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: A86719

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-242 <STO>

A;Cross-references: GB:AE005176; PID:G12723669; PIDN:AAK04851.1; GSPDB:GN00146

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: yhgA

C;Superfamily: NADPH-flavin oxidoreductase homolog

Query Match 44.8%; Score 43; DB 2; Length 242;
 Best Local Similarity 41.7%; Pred. No. 17;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17

DB 43 WKNFQSYVIVV 54

RESULT 15

JC5942
chemokine receptor - human
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JC5942
R:Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A:Title: Cloning and characterization of a novel human chemokine receptor.
A:Reference number: JC5942; MUID:98139902; PMID:9473515
A:Accession: JC5942
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-344 <P>
A:Cross-references: GB:U97123; NID:92897070; PIDN:AAC39595.1; PID:g2897071
C:Superfamily: vertebrate rhodopsin

Query Match 44.8%; Score 43; DB 2; Length 344;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 5 FWKNFQTLKIVL 16
|||:||||:
Db 195 FWKHFLTKWNI 206

RESULT 16
G98183
periplasmic sorbitol-binding protein, smcB (AF018073) [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C:Accession: G98183
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G98183
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-475 <K>
A:Cross-references: GB:AE007870; PIDN:AAK8993.1; PID:g15158779; GSPDB:GX00170
C:Genetics:
A:Gene: AGR_L_841
A:Map position: linear chromosome

Query Match 44.8%; Score 43; DB 2; Length 475;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 5 FWKNFQTLKIVL 18
|||:||||:
Db 34 FWEEDMTLKILG 47

RESULT 17
140486
surfactin synthetase component II - Bacillus subtilis
N:Alternate names: surfactin synthetase srfA2; surfactin synthetase/competence protein srfA2
C:Species: Bacillus subtilis
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 03-Nov-2000
C:Accession: I40486; S60866; C69718; S46368; S35518; S25658; S34986
R:Cosmina, P.; Rodriguez, F.; de Ferra, F.; Grandi, G.; Perego, M.; Venema, G.; van Sinderen, D.; Mol. Microbiol. 8, 821-831, 1993
A:Title: Sequence and analysis of the genetic locus responsible for surfactin synthesis
A:Reference number: I40485; MUID:93360813; PMID:8355609
A:Accession: I40486
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3587 <RES>
A:Cross-references: EMBL:X70356; NID:g396480; PIDN:CAA49817.1; PID:g396482
A:Experimental source: strain W168 derivative of JH642
R:Hamoen, L.W.; Eshuis, H.; Jongbloed, J.; Venema, G.; van Sinderen, D.

Mol. Microbiol. 15, 55-63, 1995
A:Title: A small gene, designated comS, located within the coding region of the fourth an
A:Reference number: S60866; MUID:95272393; PMID:7752896
A:Accession: S60866
A:Molecule type: DNA
A:Residues: 977-1104 <HAM>
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C:Bron, S.; Brouillette, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A:Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Boulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
A:Residues: 1-3587 <KUN>
A:Cross-references: GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB12143.1; PID:g2632635
A:Experimental source: strain 168
R:Fabret, C.; Quentin, Y.; Guisepi, A.; Busuttill, J.; Haiteh, J.; Denizot, F.
Submitted to the EMBL Data Library, March 1993
A:Reference number: S46967
A:Accession: S46968
A:Molecule type: DNA
A:Residues: 1-32, F, 34-41, G, 43-109, D, 111-114, G, 116-138, V, 140-258, W, 260-308, A, 1
1956-1914, PK, 1917-2138, SRU, 2142, DSLN, 2146-2441, Q, 2446-2712, H, 2714-2722, H, 272
A:Cross-references: EMBL:X72672; NID:9516358; PIDN:CAA51223.1; PID:g516360
R:Fuma, S.; Fujishima, Y.; Corbelli, N.; D'Souza, C.; Nakano, M.M.; Zuber, P.; Yamane, K.
Nucleic Acids Res. 21, 93-97, 1993
A:Title: Nucleotide sequence of 5' portion of srfA that contains the region required for
A:Reference number: S35517; MUID:93181186; PMID:8441623
A:Accession: S35518
A:Status: significant sequence differences
A:Molecule type: DNA
A:Cross-references: EMBL:D13262; NID:g216345; PID:g216347
A:Experimental source: strain 168 trpC2
R:Borchert, S.; Patil, S.S.; Marahiel, M.A.
FEBS Microbiol. Lett. 92, 175-180, 1992
A:Title: Identification of putative multifunctional peptide synthetase genes using highly
A:Reference number: S25658
A:Accession: S25658
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 168, C, 170-171, 281-283, 514-595, 597-647, R, 649-679, ETL, 683-693, DKR, 697, A
A:Cross-references: EMBL:X65835; NID:940202; PIDN:CAA46678.1; PID:g40203
A:Experimental source: strain ATCC 21332
C:Comment: This protein contains several amino acid-activating domains for the synthesis
the amino-terminal region of this protein, appear to be required for the development of
C:Genetics:
A:Gene: srfA2
C:Superfamily: surfactin synthetase; acetate-CoA ligase homology; acyl carrier protein ho
F:Keywords: antibiotic biosynthesis; carrier protein; duplication; ligase; phosphopanteti
F:511-951/Domain: acetate-CoA ligase homology <ACLI>
F:968-1035/Domain: acyl carrier protein homology <ACP1>
F:1036-1481/Domain: repeat <RPT1>
F:1549-1995/Domain: acetate-CoA ligase homology <ACLI2>
F:2013-2081/Domain: acyl carrier protein homology <ACP2>
F:2082-2529/Domain: repeat <RPT2>
F:2591-3108/Domain: acetate-CoA ligase homology <ACLI3>
F:3041-3108/Domain: acyl carrier protein homology <ACP3>
F:999,2045,3073/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 44.8%; Score 43; DB 2; Length 3587;
Best Local Similarity 33.3%; Pred. No. 2.7e+02;

hypothetical protein AGR_C_4995 [imported] - Agrobacterium tumefaciens (strain C58, Cer
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C/Accession: E97689
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2322-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Acession: E97689
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-421 <CUR>
A/Cross-references: GB:AE007869; PIDN:AAK88470.1; PID:g15157975; GSPDB:GN00169
C/Genetics:
A/Gene: AGR_C_4995
A/Map position: circular chromosome
C/Superfamily: ubiH protein

Query Match 43.8%; Score 42; DB 2; Length 421;
Best Local Similarity 46.2%; Pred. No. 44;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 QYQFWKNFOTLKI 14
::|::|::|::|
Db 349 RYQSWRRFDTLRM 361

RESULT 23
C84678
hypothetical protein At2g27900 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-feb-2001 #text_change 02-Feb-2001
C/Accession: C84678
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VarAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Acession: C84678
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-496 <STO>
A/Cross-references: GB:AE002093; NID:g4510426; PIDN:AAD21512.1; GSPDB:GN00139
C/Genetics:
A/Gene: At2g27900
A/Map position: 2

Query Match 43.8%; Score 42; DB 2; Length 496;
Best Local Similarity 52.9%; Pred. No. 52;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 SQYQFWKNFOTLKIVIL 17
|||::|::|::|
Db 100 SIHQFLKNYEDLSIFIL 116

RESULT 24
H81442
hypothetical protein Cj0249 [imported] - Campylobacter jejuni (strain NCTC 11168)
C/Species: Campylobacter jejuni
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C/Acession: H81442
R/Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chiller
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A/Reference number: A81250; MUID:20150912; PMID:10688204
A/Acession: H81442
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-159 <PAR>

A;Cross-references: GB:ALU39074; GB:ALU11168; NID:g6967505; PIDN:CAB72717.1; PID:g696772

A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics:

A;Gene: Cj0249

C;Superfamily: Campylobacter jejuni hypothetical protein Cj0249

Query Match 43.2%; Score 41.5; DB 2; Length 159;
Best Local Similarity 40.0%; Pred. No. 20;
Matches 8; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

QY 3 YQFWKN-----FQTUKIVIL 17
| | | | | : | : |
DB 33 YKFWNAEIGRYQGTRLIIFL 52

RESULT 25

S16296
ferric enterobactin transport protein fepD - Escherichia coli (strain K-12)

N;Alternate names: ferricenterobactin permease fepD

C;Species: Escherichia coli

C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 01-Mar-2002

C;Accession: S16296; S16305; D64792; S14841

R;Shea, C.M.; McIntosh, M.A.

Mol. Microbiol. 5, 1415-1428, 1991

A;Title: Nucleotide sequence and genetic organization of the ferric enterobactin transporter

A;Reference number: S16295; MUID:92157868; PMID:1838574

A;Accession: S16296

A;Molecule type: DNA

A;Residues: 1-334 <SHE>

A;Cross-references: EMBL:X57471; NID:g41429; PIDN:CAA40707.1; PID:g41430

R;Chenault, S.S.; Earhart, C.F.

Mol. Microbiol. 5, 1405-1413, 1991

A;Title: Organization of genes encoding membrane proteins of the Escherichia coli ferrier

A;Reference number: S16305; MUID:92157867; PMID:1787794

A;Accession: S16305

A;Molecule type: DNA

A;Residues: 1-232, 'AL', 235-334 <CHE>

A;Cross-references: EMBL:X59402; NID:g41433; PIDN:CAA42043.1; PID:g41434

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

A.; Rose, D.J.; Mau, B.; Shaoh, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: D64792

A;Status: nucleic acid sequence not shown; translation not shown

A;Residues: 1-334 <BLAT>

A;Cross-references: GB:A5000164; GB:U00096; NID:g1786800; PIDN:AACT3691.1; PID:g1786805;

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: fepD

A;Map position: 14 min

C;Superfamily: vitamin B12 transport protein btuC

C;Keywords: transmembrane protein

F;16-32/Domain: transmembrane #status predicted <TM1>

F;65-81/Domain: transmembrane #status predicted <TM2>

F;94-110/Domain: transmembrane #status predicted <TM3>

F;121-137/Domain: transmembrane #status predicted <TM4>

F;156-172/Domain: transmembrane #status predicted <TM5>

F;198-214/Domain: transmembrane #status predicted <TM6>

F;240-256/Domain: transmembrane #status predicted <TM7>

F;284-300/Domain: transmembrane #status predicted <TM8>

F;310-326/Domain: transmembrane #status predicted <TM9>

Query Match 43.2%; Score 41.5; DB 2; Length 334;
Best Local Similarity 34.8%; Pred. No. 42;
Matches 8; Conservative 5; Mismatches 3; Indels 7; Gaps 1;

QY 2 QYQFW-----KNFTUKIVIL 17
| | | | | : | | | | |
DB 179 QLRFWQAGSLDIRNLTKVILI 201

RESULT 26

A85558
 ferric enterobactin (enterochelin) transport [imported] - Escherichia coli (strain O157:H7)
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
 C:Accession: A85558
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: A85558
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-334 <STO>
 A:Cross-references: GB:AE005174; NID:G12513480; PIDN:AAG54925.1; GSPDB:GN00145; UWGP:Z07
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: fepp
 C:Superfamily: vitamin B12 transport protein btuC

Query Match 43.2%; Score 41.5; DB 2; Length 334;
 Best Local Similarity 34.8%; Pred. No. 42;
 Matches 8; Conservative 5; Mismatches 3; Indels 7; Gaps 1;

QY 2 QYQFW-----KNFQTLKIVIL 17
 DB 179 QLRFWQAGSLDIRNLHTLKVLI 201

RESULT 27

E90707
 ferric enterobactin (enterochelin) transport Ecs0629 [imported] - Escherichia coli (stra
 C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
 C:Accession: E90707
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: E90707
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-334 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA034052.1; PID:G13360087; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RWD 0509952
 C:Genetics:
 A:Gene: Ecs0629
 C:Superfamily: vitamin B12 transport protein btuC

Query Match 43.2%; Score 41.5; DB 2; Length 334;
 Best Local Similarity 34.8%; Pred. No. 42;
 Matches 8; Conservative 5; Mismatches 3; Indels 7; Gaps 1;

QY 2 QYQFW-----KNFQTLKIVIL 17
 DB 179 QLRFWQAGSLDIRNLHTLKVLI 201

RESULT 28

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - siamang mitochondrion (fragment)
 C:Species: Mitochondrion Hylobates syndactylus (siamang)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 03-Jun-2002
 C:Accession: I37047
 R:Horai, S.; Satta, Y.; Hayaoka, K.; Kondo, R.; Inoue, T.; Ishida, T.; Hayashi, S.; Tak
 J. Mol. Evol. 35, 32-43, 1992
 A>Title: Man's place in Hominoidea revealed by mitochondrial DNA genealogy.
 A:Reference number: I37047; MUID:92389366; PMID:1518083
 A:Accession: I37047
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-46 <HOR>
 A:Cross-references: GB:D38484; NID:G558513; PIDN:BAA07494.1; PID:G558514
 C:Genetics:
 A:Gene: ND1
 A:Genome: mitochondrion
 A:Genetic code: SGCI
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 1
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c

Query Match 42.7%; Score 41; DB 2; Length 46;
 Best Local Similarity 46.7%; Pred. No. 6.7;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 YQFWKNFQTLKIVIL 17
 DB 15 YLLWKNFQTLKIVIL 29

RESULT 29

H83734
 hypothetical protein BH0680 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: H83734
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
 Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and s
 A:Reference number: A83650; MUID:20512592; PMID:11058132
 A:Accession: H83734
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-118 <STO>
 A:Cross-references: GB:AP001509; GB:BA000004; NID:G10173176; PIDN:BA04399.1; GSPDB:GN001
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH0680

Query Match 42.7%; Score 41; DB 2; Length 118;
 Best Local Similarity 41.2%; Pred. No. 17;
 Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 QYQFWKNFQTLKIVILG 18
 DB 70 QYEWKHTQIIDVVDG 86

RESULT 30

S03215
 hypothetical protein D-244 - Sulfolobus particle SSV1
 C:Species: Sulfolobus particle SSV1
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Apr-2000
 C:Accession: S03215
 R:Palm, P.; Grampp, B.; Zillig, W.; Yeats, S.; McWilliams, P.; Reiter, W.D.
 submitted to the EMBL Data Library, March 1988
 A:Reference number: S03211
 A:Accession: S03215
 A:Molecule type: DNA
 A:Residues: 1-244 <PAL>
 A:Cross-references: EMBL:X07234; NID:G46703; PIDN:CAA30214.1; PID:G46708
 C:Superfamily: Sulfolobus particle SSV1 hypothetical protein D-244

Query Match 42.7%; Score 41; DB 2; Length 244;
 Best Local Similarity 40.0%; Pred. No. 37;
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 QYQFWKNFQTLKIVILG 18
 DB 216 QYWKNTDLRVSLKG 230

RESULT 31

A84494
 envelope-like protein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A89494

M.;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umavam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUJD:20083487; PMID:10617197

A;Accession: B84494

A>Status: preliminary

A:Molecule type: DNA

A;Residues: 1-285 <STO>

A;Cross-references: GB:AE002093; NID:g47333967; PIDN:AAD28650.1; GSPDB:GN00139

C;Genetics:

A;Gene: Atg10850

A;Map position: 2

Query Match 42.7%; Score 41; DB 2; Length 285;
Best Local Similarity 41.7%; Pred.No. 43;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 YQWKNFQTLLKI 14
Db 173 FEFWANPTMKV 184
 :||| | ||:
 +-----+

RESULT 32

I40547

oligopeptide ABC transporter (permease) appC - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 20-Jun-2000

C;Accession: I40547; E69586

R/Koide, A.; Hoch, J.A.
Mol. Microbiol. 13, 417-426, 1994

A>Title: Identification of a second oligopeptide transport system in Bacillus subtilis

A;Reference number: I40543; MUJD:95089678; PMID:7997159

A;Accession: I40547

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A;Residues: 1-303 <RES>

A;Cross-references: EMBL:U0909; NID:g677942; PIDN:AAA62360.1; PID:g677947

R;Kunst, F.; Ogawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Giballet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapides, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
y, M.; Ogawa, K.; Ogijwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohli, T.M.; Portelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Serot
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstra, P.; Togroni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wiopat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUJD:98044033; PMID:9384377

A;Accession: B69586

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A;Residues: 1-303 <LIN>

A;Cross-references: GB:E99110; GB:AL009126; NID:g2633472; PIDN:CAB12997.1; PID:g2633494

A;Experimental source: strain 168

C;Genetics:

A;Gene: appC

C;Superfamily: oligopeptide permease protein oppB

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Query Match      42.7%; Score 41; DB 2; Length 303;
Best local Similarity 50.0%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 5 FWRNFQTLKIVILG 18

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Db      29 FWEKFSKNLAILG 42
      ||: | | : |||
RESULT 33
T22197
hypochothetical protein F44G3.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T22197
R/McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19529
A:Accession: T22197
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-316 <WIL>
A:Cross-references: EMBL:Z83109; PIDN:CAB05515.1; GSPDB:GN00023; CESP:F44G3
C:Genetics:
A:Gene: CESP:F44G3.5
A:Map position: 5
A:Introns: 142/3; 185/3; 256/3
Query Match 42.7%; Score 41; DB 2; Length 316;
Best Local Similarity 57.1%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps
Qy 4 QFWKFPQILKIVIL 17
      ||: | | : |||
Db 36 QFFKNYFNLIKTFVL 49
RESULT 34
Tl1833
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - common gibbon mitochondrion
C/Species: mitochondrion Hylobates lar (common gibbon, white-handed gibbon)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C/Accession: Tl1833
R/Arason, U.; Gullberg, A.; Xu, X.
Hereditas 124, 185-189, 1996
A:Title: A complete mitochondrial DNA molecule of the white-handed gibbon,
A:Reference number: Z17353
A:Accession: Tl1833
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-318 <ARN>
A:Cross-references: EMBL:X99256; PIDN:CAA67628.1
A:Experimental source: isolate Ester
C:Genetics:
A:Genome: mitochondrion
A:Gene: NADH1
A:Note: NADH1
C/Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation
Query Match 42.7%; Score 41; DB 2; Length 318;
Best Local Similarity 46.7%; Pred. No. 48;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps
Qy 3 YQFWKFPQILKIVIL 17
      ||: | | : |||
Db 287 YLLWKNFPLPLTILL 301

```

RESULT 35
D83385
hypothetical protein PA2090 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83385
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larrabie
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey

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.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: AB2950; MUID:20437337; PMID:10964043
A:Accession: D83385
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <STO>
A:Cross-references: GB:AE004636; GB:AE004091; NID:59948093; PIDN:AG05478.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2090

Query Match 42.7%; Score 41; DB 2; Length 359;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 9; Conservative 2; Mismatches 0; Indels 4; Gaps 1;

QY 4 QPWNFQTLKIVILG 18
DB 233 KFWKHFQ-----VILG 243

RESULT 36
E42594
hypothetical protein ORF5 hycC 3'-region, hycE 5'-region - Pseudomonas sp. plasmid PHN67
C:Species: Pseudomonas sp.
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: E42594; A41895
R:Watabe, K.; Ishikawa, T.; Mukohara, Y.; Nakamura, H.
J. Bacteriol. 174, 962-969, 1992
A>Title: Cloning and sequencing of the genes involved in the conversion of 5-substituted
A:Reference number: A42594; MUID:92121137; PMID:1733229
A:Accession: E42594
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <WAT>
A:Cross-references: GB:D10494; GB:D90469; NID:G216829; PIDN:BAA01380.1; PID:G216834
A:Note: sequence extracted from NCBI backbone (NCBIN:77753, NCBI:77764)
R:Watabe, K.; Ishikawa, T.; Mukohara, Y.; Nakamura, H.
J. Bacteriol. 174, 3461-3466, 1992
A>Title: Identification and sequencing of a gene encoding a hydantoin racemase from the
A:Reference number: A41895; MUID:92276321; PMID:1339422
A:Accession: A41895
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 244-456 <WAT>
A:Experimental source: strain NS671
A:Note: sequence extracted from NCBI backbone (NCBIN:104597, NCBI:104598)
C:Genetics:
A:Genome: plasmid
C:Superfamily: Escherichia coli probable transport protein b0511

Query Match 42.7%; Score 41; DB 1; Length 456;
Best Local Similarity 42.9%; Pred. No. 69;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 QYQFKNFQTLKIV 15
DB 382 QYKWNVNPAAII 395

RESULT 37
S47920
pre-mRNA splicing factor PRP39 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YN9827.06; protein YML046w
C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C:Accession: S47920; S50946
R:Lockhart, S.R.; Rymond, B.C.
Mol. Cell. Biol. 14, 3623-3633, 1994
A>Title: Commitment of yeast pre-mRNA to the splicing pathway requires a novel U1 small
A:Reference number: S47920; MUID:94254821; PMID:8196608
A:Accession: S47920

```

```

A:Molecule type: DNA
A:Residues: 1-629 <LOC>
A:Cross-references: EMBL:L29224; NID:G460045; PIDN:AAA20131.1; PID:G460046
A:Note: the authors translated the codon GAC for residue 29 as Ala
R:Odell, C.; Bowman, S.
submitted to the EMBL Data Library, January 1995
A:Reference number: S50941
A:Accession: S50946
A:Molecule type: DNA
A:Residues: 1-629 <CODE>
A:Cross-references: EMBL:Z47816; NID:G642303; PID:G642309; MIPS:YML046w
C:Genetics:
A:Gene: SGD:PRP39
A:Cross-references: SGD:S0004509; MIPS:YML046w
A:Map position: 13L
C:Function:
A:Description: pre-mRNA splicing
A:Note: necessary for the stable interaction of mRNA precursors with the snRNP components
C:Keywords: nucleus; pre-mRNA splicing; transmembrane protein
F:429-445/Domain: transmembrane #status predicted <TMM>

Query Match 42.7%; Score 41; DB 2; Length 629;
Best Local Similarity 37.5%; Pred. No. 96;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 YQFKNFQTLKIVILG 18
DB 88 FGFWRKFAIEYQLFG 103

RESULT 38
T48016
probable zinc-finger protein - Arabidopsis thaliana
N:Alternate names: protein T17J13.200
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T48016
R:Riegler, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, F.
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24482
A:Accession: T48016
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-812 <RIE>
A:Cross-references: EMBL:AL138651
A:Experimental source: cultivar Columbia; BAC clone T17J13
C:Genetics:
A:Map position: 3
A:Introns: 56/3; 159/3; 229/2; 245/3; 275/3; 296/3
A:Note: T17J13.200

Query Match 42.7%; Score 41; DB 2; Length 812;
Best Local Similarity 46.2%; Pred. No. 1.2e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYQFKNFQTLKI 14
DB 234 QYEYKNYDDLEI 246

RESULT 39
T49799
related to TOM1 protein [imported] - Neurospora crassa
N:Alternate names: protein B11B22.10
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49799
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49799
A:Status: preliminary
A:Molecule type: DNA

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A;Residues: 1-3839 <SCH>
A;Cross-references: ENBL:ALJ56934; GSPDB:GN00116; NCSP:B11B22.10
A;Experimental source: BAC clone B11B22; strain OR74A
C;Genetics:
A;Gene: NCSP:B11B22.10
A;Map position: 6
A;Introns: 16/3; 2607/1; 2623/1; 2658/1; 2845/1; 2987/2; 3204/3; 3594/1; 3809/1

Query Match 42.7%; Score 41; DB 2; Length 3839;
Best Local Similarity 54.5%; Pred. No. 6e+02;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WKNFQTLKIVI 15
:|||||:::
Db 1219 YKNFQTLRVLL 1229

RESULT 40
H91193
DNA-damage-inducible protein [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: H91193
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yaunegara, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H91193
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-278 <HAY>
A;Cross-references: GB:BA000007; PID:BA037943.1; PID:g13363995; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECS4520

```

Query Match      42.2%; Score 40.5; DB 2; Length 278;
Best Local Similarity 25.6%; Pred. No. 50;
Matches 10; Conservative 4; Mismatches 2; Indels 23; Gaps 1;

Cq 3 YQFWKNFQ-----TUKVILG 18
   | : | | | |
Db 37 YRWRNFKVLARQACEASNOASHDFVETIKGVVLG 75

```

Search completed: September 28, 2004, 09:07:09
Job time : 11.925 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:55:11 ; Search time 5.625 Seconds
(without alignments)
166.624 Million cell updates/sec

Title: US-10-084-813-13
Sequence: 1 SQYQFWKNFQTLKIVILG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	96	100.0	352	1 CCR5_CERAE	P56493 cercoptithec
2	96	100.0	352	1 CCR5_CERP	Q9t442 cercoptithec
3	96	100.0	352	1 CCR5_CERTO	O62743 cercocebus
4	96	100.0	352	1 CCR5_GORGO	P56439 gorilla gor
5	96	100.0	352	1 CCR5_HUMAN	P51681 homo sapien
6	96	100.0	352	1 CCR5_HYLLE	O97883 hyllobates l
7	96	100.0	352	1 CCR5_HYML	Q95nc0 hyllobates m
8	96	100.0	352	1 CCR5_HYLSY	Q95nc5 hyllobates s
9	96	100.0	352	1 CCR5_PANTR	P56440 pan troglod
10	96	100.0	352	1 CCR5_PAPHA	P56441 papio hamad
11	96	100.0	352	1 CCR5_PONPY	O97881 pongo pygma
12	96	100.0	352	1 CCR5_PYGBI	O97880 pygathrix b
13	96	100.0	352	1 CCR5_PYGNE	O97882 pygathrix n
14	96	100.0	352	1 CCR5_TRAPR	O97878 trachypithe
15	96	100.0	352	1 CCR5_TRAPH	O97879 trachypithe
16	93	96.9	352	1 CCR5_MACMU	P79436 macaca mula
17	74	77.1	354	1 CCR5_MOUSE	P51682 mus musculu
18	74	77.1	354	1 CCR5_RAT	O08556 rattus norv
19	47	49.0	355	1 CCR1_MOUSE	P51675 mus musculu
20	46	47.9	373	1 CCR2_MOUSE	P51675 mus musculu
21	45	46.9	355	1 CCR1_MACMU	P56482 macaca mula
22	45	46.9	634	1 DYXB_HUMAN	P31916 euglena gra
23	45	46.9	4523	1 CCR3_CERAE	Q964t5 homo sapien
24	44	45.8	616	1 SECD_HAEN	P44591 haemophilus
25	43	44.8	300	1 PYRB_MYCPE	O8eux9 mycoplasma
26	43	44.8	355	1 CCR3_CERAE	P56492 cercoptithec
27	43	44.8	355	1 CCR3_MACMU	P56483 macaca mula
28	43	44.8	373	1 VIOB_CHRVO	Q983us chromobacte
29	43	44.8	3587	1 UTR4_BACSU	Q04747 bacillus su
30	42	43.8	241	1 UTR2_YEAST	P32626 saccharomyc
31	41.5	43.2	334	1 FEPD_ECOLI	P23876 escherichia
32	41	42.7	244	1 Y28K_SSV1	P20213 sulfolobus
33	41	42.7	303	1 APPC_BACSU	P42063 bacillus su

34	41	42.7	318	1 NUIM_HYLLA	Q96126 hyllobates l
35	41	42.7	358	1 CCR3_CAVPO	Q922i3 cavia porce
36	41	42.7	373	1 CCR2_RAT	O519i3 rattus norv
37	41	42.7	397	1 O22B_DROME	P81910 drosophila
38	41	42.7	461	1 FCMD_HUMAN	O75072 homo sapien
39	41	42.7	629	1 PR39_YEAST	P39682 saccharomyc
40	40	41.7	284	1 SUHA_HUMAN	Q06520 homo sapien
41	40	41.7	309	1 YBCK_HAEN	P44298 haemophilus
42	40	41.7	355	1 CCR1_HUMAN	P32246 homo sapien
43	40	41.7	371	1 Y180_CLOAB	Q04354 clostridium
44	40	41.7	437	1 ARLY_CLOAB	Q97ke5 clostridium
45	40	41.7	501	1 AMPA_BUCBP	Q89ag2 buchnera ap

ALIGNMENTS

RESULT 1
CKR5_CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98001387; PubMed=9343222;
RA "Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
[2]
RN SEQUENCE FROM N.A.
RP Murayama Y., Matsunaga S., Inoue-Murayama M.;
RA "cDNA sequence of African green monkey CCR-5 chemokine receptor
RT gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC -----
CC EMBL; U83324; AAC51795.1; -
CC EMBL; U83325; AAC51796.1; -
CC EMBL; AB015944; BAA31328.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00003; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
CC Polymorphism.
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

us-10-084-813-13.rsp

Tue Sep 28 15:49:57 2004

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FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 5 (POTENTIAL).
FT TRANSMEM 199 218 6 (POTENTIAL).
FT DOMAIN 219 235 7 (POTENTIAL).
FT TRANSMEM 236 260 8 (POTENTIAL).
FT DOMAIN 261 277 9 (POTENTIAL).
FT TRANSMEM 278 301 10 (POTENTIAL).
FT DOMAIN 302 352 11 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT VARIANT 14 14 N -> Y.
FT VARIANT 352 352 F -> L.
SQ SEQUENCE 352 AA; 40561 MW; 7F52B690C72EC29A CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVILG 18
|||
DB 185 SOYQFWKFNQTLKIVILG 202

RESULT 2
CKR5_CERY
ID CKR5_CERY STANDARD; PRT; 352 AA.
AC Q9TVI2;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKR5.
OS Cercopithecus pygerythrus (Vervet monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OC NCBI_TaxID=60710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=100;
RX MEDLINE=99335215; PubMed=10408730;
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,
RA Diop O., Rigoulet J., Barre-Sinoussi F., Ponsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with HIV
RT carrier status in African nonhuman primates."
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF035222; AAD44015.1;
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm1.1;

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DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECP F1.1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 5 (POTENTIAL).
FT TRANSMEM 199 218 6 (POTENTIAL).
FT DOMAIN 219 235 7 (POTENTIAL).
FT TRANSMEM 236 260 8 (POTENTIAL).
FT DOMAIN 261 277 9 (POTENTIAL).
FT TRANSMEM 278 301 10 (POTENTIAL).
FT DOMAIN 302 352 11 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3DB0 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVILG 18
|||
DB 185 SOYQFWKFNQTLKIVILG 202

RESULT 3
CKR5_CERTO
ID CKR5_CERTO STANDARD; PRT; 352 AA.
AC Q62743; Q62744; Q62745; Q62746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKR5.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OC NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate 079, 085, 087, and 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gattie A., Ho D.D., Marx P.A.;
RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys
RT naturally infected in west Africa: a comparison of coreceptor usage
RT of primary SIVsm, HIV-2, and SIVmac."
RL Virology 246:113-124(1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF035222; AAD44015.1;
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm1.1;

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DR EMBL; AF051902; AAC39830.1; -
DR EMBL; AF051903; AAC39831.1; -
DR EMBL; AF051904; AAC39832.1; -
DR EMBL; AF051905; AAC39833.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 325
FT TRANSMEM 326 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT VARIANT 2 2
FT VARIANT 3 3
FT VARIANT 25 25
FT VARIANT 100 100
FT VARIANT 107 107
FT VARIANT 134 134
FT VARIANT 146 146
FT VARIANT 340 340
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;
Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Indels 0; Gaps 0;
Qy 1 SQYQFWKFNFTLKIVILG 18
Db 185 SQYQFWKFNFTLKIVILG 202
RESULT 4
CKR5_GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CNKBR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CKR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by

CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF005659; AAB62553.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 325
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;
Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Indels 0; Gaps 0;
Qy 1 SQYQFWKFNFTLKIVILG 18
Db 185 SQYQFWKFNFTLKIVILG 202
RESULT 5
CKR5_HUMAN STANDARD; PRT; 352 AA.
ID P51581; O14692; O14593; O14695; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
AC O14708; O15538; Q9UPA4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
GN CKR5 OR CNKBR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=962411590; PubMed=8639485;
RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
RT "Molecular cloning and functional expression of a new human

CC-chemokine receptor gene.";
RA Biochemistry 35:3362-3367(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96291862; PubMed=8663314;
RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.P.;
RT "Molecular Cloning and functional characterization of a novel human
CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";
RN J. Biol. Chem. 271:17161-17166(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96295970; PubMed=8699119;
RA Conbadriere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
RT "Cloning and functional expression of CC CKR5, a human monocyte CC
chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
RANTES.";
RN J. Leukoc. Biol. 60:147-152(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=9601387; PubMed=9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses.";
RN J. Virol. 71:8642-8656(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang B.,
Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RN AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=98049523; PubMed=9388201;
RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
RT "The human CC chemokine receptor 5 (CCR5) gene: Multiple transcripts
with 5'-end heterogeneity, dual promoter usage, and evidence for
polymorphisms within the regulatory regions and noncoding exons.";
RN J. Biol. Chem. 272:30662-30671(1997).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=98049523; PubMed=9388201;
RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
RT "The human CC chemokine receptor 5 (CCR5) gene: Multiple transcripts
with 5'-end heterogeneity, dual promoter usage, and evidence for
polymorphisms within the regulatory regions and noncoding exons.";
RN J. Biol. Chem. 272:30662-30671(1997).
RN [8]
RP SEQUENCE FROM N.A., AND VARIANT ARG-178.
RA Magierowska M., Barre-Sinoussi F., Issatras H., Theodorou I.,
Debre P.;
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=96260017; PubMed=8649511;
RA Deng H., Liu R., Ellmeier W., Choe S., Untchaz D., Burkhardt M.,
RA Di Marzio P., Mamon S., Sutton R.E., Hill C.M., Davis C.B.,
RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
RT "Identification of a major co-receptor for primary isolates of
HIV-1.";
RN Nature 381:661-666(1996).
RN [10]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE=96260017; PubMed=8649511;
RA Deng H., Liu R., Ellmeier W., Choe S., Untchaz D., Burkhardt M.,
RA Di Marzio P., Mamon S., Sutton R.E., Hill C.M., Davis C.B.,
RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
RT "Identification of a major co-receptor for primary isolates of
HIV-1.";
RN Nature 381:661-666(1996).
RN [11]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE=96260018; PubMed=8649512;
RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
Nagashima K.A., Cayanan C., Madden P.J., Koup R.A., Moore J.P.,
Paxton W.A.;
RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
CC-CCR-5.";
RN Nature 381:667-673(1996).
RN [12]
RP SULFATION.
RX MEDLINE=99189752; PubMed=10089882;
RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
entry.";
RN Cell 96:667-676(1999).
RN [13]
RP FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and rantes and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation. Acts as co-receptor with CD4 for primary non-
syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1
virus. It promotes Env-mediated fusion of the virus.
RN [14]
RP SUBCELLULAR LOCATION: Integral membrane protein.
RN [15]
RP TISSUE SPECIFICITY: Found in promyelocytic cells.
RN [16]
PTM: Sulfation contributes to the efficiency of HIV-1 entry.
RN [17]
PTM: Modified by O-linked glycosylation, but not by N-linked
glycosylation.
RN [18]
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
RN [19]
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RN [20]
EMBL; X91492; CAA62796.1; -
DR EMBL; U54994; AAC50598.1; -
DR EMBL; U57840; AAB17071.1; -
DR EMBL; U95626; AAB57793.1; -
DR EMBL; U83326; AAC51797.1; -
DR EMBL; AF011500; AAB65700.1; -
DR EMBL; AF011501; AAB65701.1; -
DR EMBL; AF011502; AAB65702.1; -
DR EMBL; AF011503; AAB65703.1; -
DR EMBL; AF011504; AAB65704.1; -
DR EMBL; AF011505; AAB65705.1; -
DR EMBL; AF011506; AAB65706.1; -
DR EMBL; AF011507; AAB65707.1; -
DR EMBL; AF011508; AAB65708.1; -
DR EMBL; AF011509; AAB65709.1; -
DR EMBL; AF011510; AAB65710.1; -
DR EMBL; AF011511; AAB65711.1; -
DR EMBL; AF011512; AAB65712.1; -
DR EMBL; AF011513; AAB65713.1; -
DR EMBL; AF011514; AAB65714.1; -
DR EMBL; AF011515; AAB65715.1; -
DR EMBL; AF011516; AAB65716.1; -
DR EMBL; AF011517; AAB65717.1; -
DR EMBL; AF011518; AAB65718.1; -
DR EMBL; AF011519; AAB65719.1; -
DR EMBL; AF011520; AAB65720.1; -
DR EMBL; AF011521; AAB65721.1; -
DR EMBL; AF011522; AAB65722.1; -
DR EMBL; AF011523; AAB65723.1; -
DR EMBL; AF011524; AAB65724.1; -
DR EMBL; AF011525; AAB65725.1; -
DR EMBL; AF011526; AAB65726.1; -
DR EMBL; AF011527; AAB65727.1; -
DR EMBL; AF011528; AAB65728.1; -
DR EMBL; AF011529; AAB65729.1; -
DR EMBL; AF011530; AAB65730.1; -
DR EMBL; AF011531; AAB65731.1; -
DR EMBL; AF011532; AAB65732.1; -

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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: AF177884; AAK43382.1; --
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS: PR00237; GPCRHHODPSN.
 CC PROSITE: PS00237; G-PROTEIN RECEPTOR F1_1; 1.
 CC PROSITE: PS0262; G-PROTEIN RECEPTOR F1_2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 CC FT DOMAIN 1 30
 CC FT TRANSMEM 31 58
 CC FT DOMAIN 59 68
 CC FT TRANSMEM 69 89
 CC FT DOMAIN 90 102
 CC FT TRANSMEM 103 124
 CC FT DOMAIN 125 141
 CC FT TRANSMEM 142 166
 CC FT DOMAIN 167 198
 CC FT TRANSMEM 199 218
 CC FT DOMAIN 219 235
 CC FT TRANSMEM 236 260
 CC FT DOMAIN 261 277
 CC FT TRANSMEM 278 301
 CC FT DOMAIN 302 352
 CC FT DISULFID 101 178
 CC FT MOD_RES 3 3
 CC FT MOD_RES 10 10
 CC FT MOD_RES 14 14
 CC SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SOYQFWKFNQTLKIVILG 18
 DB 185 SOYQFWKFNQTLKIVILG 202

RESULT 8
 CKR5_HYLSY STANDARD; PRT; 352 AA.
 AC Q95NC5;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CMKBR5.
 OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=9590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RA "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC -----
 CC EMBL: AF177884; AAK43367.1; --
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS: PR00237; GPCRHHODPSN.
 CC PROSITE: PS00237; G-PROTEIN RECEPTOR F1_1; 1.
 CC PROSITE: PS0262; G-PROTEIN RECEPTOR F1_2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 CC FT DOMAIN 1 30
 CC FT TRANSMEM 31 58
 CC FT DOMAIN 59 68
 CC FT TRANSMEM 69 89
 CC FT DOMAIN 90 102
 CC FT TRANSMEM 103 124
 CC FT DOMAIN 125 141
 CC FT TRANSMEM 142 166
 CC FT DOMAIN 167 198
 CC FT TRANSMEM 199 218
 CC FT DOMAIN 219 235
 CC FT TRANSMEM 236 260
 CC FT DOMAIN 261 277
 CC FT TRANSMEM 278 301
 CC FT DOMAIN 302 352
 CC FT DISULFID 101 178
 CC FT MOD_RES 3 3
 CC FT MOD_RES 10 10
 CC FT MOD_RES 14 14
 CC SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SOYQFWKFNQTLKIVILG 18
 DB 185 SOYQFWKFNQTLKIVILG 202

RESULT 9
 CKR5_PANTR STANDARD; PRT; 352 AA.
 AC P564J0; Q02778;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CMKBR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CKR5 by macrophage and T cell tropic
 RL simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zimmerman P.A., Buckler-White A., Alkhatib G.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98022612; PubMed=9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;

RP "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RP SEQUENCE FROM N.A.
RA MEDLINE=97426118; PubMed=9282822;
RX Zacharova V., Zachar V., Goustin A.S.;
RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
FT HIV type 1 host."
RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
RP SEQUENCE FROM N.A.
RX MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1."
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RP SEQUENCE FROM N.A.
RX Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
FT phylogeny."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF005663; AAB62557.1; -
CC EMBL; U94329; AAB58446.1; -
CC EMBL; AF011542; AAB65742.1; -
CC EMBL; U97666; AAC51670.1; -
CC EMBL; AF011540; AAB65740.1; -
CC EMBL; U9797; AAC03717.1; -
CC EMBL; AF177894; AAK43377.1; -
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G PROTEIN RECP Fl 1; 1.
CC PROSITE; PS0262; G PROTEIN RECP Fl 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC
CC DOMAIN 1 30
CC TRANSMEM 31 58
CC DOMAIN 59 68
CC TRANSMEM 69 89
CC DOMAIN 90 102
CC TRANSMEM 103 124
CC DOMAIN 125 141
CC TRANSMEM 142 166
CC DOMAIN 167 198
CC TRANSMEM 199 218
CC DOMAIN 219 235
CC TRANSMEM 236 260
CC DOMAIN 261 277
CC TRANSMEM 278 301
CC DOMAIN 302 352
CC TRANSMEM 353 378
CC BY SIMILARITY.
CC SULFATION (BY SIMILARITY).
CC MOD_RES 10 10
CC MOD_RES 14 14
CC MOD_RES 15 15
CC MOD_RES 15 15
CC CARBOHYD 268
CC CONFLICT 123 123
CC SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. NO. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWNFQTLKIVILG 18
DB 185 SQYQFWNFQTLKIVILG 202

RESULT 10
CKR5_PAPHA STANDARD; PRT; 352 AA.
ID CKR5_PAPHA STANDARD; PRT; 352 AA.
AC P56441;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5) (CCR5).
GN CCR5 OR CXCR5.
OS Papio hamadryas (Hamadryas baboon), and
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557, 9555;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.H., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
CC simian immunodeficiency virus strains."
CC Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RX MEDLINE=99210133; PubMed=10195758;
RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
RT "Species-specific changes in the CCR5 gene from African and Asian
CC nonhuman primates."
CC AIDS Res. Hum. Retroviruses 15:479-483(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=P.anubis;
RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF005658; AAB62552.1; -
CC EMBL; AF105287; AAD20556.1; -
CC EMBL; AF105288; AAD20557.1; -
CC EMBL; AF105289; AAD20558.1; -
CC EMBL; AF105290; AAD20559.1; -
CC EMBL; AF023452; AAC63830.1; -
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsn.

Tue Sep 28 15:49:57 2004

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DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 4 (POTENTIAL).
FT TRANSMEM 142 166 5 (POTENTIAL).
FT DOMAIN 167 198 6 (POTENTIAL).
FT TRANSMEM 199 218 7 (POTENTIAL).
FT DOMAIN 219 235 8 (POTENTIAL).
FT TRANSMEM 236 260 9 (POTENTIAL).
FT DOMAIN 261 277 10 (POTENTIAL).
FT TRANSMEM 278 301 11 (POTENTIAL).
FT DOMAIN 302 352 12 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 352 AA; 40489 MW; 5E1504A9B1FE8B2 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVILG 18
DB 185 SOYQFWKFNQTLKIVILG 202

RESULT 11
CKR5_PONPY
ID CKR5_PONPY STANDARD; PRT; 352 AA.
AC 097881;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OC Pygathrix.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075446; AAD19858.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PS00237; GPCRHDOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 4 (POTENTIAL).
FT TRANSMEM 142 166 5 (POTENTIAL).
FT DOMAIN 167 198 6 (POTENTIAL).
FT TRANSMEM 199 218 7 (POTENTIAL).
FT DOMAIN 219 235 8 (POTENTIAL).
FT TRANSMEM 236 260 9 (POTENTIAL).
FT DOMAIN 261 277 10 (POTENTIAL).
FT TRANSMEM 278 301 11 (POTENTIAL).
FT DOMAIN 302 352 12 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVILG 18
DB 185 SOYQFWKFNQTLKIVILG 202

RESULT 12
CKR5_PYGBI
ID CKR5_PYGBI STANDARD; PRT; 352 AA.
AC 097880;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075445; AAD19857.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.

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DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1.1; 1.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1.2; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | |
DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 13
CKRS_PYGNE
ID CKRS_PYGNE STANDARD; PRT; 352 AA.
AC O97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CKR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF075448; AAD19860.1; -

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DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1.1; 1.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1.2; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40532 MW; FE4FD9D8D3B3E861 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | |
DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 14
CKRS_TRAFR
ID CKRS_TRAFR STANDARD; PRT; 352 AA.
AC O97878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CKR5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
CC EMBL; AF075448; AAD19860.1; -

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CC EMBL; AF075442; AAD19854.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_2; 1.
DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40496 MW; 43666FI48C25938F CRC64;
Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYQFWKMFQTLKIVILG 18
DB 185 SOYQFWKMFQTLKIVILG 202
RESULT 15
CKRS_TRAPH STANDARD; PRT; 352 AA.
AC O97879;
DT 30-MAY-2000 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKRS.
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC EMBL; AF075443; AAD19855.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_2; 1.
DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40509 MW; 43666FI48D3A5938F CRC64;
Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYQFWKMFQTLKIVILG 18
DB 185 SOYQFWKMFQTLKIVILG 202
RESULT 16
CKRS_MACMU STANDARD; PRT; 352 AA.
AC P79436; O02746;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKRS.
OS Macaca mulatta (Rhesus macaque).
OS Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RX SPECIES=M.mulatta;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RT Newman W., Gerard N., Gerard C., Sodroski J.;
RT "Utilization of C-C chemokine receptor 5 by the envelope
RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT SIVmac239.";
RL J. Virol. 71:2522-2527(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=Indian macaque;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CCR5 as a coreceptor for entry.";
RL J. Virol. 71:2705-2714(1997).

[3] SEQUENCE FROM N.A.
RC SPECIES=M.mullatta;
RX MEDLINE=21354176; PubMed=11461684;
RA Magdallies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
receptors.";
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [4]
SEQUENCE FROM N.A.
RC SPECIES=M.mullatta, M.fascicularis, and M.nemestrina;
RX MEDLINE=97269687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [5]
-1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC ENBL; U77672; AAC51109.1; -
DR ENBL; U72739; AAC51158.1; -
DR ENBL; U96762; AAC34132.1; -
DR ENBL; AF005660; AAB62554.1; -
DR ENBL; AF005661; AAB62555.1; -
DR ENBL; AF005662; AAB62556.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECPT_F2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 241 241 M -> I (IN REF. 3).
FT CONFLICT 292 292 I -> M (IN REF. 3).
SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACE2 CRC64;

Query Match 96.9%; Score 93; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 2e-07;

Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYQFWKNFQTLKIVILG 18
DB 185 SOYQFWKNFQTLKIVILG 202
RESULT 17
CKR5_MOUSE
ID CKR5_MOUSE STANDARD; PRT; 354 AA.
AC P51682; O35313; O35891; P97308; P97405; Q61867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
alpha receptor).
OS CCR5 OR CMKBR5.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Spleen;
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
chemoattractant protein 1) and murine macrophage inflammatory protein
1alpha receptors: evidence for two closely linked C-C chemokine
receptors on chromosome 9.";
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96278910; PubMed=8662890;
RA Meyer A., Coyle A.J., Froufoot A.E.I., Wells T.N.C., Power C.A.;
RT "Cloning and characterization of a novel murine macrophage
inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 271:14445-14451(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Ola;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.F., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=97404635; PubMed=9261347;
RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
RT "Two distinct CCR5 domains can mediate coreceptor usage by human
immunodeficiency virus type 1.";
RL J. Virol. 71:6305-6314(1997).
RN [6]
RP SEQUENCE FROM N.A.
RA Guo B., Kuno K., Harada A., Matsushima K.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
but not in nonhematopoietic cell lines.

RT Molecular cloning and functional expression of murine JE (monocyte
 RT chemoattractant protein 1) and murine macrophage inflammatory protein
 RT alpha receptors: evidence for two closely linked C-C chemokine
 RT receptors on chromosome 9.;
 RL J. Biol. Chem. 271:7551-7558(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=95216064; PubMed=8662823;
 RA Kurihara I., Bravo R.;
 RT "Cloning and functional expression of mCCR2, a murine receptor for
 RT the C-C chemokines JE and FIC.";
 RL J. Biol. Chem. 271:11603-11606(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97026720; PubMed=8872898;
 RA Heesen M., Tanabe S., Herman M.A., Yoshizawa I., Luo Y., Kim R.,
 RA Post T.W., Gerard C., Dorf M.E.;
 RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
 RT transcriptase-polymerase chain reaction does not detect mRNA for the
 RT KC or new MCP-1 receptor.";
 RL J. Neurosci. Res. 45:382-391(1996).
 CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
 CC chemokines. Transduces a signal by increasing the intracellular
 CC calcium ions level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
 CC but not in nonhematopoietic cell lines.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; U47035; AAC52453.1; -;
 CC EMBL; U51717; AAC52557.1; -;
 CC EMBL; U56819; AAC52784.1; -;
 CC MGD; MGI:106185; Ccr2.
 CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
 CC GO; GO:0019955; F:Cytokine binding; IPI.
 CC GO; GO:0046066; F:cellular defense response (sensu Vertebrata); IMP.
 CC GO; GO:0030097; P:hemopoiesis; IMP.
 CC GO; GO:0006959; P:humoral immune response; IMP.
 CC GO; GO:0006954; P:inflammatory response; IMP.
 CC GO; GO:0030334; P:regulation of cell migration; IMP.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm.1.1;
 CC PRINTS; PR00237; GPCR_Rhodopsn.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
 CC G-protein coupled receptor; Transmembrane.
 KW DOMAIN 1 55 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1 55
 FT TRANSMEM 56 83
 FT DOMAIN 84 93
 FT TRANSMEM 94 114
 FT DOMAIN 115 127
 FT TRANSMEM 128 149
 FT DOMAIN 150 166
 FT TRANSMEM 167 191
 FT DOMAIN 192 219
 FT TRANSMEM 220 239
 FT DOMAIN 240 256
 FT TRANSMEM 257 281
 FT DOMAIN 282 298
 FT TRANSMEM 299 322
 FT DOMAIN 323 373
 FT TRANSMEM 126 203
 FT DISULFID 39 39
 FT CONFLICT 39 184
 FT CONFLICT 184 184

FT CONFLICT 264 264 V -> G (IN REF. 1).
 SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;
 Query Match 47.9%; Score 46; DB 1; Length 373;
 Best Local Similarity 64.3%; Pred. No. 5.8;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 4 QFQKNFQTLKIVIL 17
 DB 209 QLWKNFQIMRNIL 222
 RESULT 21
 CKR1_MACMU
 ID CKR1_MACMU STANDARD; PRT; 355 AA.
 AC P56482;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1).
 GN CCR1 OR CCR1.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9544;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors.";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC RANTES, MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
 CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
 CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
 CC PROLIFERATION
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF017282; AAB70526.1; -;
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm.1.1;
 CC PRINTS; PR00237; GPCR_Rhodopsn.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1 34
 FT TRANSMEM 35 60
 FT DOMAIN 61 64
 FT TRANSMEM 65 91
 FT DOMAIN 92 107
 FT TRANSMEM 108 129
 FT DOMAIN 130 146
 FT TRANSMEM 147 171
 FT DOMAIN 172 197
 FT TRANSMEM 198 223
 FT DOMAIN 224 239
 FT TRANSMEM 240 264
 FT DOMAIN 265 281
 FT TRANSMEM 282 305
 FT DOMAIN 306 355
 FT CARBOHYD 5 5
 FT CONFLICT 5 183
 FT DISULFID 106 183

```
SQ SEQUENCE 355 AA; 41198 MW; 41CAEA7CC19D23D4 CRC64;
Query Match 46.9%; Score 45; DB 1; Length 355;
Best Local Similarity 50.0%; Pred. No. 8;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 YQFWNFQTLKIVILG 18
: ||| ||| |||
Db 192 FQWKLFOALKINLFG 207

RESULT 22
ID YCX3_EUGGR STANDARD; PRT; 634 AA.
AC P31916; P31917;
DT 01-JUN-1993 (Rel. 26, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 78.0 kDa protein in PBSC intron 2 (ORF635).
OS Euglena gracilis.
OG Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=3039;
RN [1]
SEQUENCE FROM N.A.
STRAIN=Z / UTEX 753;
MEDLINE=93347989; PubMed=8346031;
RA Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort A.,
Orsat B., Spielmann A., Stutz E.;
RT "Complete sequence of Euglena gracilis chloroplast DNA.";
RL Nucleic Acids Res. 21:3537-3544(1993).
CC -----
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CC -----
DR EMBL; Z11874; -; NOT ANNOTATED_CDS.
DR EMBL; X70810; CAA50080.1; -.
DR PR; S34499; S34499.
DR PR; S34500; S34500.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 634 AA; 78049 MW; D966B8864519E334 CRC64;

Query Match 46.9%; Score 45; DB 1; Length 634;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 10; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

Qy 4 QFW----KNFQTLKIVIL 17
: ||| ||| ||| |||
Db 60 KFWDSQIKNFQTLKIVIL 77

RESULT 23
ID DYHB_HUMAN STANDARD; PRT; 4523 AA.
AC Q96DT5; Q9UJ82;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ciliary dynein heavy chain 11 (Axonemal beta dynein heavy chain 11).
GN DNAIL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A., VARIANT PCD GLN-3004, AND VARIANTS LEU-34;
RP ARG-639; CYS-654; ALA-1023; THR-1038; GLY-1640; ASN-2641; THR-3474;
RP VAL-3715; PRO-3765 AND ILE-4177.
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RC TISSUE=Nasal epithelium, and Testis;
RX MEDLINE=22155903; PubMed=12142464;
RA Bartoloni L., Blouin J.L., Pan Y., Gehrig C., Maiti A.K., Scamuffa N.,
Rossier C., Jorissen M., Armengot M., Meeks M., Mitchison H.M.,
Chung E.M., Delozier-Blanchet C.D., Craigen W.J., Antonarakis S.E.;
RT "Mutations in the DNAIL1 (axonemal heavy chain dynein type 11) gene
cause one form of situs inversus totalis and most likely primary
ciliary dyskinesia.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10282-10286(2002).
RN [2]
SEQUENCE OF 1904-2004 FROM N.A.
RC TISSUE=Nasal polyps;
RA Maiti A.K., Mattai M.-G., Jorissen M., Volz A., Ziegler A.,
Bouvagnet P.;
RT "Chromosomal localization of human dynein heavy chain genes.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Force generating protein of respiratory cilia. Produces
CC force towards the minus ends of microtubules. Dynein has ATPase
CC activity; the force-producing power stroke is thought to occur on
CC release of ADP.
CC -!- SUBUNIT: Consists of at least two heavy chains and a number of
CC intermediate and light chains.
CC -!- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem
CC (which binds cargo and interacts with other dynein components),
CC and the head or motor domain. The motor contains six tandemly-
CC linked AAA domains in the head, which form a ring. A stalk-like
CC structure (formed by two of the coiled coil domains) protrudes
CC between AAA 4 and AAA 5 and terminates in a microtubule-binding
CC site. A seventh domain may also contribute to this ring; it is not
CC clear whether the N-terminus or the C-terminus forms this extra
CC domain. There are four well-conserved and two non-conserved ATPase
CC sites, one per AAA domain. Probably only one of these (within AAA
CC 1) actually hydrolyzes ATP, the others may serve a regulatory
CC function.
CC -!- DISEASE: Defects in DNAIL1 are a cause of primary ciliary
CC dyskinesia (PCD) [MIM:242650]; also known as immotile cilia
CC syndrome 1 (ICS1). The phenotype of this autosomal recessive
CC disease is characterized by axonemal abnormalities of respiratory
CC cilia and sperm tails leading to bronchiectasis and sinusitis,
CC which are sometimes associated with situs inversus (Kartagener
CC syndrome) and male sterility.
CC -!- SIMILARITY: Belongs to the dynein heavy chain family.
CC -----
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CC -----
DR EMBL; AJ320497; CAC60121.1; -.
DR EMBL; AJ132087; CAA10560.1; -.
DR Genew; HGNC:2942; DNAIL1.
DR MIM; 603339; -.
DR MIM; 242650; -.
DR GO; GO:0005858; C:axonemal dynein complex; NAS.
DR GO; GO:0003775; F:axonemal motor activity; NAS.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR004273; Dynein heavy.
DR Pfam; PF03028; Dynein heavy; 1.
DR SMART; SM00382; AAA; 4.
KW Motor protein; Dynein; Microtubule; ATP-binding; Repeat; Coiled coil;
KW Polymorphism; Disease mutation.
FT DOMAIN 1 1861 STEM (BY SIMILARITY).
FT DOMAIN 1862 2083 AAA 1 (BY SIMILARITY).
FT DOMAIN 2143 2373 AAA 2 (BY SIMILARITY).
FT DOMAIN 2479 2726 AAA 3 (BY SIMILARITY).
FT DOMAIN 2824 3073 AAA 4 (BY SIMILARITY).
FT DOMAIN 3079 3410 STALK (BY SIMILARITY).
FT DOMAIN 3466 3693 AAA 5 (BY SIMILARITY).
FT DOMAIN 3903 4129 AAA 6 (BY SIMILARITY).
FT DOMAIN 1274 1327 COILED COIL (POTENTIAL).
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FT DOMAIN 3079 3143 COILED COIL (POTENTIAL).
FT DOMAIN 3319 3410 COILED COIL (POTENTIAL).
FT DOMAIN 3675 3710 COILED COIL (POTENTIAL).
FT NP_BIND 1900 1907 ATP (POTENTIAL).
FT NP_BIND 2181 2188 ATP (POTENTIAL).
FT NP_BIND 2517 2524 ATP (POTENTIAL).
FT NP_BIND 2862 2869 ATP (POTENTIAL).
FT VARIANT 34 34 E -> L (requires 2 nucleotide
FT substitutions).
FT VARIANT 639 639 /FTid=VAR_013851.
FT VARIANT 654 654 Q -> R.
FT VARIANT 1023 1023 S -> C.
FT VARIANT 1038 1038 /FTid=VAR_013852.
FT VARIANT 1640 1640 /FTid=VAR_013853.
FT VARIANT 2641 2641 V -> A.
FT VARIANT 2682 2682 /FTid=VAR_013854.
FT VARIANT 3004 3004 A -> T.
FT VARIANT 3474 3474 /FTid=VAR_013855.
FT VARIANT 3715 3715 D -> G.
FT VARIANT 3765 3765 S -> N.
FT VARIANT 4177 4177 I -> V.
FT VARIANT 4523 4523 R -> Q (in PCID; not proven to be
FT pathogenic).
FT VARIANT 520969 520969 /FTid=VAR_013859.
FT VARIANT 520969 520969 A -> T.
FT VARIANT 520969 520969 L -> V.
FT VARIANT 520969 520969 S -> P.
FT VARIANT 520969 520969 T -> I.
FT VARIANT 520969 520969 /FTid=VAR_013860.
FT VARIANT 520969 520969 /FTid=VAR_013861.
FT VARIANT 520969 520969 /FTid=VAR_013862.
FT VARIANT 520969 520969 T -> I.
FT VARIANT 520969 520969 /FTid=VAR_013863.
FT SEQUENCE 4523 AA; 520969 MW; 7C9A71C95B296889 CRC64;

Query Match 46.9%; Score 45; DB 1; Length 4523;
Best Local Similarity 50.0%; Pred. No. 97;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 FWSNQTLKIVILG 18
DB 648 FWSNFASRLYLFLG 661

RESULT 24
SECD_HAEIN STANDARD; PRT; 616 AA.
AC P44591;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein-export membrane protein secD.
GN SECD OR H10240.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrman J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae

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RT Rd";
RL Science 269:496-512(1995).
CC -!- FUNCTION: Involved in protein export (By similarity).
CC -!- SUBUNIT: Part of the prokaryotic protein translocation apparatus
CC which comprise secA, secB, secD, secE, secF, secG and secY (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (By similarity).
CC -!- SIMILARITY: Belongs to the secD/secF family. SecD family.
CC
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CC
CC EMBL; U32710; AAC21908.1; -.
CC TIGR; H10240; -.
CC InterPro; IPR005791; SecD.
CC InterPro; IPR003335; SecD_SecF.
CC Pfam; PF02355; SecD_SecF; 1.
CC PRINTS; PR01755; SECFTNLKASE.
CC TIGRFAMs; TIGR00916; 2A0604s01; 1.
CC TIGRFAMs; TIGR01129; secD; 1.
CC Protein transport; Translocation; Transmembrane; Inner membrane;
CC Complete proteome. 31 POTENTIAL.
CC TRANSMEM 11 473 POTENTIAL.
CC TRANSMEM 453 495 POTENTIAL.
CC TRANSMEM 475 517 POTENTIAL.
CC TRANSMEM 562 582 POTENTIAL.
CC TRANSMEM 585 605 POTENTIAL.
CC SEQUENCE 616 AA; 66986 MW; 7D51E4B085065F8F CRC64;

Query Match 45.8%; Score 44; DB 1; Length 616;
Best Local Similarity 38.9%; Pred. No. 20;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 SOYQZKXNFQTLKIVILG 18
DB 3 NRYPLKXNLWIFIVAIG 20

RESULT 25
PYRB_MYCPE STANDARD; PRT; 300 AA.
AC Q8EUX9;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
DE transcarbamylase) (AtCase).
GN PYRB OR MYPE7890.
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HF-2;
RX MEDLINE=22354719; PubMed=12466555;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RA "The complete genomic sequence of Mycoplasma penetrans, an
RA intracellular bacterial pathogen in humans."
RL Nucleic Acids Res. 30:5293-5300(2002).
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate
CC + N-carbamoyl-L-aspartate.
CC -!- PATHWAY: Pyrimidine biosynthesis; second step.
CC -!- SIMILARITY: Belongs to the ATCase/OtCase family.
CC

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FT	DOMAIN	63	72	CYTOPLASMIC. (POTENTIAL).
FT	TRANSMEM	73	93	2 (POTENTIAL).
FT	DOMAIN	94	107	EXTRACELLULAR. (POTENTIAL).
FT	TRANSMEM	108	129	3 (POTENTIAL).
FT	DOMAIN	130	146	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	147	171	4 (POTENTIAL).
FT	DOMAIN	172	203	EXTRACELLULAR. (POTENTIAL).

FT	DOMAIN	224	239	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	240	264	6 (POTENTIAL).
FT	DOMAIN	265	281	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	282	305	7 (POTENTIAL).
FT	DOMAIN	306	355	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	106	183	BY SIMILARITY.
SQ	SEQUENCE	355 AA;	40830 MW; 44F7A5EFEEB978FF CRC64;	
	Query Match	44.8%;	Score 43; DB 1; Length 355;	
	Best Local Similarity	58.3%;	Pred. No. 17;	
	Matches	7; Conservative	3; Mismatches	2; Indels
QV		6	WKNFOTLKIVL	17

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Db      195 WRHFHTLKWTIL 206
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RESUL 27
CKR3 MACMU
ID CKR3 MACMU PRT; 355 AA.
AC P56483:

DI 23-OUL-1998 (Rel. 36, Last annotation update)
 DE 20-FEB-2003 (Rel. 41, Last annotation update)
 CC C-terminal kinase receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
 GN CCR3 OR CMKR3
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.

NCBI_1aXID=9344;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21354176; PubMed=11461684;
RX Martgullies B. J., Hauer D.A., Clements J.E.;
RA "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."; RT
RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=98118446; PubMed=94554694;
RX Sol N., Treboute C., Gomas E., Ferchal F., Shacklett B., Alizon M.;
RA "The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor
RT for HIV-2, but not for HIV-1."; RT
RL Virology 240:213-220 (1998).
RN -!- FUNCTION: Receptor for a C-C type chemokine. Binds to ectaxin.
CC

MCF-3, MCF-4 and RW148 and subsequently transduces a signal by
 increasing the intracellular calcium ions level.
 -!- SUBCELLULAR LOCATION: Integral membrane protein.
 -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; AF017283; AAB70527.1; -.
EMBL; Y13776; CAA74107.1; -.
InterPro; IPR000376; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCR_Rhodpsn

```
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; transmembrane.
FT DOMAIN 1 34
FT TRANSMEM 35 62
FT DOMAIN 63 72
FT TRANSMEM 73 93
FT DOMAIN 94 107
FT TRANSMEM 108 129
FT DOMAIN 130 146
FT TRANSMEM 147 171
FT DOMAIN 172 203
FT TRANSMEM 204 223
FT DOMAIN 224 239
FT TRANSMEM 240 264
FT DOMAIN 265 281
FT TRANSMEM 282 305
FT DOMAIN 306 355
FT DISULFID 106 183
FT CONFLICT 180 180
FT CONFLICT 202 202
SQ SEQUENCE 355 AA; 40805 MW; E271F1E694970D9F CRC64;

Query Match 44.8%; Score 43; DB 1; Length 355;
Best Local Similarity 58.3%; Pred. No. 17;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17
DB 195 WRHFTLKWTL 206

RESULT 28
VTOD CHRVQ
ID VTOD CHRVQ STANDARD; PRT; 373 AA.
AC Q983U8; Q980N2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable tryptophan hydroxylase viod (EC 1.-.-.-).
GN VIOD OR CV3271.
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=UQM51;
RX MEDLINE=20525185; PubMed=11075927;
RA August P.R., Grossman T.H., Minor C., Draper M.P., MacNeil I.A.,
RA Pemberton J.M., Call K.M., Holt D., Osburne M.S.;
RA "Sequence analysis and functional characterization of the violacein
RT biosynthetic pathway from Chromobacterium violaceum.";
RL J. Mol. Microbiol. Biotechnol. 2:513-519(2000).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=JCM 1249;
RA Hoshino T.;
RT "Biosynthetic gene cluster for violacein pigment.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22582880; PubMed=14500782;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida J.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Arraiza J., de Araujo M.F.F.,
RA Atolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Beio A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.M.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Pegundes N., Falcao C.L.,
```

STRAIN=168;
 MEDLINE=93181186; PubMed=8441623;
 Fuma S., Fujishina Y., Corbell N., D'Souza C., Nakano M.M.,
 Zuber P., Yamane K.;
 "Nucleotide sequence of 5' portion of srfA that contains the region
 required for competence establishment in *Bacillus subtilis*.";
 Nucleic Acids Res. 21:93-97(1993).
 [2]
 SEQUENCE FROM N.A.
 RC STRAIN=168; / JH642;
 RX MEDLINE=93360813; PubMed=8355609;
 Cosmina P., Rodriguez F., de Ferra F., Grandi G., Perego M.,
 Venema G., van Sinderen D.;
 "Sequence and analysis of the genetic locus responsible for surfactin
 synthesis in *Bacillus subtilis*.";
 Mol. Microbiol. 8:821-831(1993).
 [3]
 SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=97124189; PubMed=8969502;
 Yamane K., Kumano M., Kurita K.;
 "The 25 degrees-36 degrees region of the *Bacillus subtilis*
 chromosome: determination of the sequence of a 146 kb segment and
 identification of 113 genes.";
 Microbiology 142:3047-3056(1996).
 [4]
 SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 Brouillet S., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 Chai S.K., Codani J.J., Connerion I.P., Cummings N.J., Daniel R.A.,
 Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 Ertan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 Ghim S.Y., Glaser P., Goffeau A., Golligorsky E.J., Grandi G.,
 Guseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut L.,
 Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 Joris B., Karamata D., Kasahara Y., Klauer-Blanchard M., Klein C.,
 Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 Lee S.M., Levine A., Liu H., Masuda S., Maestl D., Nakai S., Noback M.,
 Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 Rieger M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y.,
 Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone P.,
 Sirokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 Takeuchi M., Tamakoshi A., Tanaka T., Terstra P., Tognoni A.,
 Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 Viari A., Wambuit R., Wedler E., Wedler H., Weitzenecker T.,
 Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 Yoshida K., Yoshikawa H.F., Zmstein E., Yoshikawa H., Danchin A.;
 "The complete genome sequence of the Gram-positive bacterium *Bacillus*
subtilis.";
 Nature 390:249-256(1997).
 [5]
 SEQUENCE OF 514-800 FROM N.A.
 RC STRAIN=ATCC 21332;
 RX MEDLINE=92290255; PubMed=1601288;
 Borchert S., Pacl S.S., Marahiel M.A.;
 "Identification of putative multifunctional peptide synthetase genes
 using highly conserved oligonucleotide sequences derived from known
 synthetases.";
 FEMS Microbiol. Lett. 71:175-180(1992).
 -1- FUNCTION: THIS PROTEIN IS A MULTIFUNCTIONAL ENZYME ABLE TO
 ACTIVATE AND POLYMERIZE THE AMINO ACIDS LEU, GLU, ASP AND VAL.
 ACTIVATION SITES FOR THESE AA CONSIST OF INDIVIDUAL DOMAINS.
 -1- COFACTOR: Contains 3 covalently bound phosphopantetheines.

-1- PATHWAY: Cyclic peptide antibiotic surfactin biosynthesis.
 -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
 family.
 -1- SIMILARITY: Contains 3 acyl carrier domains.

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 ENBL; D13262; BAA02533.1; -;
 ENBL; X70356; CAA49817.1; -;
 ENBL; D50453; BAA08983.1; -;
 ENBL; Z99105; CAB12143.1; -;
 ENBL; X65835; CAA46678.1; -;
 PIR; I40486; I40496.
 HSSP; P14687; 1AMU
 Subtilist; BG10169; srfAB.
 InterPro; IPR000873; AMP-bind.
 InterPro; IPR001242; Condensatr.
 InterPro; IPR006163; Pp-bind.
 InterPro; IPR006162; Ppantne S.
 Pfam; PF00501; AMP-binding; 3.
 Pfam; PF00668; Condensation; 4.
 Pfam; PF00550; Pp-binding; 3.
 PRINTS; PRO0154; AMPBINDING.
 PROSITE; PS00012; PHOSPHOPANTHETHEINE; 3.
 PROSITE; PS00455; AMP BINDING; 3.
 PROSITE; PS00075; ACP DOMAIN; 3.
 Ligase; Antibiotic biosynthesis; Phosphopantetheine; Sporulation;
 Multifunctional enzyme; Repeat; Complete proteome
 REPEAT ? 1040 DOMAIN 1 (VAL-ACTIVATING).
 REPEAT ? 2036 DOMAIN 2 (ASP-ACTIVATING).
 REPEAT ? 3114 DOMAIN 3 (D-LEU-ACTIVATING).
 FT DOMAIN 970 1036
 FT ACYL CARRIER (ACP) 1.
 FT DOMAIN 2015 2082
 FT ACYL CARRIER (ACP) 2.
 FT DOMAIN 3043 3109
 FT ACYL CARRIER (ACP) 3.
 FT BINDING 999 999
 FT PHOSPHOPANTHETHEINE (POTENTIAL).
 FT BINDING 2045 2045
 FT PHOSPHOPANTHETHEINE (POTENTIAL).
 FT BINDING 3073 3073
 FT CONFLICT 33 33
 FT CONFLICT 42 42
 FT CONFLICT 110 110
 FT CONFLICT 113 113
 FT CONFLICT 139 139
 FT CONFLICT 239 239
 FT CONFLICT 309 309
 FT CONFLICT 478 480
 FT CONFLICT 596 596
 FT CONFLICT 648 648
 FT CONFLICT 680 682
 FT CONFLICT 694 698
 FT CONFLICT 788 788
 FT CONFLICT 939 940
 FT CONFLICT 1038 1038
 FT CONFLICT 1133 1133
 FT CONFLICT 1310 1310
 FT CONFLICT 1333 1333
 FT CONFLICT 1384 1384
 FT CONFLICT 1582 1582
 FT CONFLICT 1677 1682
 FT CONFLICT 1700 1700
 FT CONFLICT 1755 1755
 FT CONFLICT 1787 1787
 FT CONFLICT 1801 1822
 FT CONFLICT 1915 1916
 FT CONFLICT 2075 2075
 FT CONFLICT 2079 2079
 FT CONFLICT 2141 2145
 LG -> PK (IN REF. 1).
 R -> C (IN REF. 1).
 A -> V (IN REF. 1).
 ARLTP -> LRDSIN (IN REF. 1).
 EQSIT -> DKRIS (IN REF. 5).
 R -> A (IN REF. 1).
 TPA -> SRP (IN REF. 1).
 MISSING (IN REF. 5).
 A -> R (IN REF. 1).
 RHV -> ETL (IN REF. 1).
 EQSIT -> DKRIS (IN REF. 5).
 M -> L (IN REF. 5).
 PL -> LV (IN REF. 1).
 N -> I (IN REF. 1).
 H -> Q (IN REF. 1).
 V -> C (IN REF. 1).
 G -> V (IN REF. 1).
 P -> R (IN REF. 1).
 G -> E (IN REF. 1).
 KERADG -> S (IN REF. 1).
 C -> S (IN REF. 1).
 F -> K (IN REF. 1).
 T -> S (IN REF. 1).
 GAIAGRVDPDAFAKPTIG -> APSPOGLICMSRCIC
 ETPDNR (IN REF. 1).
 LG -> PK (IN REF. 1).
 R -> C (IN REF. 1).
 A -> V (IN REF. 1).
 ARLTP -> LRDSIN (IN REF. 1).


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DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00702; Hydrolase; 1. ID -> MH (IN REF. 2).
FT CONFLICT 70 71
FT CONFLICT 153 158 AHSDLS -> GMIRWI (IN REF. 2).
SQ SEQUENCE 241 AA; 26735 MW; BFGFBBC7FB14BSAD CRC64;

Query Match 43.8%; Score 42; DB 1; Length 241;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYQFWKKNFQTL 12
   :||:|||||
Db 231 KQGVYKNFETL 241

RESULT 31
FEPD_ECOLI STANDARD; PRT; 334 AA.
ID FEPD_ECOLI
AC P23876; P77097;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ferric enterobactin transport system permease protein fepD.
DE FEPD OR B0590.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92157868; PubMed=1838574;
RA Shea C.M., McIntosh M.A.;
RT "Nucleotide sequence and genetic organization of the ferric
RT enterobactin transport system: homology to other periplasmic binding
RT protein-dependent systems in Escherichia coli.";
RL Mol. Microbiol. 5:1415-1428(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92157867; PubMed=1787794;
RA Chenualt S.S., Earhart C.F.;
RT "Organization of genes encoding membrane proteins of the Escherichia
RT coli ferrienterobactin permease.";
RL Mol. Microbiol. 5:1405-1413(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RC Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H.,
RC Lin D., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR FERRIC ENTEROACTIN. PROBABLY RESPONSIBLE FOR THE
CC TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- INDUCTION: Controlled in part by the amount of available iron.
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family. FecCD subfamily.
-----
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EMBL; X57471; CAA40707.1; -
DR EMBL; X59402; CAA42043.1; -
DR EMBL; AE000164; AAC73691.1; -
DR EMBL; U82598; AAB40789.1; ALT_INIT.
DR EMBL; S16296; -
DR EcoGene; EG10296; fepD
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR005222; fepD.
DR Pfam; PF01032; fepD; 1.
DR ProDom; PD001557; fepD; 1.
KW Iron transport; Transp; Inner membrane; Transmembrane;
KW Complete proteome.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 54 84 POTENTIAL.
FT TRANSMEM 93 113 POTENTIAL.
FT TRANSMEM 121 141 POTENTIAL.
FT TRANSMEM 152 172 POTENTIAL.
FT TRANSMEM 193 213 POTENTIAL.
FT TRANSMEM 242 262 POTENTIAL.
FT TRANSMEM 280 300 POTENTIAL.
FT TRANSMEM 306 326 POTENTIAL.
FT CONFLICT 233 234 RV -> AL (IN REF. 2).
SQ SEQUENCE 334 AA; 33871 MW; 855939A96951B CRC64;

Query Match
Best Local Similarity 43.2%; Score 41.5; DB 1; Length 334;
Matches 8; Conservative 5; Mismatches 3; Indels 7; Gaps 1;

Qy 2 QYQFW-----KNFQTLKIVIL 17
Db 179 QLRFQWAGSLDIRNLTKVLI 201

RESULT 32
Y28K_SSV1
ID Y28K_SSV1 STANDARD; PRT; 244 AA.
AC P20213;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Hypothetical 28.5 kDa protein (ORF P-244).
OS Sulfolobus virus-like particle SSV1.
OC Viruses; dsDNA viruses, no RNA stage; Fuselloviridae; Fusellovirus.
OX NCBI_TaxID=244589;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92024080; PubMed=1926776;
RA Palm P., Schleper C., Gramp B., Yeats S., McWilliam P., Reiter W.-D., Zillig W.;
RT "Complete nucleotide sequence of the virus SSV1 of the archaeobacterium Sulfolobus shibatae.";
RL Virology 185:242-250(1991).
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DR EMBL; X07234; CAA30214.1; -
DR PIR; S03215; S03215.
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 28515 MW; 9326209BC3B9DD86 CRC64;

Query Match
Best Local Similarity 42.7%; Score 41; DB 1; Length 244;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 4 QFWKMFQTLKIVILG 18
Db 216 QYKNTLTLRVSLKG 230

RESULT 33

APPC_BACSU
ID APPC_BACSU STANDARD; PRT; 303 AA.
AC P42063;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Oligopeptide transport system permease protein appc.
GN APPC OR BSU11400.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
RX MEDLINE=95089678; PubMed=7997159;
RA Koide A., Hoch J.A.;
RT "Identification of a second oligopeptide transport system in Bacillus subtilis and determination of its role in sporulation.";
RL Mol. Microbiol. 13:417-426(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst P., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Conner I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Giuseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpatra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
RL Nature 390:249-256(1997).
CC -!- FUNCTION: This protein is a component of an oligopeptide permease, a binding protein-dependent transport system. This APP system can completely substitute for the OPP system in both sporulation and genetic competence, though, unlike OPP, is incapable of transporting tripeptides. Probably responsible for the translocation of the substrate across the membrane (by similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport system permease family. OppBC subfamily.
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DR EMBL; U20909; AAA62360.1; -;
 DR EMBL; Z99110; CAB12997.1; -;
 DR PIR; I40547; I40547.
 DR Subtilist; BG11089; appC.
 DR InterPro; IPR000515; BPD_transp.
 DR Pfam; PF00528; BPD_transp; 1.
 DR PROSITE; PS05928; ABC_TM1; 1.
 KW Competence; Sporulation; Transport; Peptide transport; Transmembrane;
 KW Complete proteome.
 FT TRANSMEM 39 59 POTENTIAL.
 FT TRANSMEM 103 123 POTENTIAL.
 FT TRANSMEM 138 158 POTENTIAL.
 FT TRANSMEM 212 232 POTENTIAL.
 FT TRANSMEM 233 253 POTENTIAL.
 FT TRANSMEM 269 289 POTENTIAL.
 FT TRANSMEM 303 344; 33420 MW; B9CD2CD936C46DC5 CRC64;
 SQ SEQUENCE 303 AA; 33420 MW; B9CD2CD936C46DC5 CRC64;

Query Match 42.7%; Score 41; DB 1; Length 303;
 Best Local Similarity 50.0%; Pred. No. 29;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 FWNKFNQTLKIVILG 18
 DB 29 FWEKFSKNKLLIG 42

RESULT 34
 ID NUIUM HYLLA STANDARD; PRT; 318 AA.
 AC Q96126;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3).
 GN MTND1 OR ND1 OR NADH1.
 OS Hylobates lar (Common gibbon).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=9580;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Uster;
 RA Aranson U., Gullberg A., Xu X.;
 RT "A complete mitochondrial DNA molecule of the white-handed gibbon,
 RT Hylobates lar, and comparison among individual mitochondrial genes of
 RT all hominoid genera."
 RL Hereditas 124:185-189(1996).
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- SIMILARITY: Belongs to the complex I subunit 1 family.
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DR EMBL; X99256; CAA67628.1; -;
 DR PIR; T11833; T11833.
 DR InterPro; IPR001694; Resp_NADH_dhl.
 DR Pfam; PF00146; NADHdh; 1.
 DR PROSITE; PS00667; COMPLEX1_ND1_1; 1.
 DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.

SQ SEQUENCE 318 AA; 35814 MW; 3988A4B0BFE13711 CRC64;
 Query Match 42.7%; Score 41; DB 1; Length 318;
 Best Local Similarity 46.7%; Pred. No. 31;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 YQFKNFQTLKIVIL 17
 DB 287 YLLWKNFLPLTLTL 301

RESULT 35
 ID CKR3_CAVPO STANDARD; PRT; 358 AA.
 AC Q9Z2I3;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
 DE (CCR3).
 DE CCR3 OR CMKBR3.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99049845; PubMed=9834099;
 RA Sabroe I., Conroy D.M., Gerard N.P., Li Y., Collins P.D., Post T.W.,
 RA Jose P.J., Williams T.J., Gerard C.J., Ponath P.D.;
 RT "Cloning and characterization of the guinea pig eosinophil ectaxin
 RT receptor, C-C chemokine receptor-3: blockade using a monoclonal
 RT antibody in vivo".
 RL J. Immunol. 161:6139-6147(1998).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to ectaxin,
 CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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DR EMBL; AF060698; AAC80428.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_3; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 44 64 POTENTIAL.
 FT DOMAIN 65 74 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 75 95 POTENTIAL.
 FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 113 133 POTENTIAL.
 FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 155 175 POTENTIAL.
 FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 227 POTENTIAL.
 FT DOMAIN 228 244 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 244 264 POTENTIAL.
 FT DOMAIN 265 287 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 288 308 POTENTIAL.
 FT DOMAIN 309 358 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 358 AA; 41623 MW; 7B73FAB7A3BC3670 CRC64;

Query Match 42.7%; Score 41; DB 1; Length 358;

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Best Local Similarity 53.8%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WNFQTLKIVILG 18
   |||||:|
Db 199 WKRFQALRMNIFG 211

RESULT 16
CKR2_RAT
ID CKR2_RAT STANDARD; PRT; 373 AA.
AC O55193;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2).
GN CCR2 OR CCR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA deHebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis";
RL J. Neuroimmunol. 86:11-12(1998).
CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
CC macrophages.
CC -!- INDUCTION: In animals in which experimental allergic
CC encephalomyelitis (EAE) has been induced.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U77349; AAC03242.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 3.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G.PROTEIN RECP FL 1; 1.
DR PROSITE: PS0262; G.PROTEIN RECP FL 2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 61 81 POTENTIAL.
FT DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 92 112 POTENTIAL.
FT DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 129 149 POTENTIAL.
FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 POTENTIAL.
FT DOMAIN 192 220 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 221 241 POTENTIAL.
FT DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 277 POTENTIAL.
FT DOMAIN 278 301 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 302 323 POTENTIAL.
FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 203 BY SIMILARITY.
SQ SEQUENCE 373 AA; 42763 MW; 2E7B012F5D6FD9 CRC64;
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Query Match 42.7%; Score 41; DB 1; Length 373;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 WNFQTLKIVIL 17
   |||||:|
Db 211 WNFQTLINRIL 222

RESULT 37
O22B_DROME
ID O22B_DROME STANDARD; PRT; 397 AA.
AC P81910; Q9U6X6; Q9VQ19;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Odorant receptor 22B.
GN OR22B OR OR22A.2 OR DOR22A.2 OR DOR67 OR ANI2 OR CG4231.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RC STRAIN=Oregon-R; TISSUE=Antenna;
RX MEDLINE=99189757; PubMed=1008987;
RA Vosehall L.B., Amrein H., Morozov P.S., Rzhetsky A., Axel R.;
RT "A spatial map of olfactory receptor expression in the Drosophila
RT antenna";
RL Cell 96:725-736(1999).
RN [2]
RP REVISION TO 58.
RA Vosehall L.B., Amrein H., Morozov P.S., Rzhetsky A., Axel R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99389723; PubMed=10458908;
RA Gao Q., Chess A.;
RT "Identification of candidate Drosophila olfactory receptors from
RT genomic DNA sequence.";
RL Genomics 60:31-39(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Colnicker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.B.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flesher C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milehina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [5]
 RP IDENTIFICATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Antenna;
 RX MEDLINE=99166868; PubMed=10069338;
 RA Clyne P.J., Warr C.G., Freeman M.R., Lessing D., Kim J., Carlson J.R.;
 RT "A novel family of divergent seven-transmembrane proteins: candidate
 RT odorant receptors in *Drosophila*.";
 RL Neuron 22:327-338(1999).
 CC -!- FUNCTION: Probable role in the odorant response, being an odorant
 CC receptor.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN 20-22 SENSORY NEURONS ON THE
 CC MEDIAL-PROXIMAL EDGE OF THE ANTENNA. THIS EXPRESSION PATTERN
 CC MATCHES THE DISTRIBUTION OF THE LARGE SENSILLA BASICONICA.
 CC EXPRESSION IS FIRST SEEN AT 60 HOURS APF IN A SUBSET OF CELLS
 CC RESTRICTED TO A SUBREGION OF THE DEVELOPING ANTENNA. EXPRESSION
 CC CONTINUES THROUGHOUT ANTENNAL DEVELOPMENT.
 CC -!- SIMILARITY: Belongs to family Dr-or of G-protein coupled
 CC receptors.
 CC
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 CC
 CC -----
 CC EMBL; AF127924; RAD26359.2; -;
 CC EMBL; AB003586; RAF51363.1; -;
 CC Flybase; Fggn0026397; Or22b.
 CC GO; GO:0016021; C:integral to membrane; NAS.
 CC GO; GO:0004984; F:olfactory receptor activity; NAS.
 CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; NAS.
 CC GO; GO:0007608; P:olfaction; NAS.
 CC InterPro; IPR004117; 7tm_6.
 CC Pfam; PF02949; 7tm_6; 1.
 CC Transmembrane; G-protein coupled receptor; Olfaction;
 KW Multigene family.
 FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 50 70 1 (POTENTIAL).
 FT DOMAIN 71 85 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 86 105 2 (POTENTIAL).
 FT DOMAIN 106 143 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 144 164 3 (POTENTIAL).
 FT DOMAIN 165 194 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 195 215 4 (POTENTIAL).
 FT DOMAIN 216 268 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 269 289 5 (POTENTIAL).
 FT DOMAIN 290 295 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 296 316 6 (POTENTIAL).
 FT DOMAIN 317 347 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 348 368 7 (POTENTIAL).
 FT DOMAIN 369 397 CYTOPLASMIC (POTENTIAL).
 FT CONFLICT 58 58 V -> L (IN REF. 3, 4 AND 5).
 FT CONFLICT 256 256 M -> T (ICFDKFFVLPYFFS (IN REF. 3)).
 FT CONFLICT 376 397 MYKLAFTVTVIVKQFNLAKEFQ -> VSIHQVEL (IN
 FT REF. 3).
 SQ SEQUENCE 397 AA; 46387 MW; EB7816E9DDA13E50 CRC64;

Query Match

Best Local Similarity 42.3%; Score 41; DB 1; Length 397;

Pred. No. 38;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 3 YQFKNFQTLKIVIL 17
 Db 48 YKLWSTFVTLVIFIL 62
 RESULT 38
 FCMD HUMAN STANDARD; PRT; 461 AA.
 ID FCMD HUMAN
 AC 075072; Q96TE1; Q9P295;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Fukutin precursor (Fukuyama-type congenital muscular dystrophy
 DE protein).
 GN FCMD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98952786; PubMed=9690476;
 RA Kobayashi K., Nakahori Y., Miyake M., Matsumura K., Kondo-Iida E.,
 RA Nomura Y., Segawa M., Yoshioka M., Saito K., Osawa M., Hamano K.,
 RA Sakakihara Y., Nonaka I., Nakagome Y., Kanazawa I., Nakamura Y.,
 RA Tokunaga K., Toda T.;
 RA "An ancient retrotransposon insertion causes Fukuyama-type congenital
 RT muscular dystrophy.";
 RL Nature 394:388-392(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21099876; PubMed=11165248;
 RA Kobayashi K., Sasaki J., Kondo-Iida E., Fukuda Y., Kinoshita M.,
 RA Sunada Y., Nakamura Y., Toda T.;
 RA "Structural organization, complete genomic sequences and mutational
 RT analyses of the Fukuyama-type congenital muscular dystrophy gene,
 RT fukutin.";
 RL FEBS Lett. 489:192-196(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Babbage A.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May interact with and reinforce a large complex
 CC encompassing the outside and inside of muscle membranes. May also
 CC be involved in brain development.
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable). May be located in the
 CC extracellular matrix.
 CC -!- TISSUE SPECIFICITY: Widely expressed with highest expression in
 CC brain, heart, pancreas and skeletal muscle.
 CC -!- DISEASE: Defects in FCMD is the cause of Fukuyama-type congenital
 CC dystrophy (FCMD) [MIM:253800]. FCMD is an autosomal recessive
 CC disorder characterized by congenital muscular dystrophy associated
 CC with brain malformation due to a defect in the migration of
 CC neurons. The disease is often due to a retrotransposon insertion
 CC of tandemly repeated sequences in the 3'-UTR of FCMD.
 CC
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 CC
 CC -----
 CC EMBL; AB008226; BAA32000.1; -;
 CC EMBL; AB038490; BAA94082.1; -;
 CC EMBL; AL158070; CAC22162.1; -;
 CC GenBank; HGNC:3622; FCMD.
 CC MIM; 607440; -;
 CC MIM; 253800; -;

DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0007517; P:muscle development; TAS.
DR GO: GO:0007399; P:neurogenesis; TAS.
KW Glycoprotein; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 461 FUKUTIN.
FT CARBOHYD 92 92 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 203 203 R -> Q (IN REF. 1).
SQ SEQUENCE 461 AA; 53724 MW; 2D11F2BE4BCDD858 CRC64;

Query Match 42.7%; Score 41; DB 1; Length 461;
Best Local Similarity 40.0%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 3; Indels 12; Gaps 1;

QY 2 QYQWKN-----FQTLKI 14
DB 116 QYHLKNVEGFWFIAENWGFQCLKI 140

RESULT 39
PR39 YEAST
ID PR39 YEAST STANDARD; PRT; 629 AA.
AC P396B2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pre-mRNA processing protein PRP39.
GN PRP39 OR YML046W OR YN9827.06.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94254821; PubMed=8196608;
RA Lockhart S.R., Rymond B.C.;
RT "Commitment of yeast pre-mRNA to the splicing pathway requires a novel U1 small nuclear ribonucleoprotein polypeptide, Prp39p.";
RL Mol. Cell. Biol. 14:3623-3633(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churche C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII.";
RL Nature 387:90-93(1997).
RN [3]
RP PARTIAL SEQUENCE.
RX MEDLINE=97165029; PubMed=9012791;
RA Neubauer G., Gottschalk A., Fabrizio P., Seraphin B., Luehrmann R., Mann M.;
RT "Identification of the proteins of the yeast U1 small nuclear ribonucleoprotein complex by mass spectrometry.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:385-390(1997).
CC -1- FUNCTION: FUNCTION PRIOR TO STABLE BRANCH POINT RECOGNITION BY THE U1 SNRNP PARTICLE TO FACILITATE OR STABILIZE THE U1 SNRNP/5' SPlice SITE INTERACTION. HAS A DIRECT ROLE IN THE ASSEMBLY OR FUNCTION OF A CATALYTICALLY ACTIVE SPLICEOSOME.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Contains 7 HAT repeats.
CC
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CC EMBL; L29224; AAA20131.1; -;
DR EMBL; Z47816; CAA87828.1; -;
DR PIR; S47920; S47920.
DR Germline; 142575; -;
DR SGD; S0004509; FAP39.
DR GO; GO:0000243; C:commitment complex; IPI.
DR GO; GO:0005685; C:snRNP U1; IDA.
DR GO; GO:0003723; P:RNA binding; IPI.
DR GO; GO:0006371; P:mRNA splicing; IMP.
DR InterPro; IPR003107; HAT.
DR SMART; SM00386; HAT; 2.
KW mRNA processing; mRNA splicing; Nuclear protein; Repeat.
FT REPEAT 68 100 HAT 1.
FT REPEAT 102 134 HAT 2.
FT REPEAT 138 173 HAT 3.
FT REPEAT 175 208 HAT 4.
FT REPEAT 233 265 HAT 5.
FT REPEAT 270 302 HAT 6.
FT REPEAT 446 480 HAT 7.
SQ SEQUENCE 629 AA; 74748 MW; 67480ED01347B6AB CRC64;

Query Match 42.7%; Score 41; DB 1; Length 629;
Best Local Similarity 37.5%; Pred. No. 60;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 YQWKNFQTLKIVILG 18
DB 88 FGFKRFATIEYQLFG 103

RESULT 40
SUHA HUMAN
ID SUHA HUMAN STANDARD; PRT; 284 AA.
AC Q06520;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alcohol sulfotransferase (EC 2.8.2.2) (hydroxysteroid sulfotransferase) (HST) (Dehydroepiandrosterone sulfotransferase)
DE (DHEA-ST) (ST2) (ST2A3).
GN SUL2A1 OR STD OR HST.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 60-64; 104-119 AND 273-284.
RC TISSUE=Liver;
RX MEDLINE=93143674; PubMed=7678732;
RA Comer K.A., Falany J.L., Falany C.N.;
RT "Cloning and expression of human liver dehydroepiandrosterone sulfotransferase.";
RL Biochem. J. 289:233-240(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 80-107 AND 176-198.
RC TISSUE=Liver;
RX MEDLINE=92269778; PubMed=1588921;
RA Ottensm F.D., Wieben E.D., Wood T.C., Watson R.W.G., Madden B.J., McCormick D.J., Weishilboum R.M.;
RT "Human liver dehydroepiandrosterone sulfotransferase: molecular cloning and expression of cDNA.";
RL Mol. Pharmacol. 41:865-872(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RX MEDLINE=96034512; PubMed=7589785;
RA Forbes K.J., Hagen M., Coughtrie M.W.H., Glatt H.R., Hume R.;
RT "Human fetal adrenal hydroxysteroid sulphotransferase: cDNA cloning, stable expression in V79 cells and functional characterisation of the expressed enzyme.";
RL Mol. Cell. Endocrinol. 112:53-60(1995).
RN [4]

SEQUENCE FROM N.A.
 RX MEDLINE=9532029; PubMed=759806;
 RA Luu-The V., Dufort I., Paquet N., Reimnitz G., Labrie F.;
 RT "Structural characterization and expression of the human
 RT dehydroepiandrosterone sulfotransferase gene.";
 RL DNA Cell Biol. 14:511-518(1995).
 RN [5]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95225980; PubMed=7710689;
 RA Oterness D.M., Her C., Aksoy S., Kimura S., Wieben E.D.,
 RA Weinschilbom R.M.;
 RT "Human dehydroepiandrosterone sulfotransferase gene: molecular
 RT cloning and structural characterization.";
 RL DNA Cell Biol. 14:331-341(1995).
 RN [6]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=92392364; PubMed=1520333;
 RA Kong A.-N.T., Yang L., Ma M., Tao D., Bjornsson T.D.;
 RT "Molecular cloning of the alcohol/hydroxysteroid form (hSta) of
 RT sulfotransferase from human liver.";
 RL Biochem. Biophys. Res. Commun. 187:448-454(1992).
 RN [7]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Catalyzes the sulfation of steroids and bile acids in
 CC the liver and adrenal glands.
 CC -!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + an alcohol =
 CC adenosine 3',5'-bisphosphate + an alkyl sulfate.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Liver, adrenal and at lower level in the
 CC kidney. Is present in human fetus in higher level in the adrenal
 CC than the liver and the kidney.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Estrogens present in maternal circulation is
 CC predominantly derived from fetal dehydroepiandrosterone sulfate
 CC which is hydrolyzed and metabolized to estrogens in placenta.
 CC -!- SIMILARITY: Belongs to the sulfotransferase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L20000; AAA35758.1; -;
 DR EMBL; X70222; CAA49755.1; -;
 DR EMBL; U08024; AAA17749.1; -;
 DR EMBL; U08025; AAA17750.1; -;

DR EMBL; X84816; CAA59274.1; -;
 DR EMBL; L36196; AAA75491.1; -;
 DR EMBL; L36191; AAA75491.1; JOINED.
 DR EMBL; L36192; AAA75491.1; JOINED.
 DR EMBL; L36193; AAA75491.1; JOINED.
 DR EMBL; L36194; AAA75491.1; JOINED.
 DR EMBL; L36195; AAA75491.1; JOINED.
 DR EMBL; U13061; AAC51353.1; -;
 DR EMBL; U13056; AAC51353.1; JOINED.
 DR EMBL; U13057; AAC51353.1; JOINED.
 DR EMBL; U13058; AAC51353.1; JOINED.
 DR EMBL; U13059; AAC51353.1; JOINED.
 DR EMBL; U13060; AAC51353.1; JOINED.
 DR EMBL; S43859; AAB23169.2; -;
 DR EMBL; BC020755; AAH20755.1; -;
 DR PIR; I53037; I38548.
 DR PDB; 1J99; 19-JUN-02.
 DR Genew; HGNC:11458; SULT2A1.
 DR MIM; 125263; -;
 DR GO; GO:0008146; F:sulfotransferase activity; TAS.
 DR GO; GO:0008202; P:steroid metabolism; TAS.
 DR InterPro; IPR000863; Sulfotransferase.
 DR Pfam; PF00685; Sulfotransfer; 1.
 DR ProDom; PD001218; Sulfotransferase; 1.
 DR Bile acid catabolism; Steroid metabolism; Transferase; 3D-structure.
 KW INIT_MET 0 0 BY SIMILARITY
 FT BINDING 248 254 PAPS BINDING SITE (POTENTIAL).
 FT CONFLICT 62 62 A -> P (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 89 89 T -> S (IN REF. 1).
 FT CONFLICT 118 118 L -> D (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 158 158 L -> V (IN REF. 6).
 SQ SEQUENCE 284 AA; 33648 MW; 3C89C7597833EBA1 CRC64;
 Query Match 41.7%; Score 40; DB 1; Length 284;
 Best Local Similarity 53.8%; Pred. No. 40;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SOYQWKNFQTLK 13
 DB 128 SCYFFWKNKPIK 140
 Search completed: September 28, 2004, 09:04:06
 Job time: 6.625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:56:16 ; Search time 28.8 Seconds
(without alignments)
197.199 Million cell updates/sec

Title: US-10-084-813-13
Perfect score: 96
Sequence: 1 SQYQFWKNFQTLKIVILG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	96	100.0	52	4 Q9PIT5	Q9pit5 homo sapien
2	96	100.0	60	4 Q9PIT4	Q9pit4 homo sapien
3	96	100.0	333	4 O14694	O14694 homo sapien
4	96	100.0	334	5 Q9TUQ7	Q9tuq7 erythrocebu
5	96	100.0	339	4 Q9UN24	Q9un24 homo sapien
6	96	100.0	339	4 Q9UN26	Q9un26 homo sapien
7	96	100.0	339	4 Q9UN23	Q9un23 homo sapien
8	96	100.0	339	4 Q9UBJ7	Q9ubj7 homo sapien
9	96	100.0	339	4 Q9UN25	Q9un25 homo sapien
10	96	100.0	339	4 Q9UN27	Q9un27 homo sapien
11	96	100.0	339	4 Q9UBT9	Q9ubt9 homo sapien
12	96	100.0	339	4 Q9UN28	Q9un28 homo sapien
13	96	100.0	339	6 Q9TQW0	Q9tqw0 hylobates c
14	96	100.0	339	6 Q9TUX1	Q9tux1 hylobates c
15	96	100.0	339	6 Q9TUW9	Q9tuw9 cercopithec
16	96	100.0	339	6 Q9TUN9	Q9tun9 hylobates c

17	96	100.0	339	6 Q9TSQ1	Q9tsq1 cercopithec
18	96	100.0	339	6 Q9TUU8	Q9tuu8 cercopithec
19	96	100.0	339	6 Q9TQW4	Q9tqw4 pan troglod
20	96	100.0	339	6 Q9TQW4	Q9tqw4 pan troglod
21	96	100.0	339	6 Q9TQW7	Q9tqw7 cercopithec
22	96	100.0	339	6 Q9TUR6	Q9tur6 cercopithec
23	96	100.0	339	6 Q9TQV6	Q9tqv6 colobus que
24	96	100.0	339	6 Q9TQW6	Q9tqw6 pan troglod
25	96	100.0	339	6 Q9TUQ9	Q9tuq9 cercopithec
26	96	100.0	339	6 Q9TUR2	Q9tur2 erythrocebu
27	96	100.0	339	6 Q9TQV0	Q9tqv0 papio papio
28	96	100.0	339	6 Q9TQUS	Q9tqv0 cercopithec
29	96	100.0	339	6 Q9TUS7	Q9tus7 papio papio
30	96	100.0	339	6 Q9TUS3	Q9tus3 pongo pygma
31	96	100.0	339	6 Q9TUS5	Q9tus5 papio papio
32	96	100.0	339	6 Q9TQV2	Q9tqv2 papio papio
33	96	100.0	339	6 Q9TQV3	Q9tqv3 cercopithec
34	96	100.0	339	6 Q9TUQ8	Q9tuq8 cercopithec
35	96	100.0	339	6 Q9TUR3	Q9tur3 erythrocebu
36	96	100.0	339	6 Q9TQW2	Q9tqw2 pongo pygma
37	96	100.0	339	6 Q9TQX2	Q9tqx2 erythrocebu
38	96	100.0	339	6 Q9TSQ4	Q9tsq4 cercopithec
39	96	100.0	339	6 Q9TQK2	Q9tkr2 gorilla gor
40	96	100.0	339	6 Q9TSQ3	Q9tsq3 cercopithec
41	96	100.0	339	6 Q9TUR0	Q9tur0 cercopithec
42	96	100.0	339	6 Q9TUN5	Q9tun5 pan troglod
43	96	100.0	339	6 Q9TUQ4	Q9tuq4 erythrocebu
44	96	100.0	339	6 Q9TQK6	Q9tkq6 erythrocebu
45	96	100.0	339	6 Q9TUR8	Q9tur8 papio papio

ALIGNMENTS

RESULT 1

Q9PIT5 PRELIMINARY; PRT; 52 AA.
AC Q9PIT5;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Mutant chemokine receptor CCR5 (Fragment).
GN CCR5.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9392755; PubMed=10465086;
RA Aikhiobare F.O., Newman C., Womack C., Roth W.W., Stringer H.G. Jr.,
RA Bond V.C.;
RT "Characterization of a third CCR5 amplicon from CCR5-delta32-
RT heterozygous HIV-1-infected individuals.";
RL AIDS 13:1585-1586(1999).
DR EMBL; AF056019; AAF65578.1; -;
DR GO; GO:0004872; FAF65578.1; -;
KW Receptor.
FT NON_TER 1 1
FT VARIANT 41 41 P -> S.
SQ SEQUENCE 52 AA; 5962 MW; DAEB2A5A9529C3A9 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18

Db 11 SQYQFWKNFQTLKIVILG 28

RESULT 2

Q9PIT4


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ID Q9PIT4 PRELIMINARY; PRT; 60 AA.
AC Q9PIT4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chemokine receptor CCR5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99392755; PubMed=10465086;
RA Aikihonbare F.O., Newman C., Roth W.W., Stringer H.G. Jr.,
RT Bond V.C.,
RL "Characterization of a third CCR5 amplicon from CCR5-delta32-
RT heterozygous HIV-1-infected individuals.";
RL AIDS 13:1585-1586(1999).
DR EMBL; AF056020; AAF65579.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 7156 MW; AFF4B9CAF6B80AFB CRC64;

Query Match 100.0%; Score 96; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
DB 11 SOYQFWKNFQTLKIVILG 28

RESULT 3
ID O14694 PRELIMINARY; PRT; 333 AA.
AC O14694;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RT Ho D.D.;
RL "Hiv-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011504; AAB65704.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS0237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 333 333
SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

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Query Match 100.0%; Score 96; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
DB 166 SOYQFWKNFQTLKIVILG 183

RESULT 4
ID Q9TUQ7 PRELIMINARY; PRT; 334 AA.
AC Q9TUQ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162049; AAD47804.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS0237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 334
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 334;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
DB 173 SOYQFWKNFQTLKIVILG 190

RESULT 5
ID Q9UN24 PRELIMINARY; PRT; 339 AA.
AC Q9UN24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian

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RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161919; AAD47676.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PRO0237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
|||||
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 6
Q9UN26 PRELIMINARY; PRT; 339 AA.
AC Q9UN26
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161916; AAD47673.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PRO0237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39162 MW; A56369F80529F4AB CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
|||||
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 7
Q9UN23 PRELIMINARY; PRT; 339 AA.
ID Q9UN23
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Q9UN23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PRO0237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
|||||
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 8
Q9UBJ7 PRELIMINARY; PRT; 339 AA.
ID Q9UBJ7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR EMBL; AF161917; AAD47674.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PRO0237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
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FT  NON TER      1
FT  NON TER    339
SQ  SEQUENCE    339 AA; 39128 MW;  9C3369FF1F2F27A CRC64;

Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SOYQFWKQFQTLKIVILG 18
    |||||
DB  178 SOYQFWKQFQTLKIVILG 195

RESULT 9
QUN25
ID  Q9UN25      PRELIMINARY;      PRT;      339 AA.
AC  Q9UN25
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  C-C chemokine receptor 5 (Fragment).
GN  CCR5.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA  Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT  "Sequences of the CCR5 genes from diverse simian and prosimian
RT  species.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF161918; AAD47675.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHHODPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
FT  NON TER      1
FT  NON TER    339
SQ  SEQUENCE    339 AA; 39146 MW;  10FE05FE5371D4B3 CRC64;

Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SOYQFWKQFQTLKIVILG 18
    |||||
DB  178 SOYQFWKQFQTLKIVILG 195

RESULT 10
QUN27
ID  Q9UN27      PRELIMINARY;      PRT;      339 AA.
AC  Q9UN27
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  C-C chemokine receptor 5 (Fragment).
GN  CCR5.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,

```

```

RA  Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT  "Sequences of the CCR5 genes from diverse simian and prosimian
RT  species.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF161914; AAD47671.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHHODPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
FT  NON TER      1
FT  NON TER    339
SQ  SEQUENCE    339 AA; 39086 MW;  88AD8B44E2CB4EC2 CRC64;

Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SOYQFWKQFQTLKIVILG 18
    |||||
DB  178 SOYQFWKQFQTLKIVILG 195

RESULT 11
QUN29
ID  Q9UN29      PRELIMINARY;      PRT;      339 AA.
AC  Q9UN29
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  C-C chemokine receptor 5 (Fragment).
GN  CCR5.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA  Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT  "Sequences of the CCR5 genes from diverse simian and prosimian
RT  species.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF161915; AAD47672.1; -.
DR  EMBL; AF161909; AAD47666.1; -.
DR  EMBL; AF161910; AAD47667.1; -.
DR  EMBL; AF161911; AAD47668.1; -.
DR  EMBL; AF161912; AAD47669.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHHODPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
FT  NON TER      1
FT  NON TER    339
SQ  SEQUENCE    339 AA; 39114 MW;  3C6369F92C29F4A7 CRC64;

Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SOYQFWKQFQTLKIVILG 18
    |||||

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```
Db 178 SQYQFWKNFQTLKIVILG 195
RESULT 12
Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
|||||
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 13
Q9TQW0 PRELIMINARY; PRT; 339 AA.
AC Q9TQW0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

Db 178 SQYQFWKNFQTLKIVILG 195
|||||
Qy 1 SQYQFWKNFQTLKIVILG 18
|||||
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 14
Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257F8B834C4AE CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
|||||
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 15
Q9TUU9 PRELIMINARY; PRT; 339 AA.
AC Q9TUU9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.

OX NCBI_TaxID=36224;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161949; AAD47704.1; -

DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0004872; F: receptor activity; IEA.

DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.

DR Pfam; PF00001; 7tm 1; 1.

DR PRINTS; PR00237; GPCR_Rhodopsin.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON_TER 1

FT NON_TER 339

SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVILG 18

|||||

Db 178 SOYQFWKFNQTLKIVILG 195

RESULT 16

Q9TUW9

ID Q9TUW9 PRELIMINARY; PRT; 339 AA.

AC Q9TUW9;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Hylobates concolor (crested gibbon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.

OX NCBI_TaxID=29089;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

RT species.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161890; AAD47647.1; -

DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0004872; F: receptor activity; IEA.

DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.

DR Pfam; PF00001; 7tm 1; 1.

DR PRINTS; PR00237; GPCR_Rhodopsin.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON_TER 1

FT NON_TER 339

SQ SEQUENCE 339 AA; 39024 MW; EC4CE48DEEF107E CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVILG 18

|||||

Db 178 SOYQFWKFNQTLKIVILG 195

RESULT 17

Q9TSQ1

ID Q9TSQ1 PRELIMINARY; PRT; 339 AA.

AC Q9TSQ1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Cercopithecus aethiops (Green monkey) (Grivet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Cercopithecus.

OX NCBI_TaxID=9534;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

RT species.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF162023; AAD47778.1; -

DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0004872; F: receptor activity; IEA.

DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm 1; 1.

DR PRINTS; PR00237; GPCR_Rhodopsin.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON_TER 1

FT NON_TER 339

SQ SEQUENCE 339 AA; 39216 MW; 847E935FA403E52D CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVILG 18

|||||

Db 178 SOYQFWKFNQTLKIVILG 195

RESULT 18

Q9TUU8

ID Q9TUU8 PRELIMINARY; PRT; 339 AA.

AC Q9TUU8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Cercopithecus diana (Diana monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Cercopithecus.

OX NCBI_TaxID=36224;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

RT species.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161949; AAD47705.1; -

DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 33049 MW; 6D1A93F66270F3ED CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 19
Q9TQW4 Q9TQW4 PRELIMINARY; PRT; 339 AA.
AC Q9TQW4;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47662.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39129 MW; 4A88F8B601D46A4 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 20
Q9TQW4 Q9TQW4 PRELIMINARY; PRT; 339 AA.
AC Q9TQW4;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47662.1; -.
DR EMBL; AF161898; AAD47655.1; -.
DR EMBL; AF161901; AAD47658.1; -.
DR EMBL; AF161904; AAD47661.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39129 MW; 4A88F8B601D46A4 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 20
Q9TQW4 Q9TQW4 PRELIMINARY; PRT; 339 AA.
ID Q9TQW4
AC Q9TQW4 PRELIMINARY; PRT; 339 AA.
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -.
DR EMBL; AF162042; AAD47797.1; -.
DR EMBL; AF162044; AAD47799.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

us-10-084-813-13.rspt

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DR PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 8475F92BB03E6E2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 96; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
DB 178 SOYQFWKNFQTLKIVILG 195

RESULT 22
Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162005; AAD47760.1; -
DR EMBL; AF162000; AAD47755.1; -
DR EMBL; AF162001; AAD47756.1; -
DR EMBL; AF162002; AAD47757.1; -
DR EMBL; AF162003; AAD47758.1; -
DR EMBL; AF162004; AAD47759.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 844BF72F8BFF566F CRC64;

Query Match
Best Local Similarity 100.0%; Score 96; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
DB 178 SOYQFWKNFQTLKIVILG 195

RESULT 24
Q9TUM6 PRELIMINARY; PRT; 339 AA.
AC Q9TUM6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161900; AAD47657.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 90DF2A6F446C5A5D CRC64;

Query Match
Best Local Similarity 100.0%; Score 96; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
DB 178 SOYQFWKNFQTLKIVILG 195

RESULT 23
Q9TQV6 PRELIMINARY; PRT; 339 AA.
AC Q9TQV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Colobus quereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae;
OC Colobus.

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Best Local Similarity		100.0%;	Pred. No. 2e-07;	
Matches		18;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	SOYQFWKNFQTLKIVILG 18		
DB	178	SOYQFWKNFQTLKIVILG 195		
RESULT 25				
Q9TUQ9		PRELIMINARY;	PRT;	339 AA.
ID	Q9TUQ9			
AC	Q9TUQ9;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	C-C chemokine receptor 5 (Fragment).			
GN	CCR5.			
OS	Cercopithecus mona.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
OC	Cercopithecinae; Cercopithecus.			
NCBI_TaxID=36226;				
NCBI_TaxID=36226;				
RP	SEQUENCE FROM N.A.			
RA	Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,			
RA	Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;			
RT	"Sequences of the CCR5 genes from diverse simian and prosimian			
RT	species.";			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF162041; AAD47796.1; -.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.			
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.			
DR	InterPro; IPR000276; GPCR_Rhodopsn.			
DR	Pfam; PF00001; 7tm1; 1.			
DR	PRINTS; PR00237; GPCRHHODOPSN.			
DR	PROSITE; PS00237; G PROTEIN RECEPT F1_1; 1.			
DR	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.			
KW	Receptor.			
FT	NON_TER	1		
FT	NON_TER	339		
FT	NON_TER	339		
SEQ	SEQUENCE	339 AA; 39019 MW; 7176F940AFl1F3ED CRC64;		
Query Match		100.0%;	Score 96;	DB 6; Length 339;
Best Local Similarity		100.0%;	Pred. No. 2e-07;	
Matches		18;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	SOYQFWKNFQTLKIVILG 18		
DB	178	SOYQFWKNFQTLKIVILG 195		
RESULT 26				
Q9TUR2		PRELIMINARY;	PRT;	339 AA.
ID	Q9TUR2			
AC	Q9TUR2;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	C-C chemokine receptor 5 (Fragment).			
GN	CCR5.			
OS	Erythrocybus patas (Red guenon) (Hussar).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
OC	Cercopithecinae; Erythrocybus.			
NCBI_TaxID=9538;				
NCBI_TaxID=9538;				
RP	SEQUENCE FROM N.A.			
RA	Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,			
RA	Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;			
RT	"Sequences of the CCR5 genes from diverse simian and prosimian			
RT	species.";			

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ID Q9TQUS PRELIMINARY; PRT; 339 AA.
AC Q9TQUS;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecius.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162046; AAD47801.1; -.
DR EMBL; AF162043; AAD47798.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39178 MW; 847F8F936B00E6E2 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
Db 178 SOYQFWKNFQTLKIVILG 195

RESULT 29
Q9TUS7 PRELIMINARY; PRT; 339 AA.
AC Q9TUS7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161995; AAD47750.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.

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DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39068 MW; 84EB018085DC0A62 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
Db 178 SOYQFWKNFQTLKIVILG 195

RESULT 30
Q9TUM3 PRELIMINARY; PRT; 339 AA.
AC Q9TUM3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161908; AAD47665.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39103 MW; 4350C4625FB0657C CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
Db 178 SOYQFWKNFQTLKIVILG 195

RESULT 31
Q9TUS5 PRELIMINARY; PRT; 339 AA.
AC Q9TUS5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=100937;

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DR EMBL; AF162045; AAD47800.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; -.
DR PRINTS; PS00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39148 MW; 0CA289CDBDEDE831 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred.No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 35
Q9TUR3 PRELIMINARY; PRT; 339 AA.
AC Q9TUR3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CC5.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161907; AAD47664.1; -.
DR EMBL; AF161906; AAD47663.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39117 MW; 4C4E35825BD54E9C CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred.No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 37
Q9TOX2 PRELIMINARY; PRT; 339 AA.
AC Q9TOX2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CC5.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162053; AAD47808.1; -.
DR EMBL; AF162035; AAD47790.1; -.
DR EMBL; AF162036; AAD47791.1; -.
DR EMBL; AF162048; AAD47803.1; -.
DR EMBL; AF162050; AAD47805.1; -.
DR EMBL; AF162052; AAD47807.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred.No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 36
Q9TQW2 PRELIMINARY; PRT; 339 AA.
AC Q9TQW2

```

```
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39154 MW; 09715882A6074884 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 38
Q9TSQ4 PRELIMINARY; PRT; 339 AA.
AC Q9TSQ4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciniae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162006; AAD47761.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; -
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39164 MW; 85CF8E22DB00E6E3 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 39
Q9TSQ2 PRELIMINARY; PRT; 339 AA.
AC Q9TSQ2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161897; AAD47654.1; -
DR EMBL; AF161891; AAD47648.1; -
DR EMBL; AF161892; AAD47649.1; -
DR EMBL; AF161893; AAD47650.1; -
DR EMBL; AF161895; AAD47652.1; -
DR EMBL; AF161896; AAD47653.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; -
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39105 MW; F5400A7AB56FF7AB9 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 40
Q9TSQ3 PRELIMINARY; PRT; 339 AA.
AC Q9TSQ3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciniae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162007; AAD47762.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; -
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39219 MW; BFFE9138E82933D0 CRC64;
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Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
|||
Db 178 SOYQFWKNFQTLKIVILG 195

Search completed: September 28, 2004, 09:06:19
Job time : 29.8 secs

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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:51:21 ; Search time 52.525 Seconds
(without alignments)
118.345 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APYNIVLLNTFQEFFGLNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1_A_Geneseq_29Jan04:*
1: Geneseqp1950s:*
2: Geneseqp1950s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	22	4 AAB88996	Aab88996 HIV gp120
2	118	100.0	268	7 ADC10142	Adc10142 Human NOV
3	118	100.0	268	7 ADC10144	Adc10144 Human NOV
4	118	100.0	332	2 AAW25765	Aaw25765 Human CCR
5	118	100.0	352	2 AAW27407	Aaw27407 Human CCR
6	118	100.0	352	2 AAW27123	Aaw27123 Human che
7	118	100.0	352	2 AAW27125	Aaw27125 Macaque c
8	118	100.0	352	2 AAW07602	Aaw07602 Human G-p
9	118	100.0	352	2 AAW23835	Aaw23835 Human CC
10	118	100.0	352	2 AAW82322	Aaw82322 HIV-1 co-
11	118	100.0	352	3 AAY80128	Aay80128 Human G-p
12	118	100.0	352	4 AAG79089	Aag79089 Amino aci
13	118	100.0	352	4 AAE07046	Aae07046 Human G-p
14	118	100.0	352	4 AAE07048	Aae07048 Human G-p
15	118	100.0	352	4 AAG80111	Aag80111 Human CCR
16	118	100.0	352	4 AAE04321	Aae04321 Human che
17	118	100.0	352	4 AAE07037	Aae07037 Human G-p
18	118	100.0	352	4 AAE07039	Aae07039 Human G-p
19	118	100.0	352	4 AAB46858	Aab46858 Human HDG
20	118	100.0	352	4 AAB56342	Abb56342 Non-endog
21	118	100.0	352	4 AAB83354	Aab83354 Human CCR
22	118	100.0	352	4 AAB82948	Aab82948 Human HIV
23	118	100.0	352	5 AAU97150	Aau97150 Human G-p
24	118	100.0	352	5 AAU97152	Aau97152 Human G-p
25	118	100.0	352	5 AAM52829	Aam52829 Human CCR

26	118	100.0	352	5 AAM52828	Aam52828 Human CC
27	118	100.0	352	5 ABG70597	Abg70597 Human G-p
28	118	100.0	352	5 ABG92883	Abg92883 Human Imm
29	118	100.0	352	5 ABG92880	Abg92880 Human G-p
30	118	100.0	352	5 AAE25808	Aae25808 Human G-p
31	118	100.0	352	5 AAE25811	Aae25811 Human G-p
32	118	100.0	352	5 ABB81054	Abb81054 G-protein
33	118	100.0	352	5 ABB80343	Abb80343 Human che
34	118	100.0	352	6 ABG75540	Abg75540 Human G-p
35	118	100.0	352	6 ABR58602	Abt58602 Human can
36	118	100.0	352	6 AAO29514	Aao29514 Human G-C
37	118	100.0	352	6 ABU61654	Abu61654 Human G-p
38	118	100.0	352	6 ABP97728	Abp97728 Amino aci
39	118	100.0	352	6 ABP81933	Abp81933 Human C-C
40	118	100.0	352	7 ADC03341	Adc03341 Human che
41	118	100.0	352	7 ADC03359	Adc03359 Macaque c
42	118	100.0	371	2 AAW23834	Aaw23834 Human CC
43	118	100.0	439	2 AAY41280	Aay41280 Fusion pr
44	108	91.5	354	2 AAW54037	Aaw54037 Mouse CC-
45	105	89.0	354	7 ADD44859	Add44859 Rat Prote

ALIGNMENTS

RESULT 1

AAB88996
ID AAB88996 standard; peptide; 22 AA.

XX
AC AAB88996;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #89.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.

XX WO200116182-A2.

XX PD 08-MAR-2001.

XX PF 25-AUG-2000; 2000WO-US023505.

XX PR 27-AUG-1999; 99US-0151270P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions.

XX Claim 21; Page 38; 114pp; English.

XX The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention

SQ Sequence 22 AA;

Query Match 100.0%; Score 118; DB 4; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.1e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22

DB 1 APYNIVLLNTFOEFFGLNCS 22
 RESULT 2
 ADC10142
 ID ADC10142 standard; protein; 268 AA.
 AC ADC10142;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human NOVX polypeptide SEQ ID NO: 162.
 KW cytotatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
 KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
 KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
 KW inflammatory disorder; chromosome mapping; tissue typing;
 KW predictive medicine.
 XX
 OS Homo sapiens.
 XX
 PN WO2003000842-A2.
 XX
 PD 03-JAN-2003.
 XX
 PF 04-JUN-2002; 2002WO-US017443.
 PR 04-JUN-2001; 2001US-0295607P.
 PR 04-JUN-2001; 2001US-0295661P.
 PR 06-JUN-2001; 2001US-0296404P.
 PR 06-JUN-2001; 2001US-0296418P.
 PR 07-JUN-2001; 2001US-0296575P.
 PR 11-JUN-2001; 2001US-0297414P.
 PR 12-JUN-2001; 2001US-0295573P.
 PR 12-JUN-2001; 2001US-0297567P.
 PR 14-JUN-2001; 2001US-0298285P.
 PR 15-JUN-2001; 2001US-0298528P.
 PR 18-JUN-2001; 2001US-0299133P.
 PR 19-JUN-2001; 2001US-0299230P.
 PR 21-JUN-2001; 2001US-0299949P.
 PR 22-JUN-2001; 2001US-0300177P.
 XX
 XX (CURA-) CURAGEN CORP.
 PI Agae ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
 PI Dippio VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
 PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;
 PI Khramtsov NV, Liu L, Liu X, Malyankar UM, Miller CE, Millet I;
 PI Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
 PI Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;

PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
 PI Burgess CE, Lepley DM;
 XX
 DR WPI: 2003-210149/20.
 DR N-PSDB; ADC10141.
 XX
 PT New isolated NOVX polypeptides and nucleic acid molecules useful for
 PT treating, preventing and diagnosing pathological conditions with NOVX-
 PT associated disorders, such as cancer, obesity, diabetes and inflammatory
 PT or CNS diseases.
 XX
 XX Claim 1; SEQ ID NO 162; 772pp; English.
 XX
 CC The invention relates to novel isolated polypeptides, mature form of the
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the
 CC polypeptide comprising one or more conservative substitutions. The NOVX
 CC polypeptide is useful for treating or preventing a pathology associated
 CC with the polypeptide e.g. disorders associated with aberrant expression
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
 CC endocrine, CNS and inflammatory disorders. They can also be used in
 CC various detection and screening assays, chromosome mapping, tissue typing
 CC and predictive medicine. This sequence corresponds to one of the
 CC polypeptides of the invention.
 XX
 SQ Sequence 268 AA;
 Query Match 100.0%; Score 118; DB 7; Length 268;
 Best Local Similarity 100.0%; Pred. No. 2.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLNTFOEFFGLNCS 22
 DB 165 APYNIVLLNTFOEFFGLNCS 136
 RESULT 3
 ADC10144
 ID ADC10144 standard; protein; 268 AA.
 AC ADC10144;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human NOVX polypeptide SEQ ID NO: 164.
 KW cytotatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
 KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
 KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
 KW inflammatory disorder; chromosome mapping; tissue typing;
 KW predictive medicine.
 XX
 OS Homo sapiens.
 XX
 PN WO2003000842-A2.
 XX
 PD 03-JAN-2003.
 XX
 PF 04-JUN-2002; 2002WO-US017443.
 PR 04-JUN-2001; 2001US-0295607P.
 PR 04-JUN-2001; 2001US-0295661P.
 PR 06-JUN-2001; 2001US-0296404P.
 PR 06-JUN-2001; 2001US-0296418P.
 PR 07-JUN-2001; 2001US-0296575P.
 PR 11-JUN-2001; 2001US-0297414P.
 PR 12-JUN-2001; 2001US-0295573P.
 PR 12-JUN-2001; 2001US-0297567P.
 PR 14-JUN-2001; 2001US-0298285P.
 PR 15-JUN-2001; 2001US-0298528P.
 PR 18-JUN-2001; 2001US-0299133P.
 PR 19-JUN-2001; 2001US-0299230P.
 PR 21-JUN-2001; 2001US-0299949P.
 PR 22-JUN-2001; 2001US-0300177P.

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PR 26-JUN-2001; 2001US-0300893P.
PR 28-JUN-2001; 2001US-0301530P.
PR 28-JUN-2001; 2001US-0301550P.
PR 03-JUL-2001; 2001US-0302951P.
PR 31-JUL-2001; 2001US-030890P.
PR 14-SEP-2001; 2001US-0322297P.
PR 25-SEP-2001; 2001US-0324659P.
PR 03-DEC-2001; 2001US-0337477P.
PR 14-DEC-2001; 2001US-0341562P.
PR 21-FEB-2002; 2002US-0358565P.
PR 21-FEB-2002; 2002US-0359122P.
PR 22-FEB-2002; 2002US-0358978P.
PR 22-FEB-2002; 2002US-0359034P.
PR 22-FEB-2002; 2002US-0359035P.
PR 22-FEB-2002; 2002US-0359121P.
PR 27-FEB-2002; 2002US-0359964P.
PR 01-MAR-2002; 2002US-0360858P.
PR 12-MAR-2002; 2002US-0363430P.
PR 12-MAR-2002; 2002US-0363676P.
PR 10-APR-2002; 2002US-0371346P.
PR 10-MAY-2002; 2002US-0379444P.
PR 04-JUN-2002; 2002US-00379444.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Agee MJ, Anderson DW, Berghs C, Casman SJ, Catterton E,
XX Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA,
XX Giralach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R,
XX Kurantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I,
XX Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK,
XX Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK,
XX Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP,
XX Burgess CE, : Lepley DM;
XX
XX WPI; 2003-210149/20.
XX N-PSDB; ADC10143.
XX
XX New isolated NOVX polypeptides and nucleic acid molecules useful for
XX treating, preventing and diagnosing pathological conditions with NOVX-
XX associated disorders, such as cancer, obesity, diabetes and inflammatory
XX or CNS diseases.
XX
XX Claim 1; SEQ ID NO 164; 772pp; English.
XX
XX The invention relates to novel isolated polypeptides, mature form of the
XX polypeptide, a sequence that is 95% identical to the polypeptide or the
XX polypeptide comprising one or more conservative substitutions. The NOVX
XX polypeptide is useful for treating or preventing a pathology associated
XX with the polypeptide e.g. disorders associated with aberrant expression
XX or activity of the polypeptide, such as cancer, diabetes, obesity, and
XX endocrine, CNS and inflammatory disorders. They can also be used in
XX various detection and screening assays, chromosome mapping, tissue typing
XX and predictive medicine. This sequence corresponds to one of the
XX polypeptides of the invention.
XX
XX Sequence 268 AA;
XX
XX Query Match 100.0%; Score 118; DB 7; Length 268;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 APYNIVLLNTFOEFFGLNCS 22
XX 165 APYNIVLLNTFOEFFGLNCS 186
XX
XX RESULT 4
XX AAW26766
XX ID AAW26766 standard; protein; 332 AA.
XX
XX AAW26766;
XX
XX 21-MAY-1998 (first entry)

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```

XX Human chemokine receptor MMLR-CCR.
XX
XX Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human;
XX monocyte; macrophage; chemotaxis; haematopoiesis; infection; tumour;
XX inflammation; proliferative disease; cardiovascular disease; tumour;
XX rheumatoid arthritis; alveolitis; atherosclerosis;
XX chronic granulomatous disease; asthma; myasthenia gravis; diabetes;
XX inflammatory bowel disease; toxic shock syndrome; septic shock;
XX Chediak-Higashi syndrome; therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 107..128
XX /note= "conserved peptide"
XX
XX Misc-difference 121
XX /note= "a claimed polypeptide has isoleucine at residue
XX 121"
XX
XX WO9741225-A2.
XX
XX 06-NOV-1997.
XX
XX 25-APR-1997; 97WO-US006993.
XX
XX 26-APR-1996; 96US-00638081.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Au-Young J, Bandman O, Coleman R, Wilde CG;
XX
XX WPI; 1997-549729/50.
XX N-PSDB; AAT99542.
XX
XX Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful
XX to study, diagnose and treat, e.g. infection, inflammation, solid tumour
XX and proliferative and cardiovascular disease.
XX
XX Claim 8; Page 37-38; 59pp; English.
XX
XX This protein comprises human MMLR-CCR, a novel C-C chemokine receptor
XX associated with monocyte/macrophage infiltration and chemotaxis and
XX haematopoiesis. The amino acid sequence was deduced from a cDNA clone
XX (see AAT99542) obtained from a cDNA library made from mononuclear cells
XX collected on day 2 of a mixed lymphocyte culture, i.e. cells associated
XX with inflammation and immunomodulation. Another novel chemokine receptor,
XX MPHG-CCR (see AAW36767), is also claimed. MMLR-CCR contains 7
XX transmembrane spanning segments connected by a series of intracellular
XX and extracellular loops. MMLR-CCR and MPHG-CCR can be used to study,
XX diagnose and treat disease states in which normal leukocyte function is
XX perturbed by normal leukopoiesis or inappropriate activation via
XX chemokine agonists or antagonists, such as infection, inflammation,
XX proliferative disease, tumorigenesis, autoimmune disease, abnormal cell
XX proliferation, solid tumours, cardiovascular disease, rheumatoid
XX arthritis, alveolitis, atherosclerosis, chronic granulomatous disease,
XX asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic
XX shock syndrome, septic shock and Chediak-Higashi syndrome
XX
XX Sequence 332 AA;
XX
XX Query Match 100.0%; Score 118; DB 2; Length 332;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 APYNIVLLNTFOEFFGLNCS 22
XX 229 APYNIVLLNTFOEFFGLNCS 250
XX
XX RESULT 5
XX AAW27407
XX ID AAW27407 standard; protein; 352 AA.

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XX DT 14-DEC-1997 (first entry)
XX PN Macaque chemokine receptor 88C.
XX DE
XX KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
XX KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
XX KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
XX KW modulator; antibody.
XX OS
XX OS Macaca sp.
XX PN WO9722698-A2.
XX PD 26-JUN-1997.
XX PF 20-DEC-1996; 96WO-US020759.
XX PR 20-DEC-1995; 95US-00575967.
XX PR 07-JUN-1996; 96US-00661393.
XX PF (ICOS-) ICOS CORP.
XX PI Gray PW, Schweickart VL, Raport CJ;
XX DR WPI; 1997-341689/31.
XX DR N-PSDB; AAT85163.
XX CC New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX PT tumours, viral infections, auto-immune diseases, etc.
XX PS Claim 36; Page 57-58; 65pp; English.
XX CC This polypeptide sequence comprises Macaque chemokine receptor 88C, a G
XX CC protein coupled receptor that is involved in leukocyte trafficking. Its
XX CC amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR
XX CC amplification. It shows 97% identity to human 88C (AAW27123). 88C
XX CC receptors and their polypeptide fragments can be produced in transformed
XX CC host cells. The receptors, peptides comprising one or more of the
XX CC extracellular or intracellular domains, and anti-receptor antibodies can
XX CC be used to modulate receptor activities, particularly ligand and G
XX CC protein binding, and are potentially useful in the treatment
XX CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX CC infection, AIDS, inflammatory conditions, pathological immune response,
XX CC abnormal haematopoietic processes etc. A hybridoma that produces an
XX CC antibody that specifically binds to Macaque 88C is claimed
XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
DB 249 APYNIVLLNTFQFFGLNCS 270

RESULT 8
AAW07602
ID AAW07602 standard; protein; 352 AA.
AC AAW07602;
XX DT 26-FEB-1997 (first entry)
XX DE Human G-protein chemokine receptor HDGNR10.
XX KW G-protein chemokine receptor; HDGNR10; signal transduction;
XX KW haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
XX KW therapy.

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OS Homo sapiens.
XX PN WO9639437-A1.
XX PD 12-DEC-1996.
XX PF 06-JUN-1995; 95WO-US007173.
XX PR 06-JUN-1995; 95WO-US007173.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Li Y, Ruben SM;
XX DR WPI; 1997-043072/04.
XX DR N-PSDB; AAT44042.
XX CC Human G-protein chemokine receptor, HDGNR10 - useful to identify
XX PT (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and
XX PT acute inflammation, rheumatoid arthritis, etc.
XX PS Claim 1; Page 44-46; 61pp; English.
XX CC Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7
XX CC -transmembrane protein involved in signal transduction. Its amino acid
XX CC sequence was deduced from a cDNA clone (AAT44042) isolated from a human
XX CC monocyte library. Isolation of the cDNA allows prodn. of recombinant
XX CC HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant
XX CC receptor can be used to identify agonists or antagonists of the receptor;
XX CC such cpds. can be used to treat conditions related to the under- and over
XX CC -expression of G-protein chemokine receptors
XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
DB 249 APYNIVLLNTFQFFGLNCS 270

RESULT 9
AAW23835
ID AAW23835 standard; protein; 352 AA.
XX AC AAW23835;
XX DT 08-JUN-1998 (first entry)
XX DE Human CC chemokine receptor 5 (CCR5).
XX KW CC chemokine receptor 5; CCR5; G-protein coupled receptor;
XX KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Domain 29..55
XX FT /label= I
XX FT /note= "transmembrane domain"
XX FT Domain 104..126
XX FT /label= III
XX FT /note= "transmembrane domain"
XX FT Region 109..120
XX FT /note= "extracellular loop-1 (Claim 19)"
XX FT Domain 143..171
XX FT /label= IV
XX FT /note= "transmembrane domain"
XX FT Region 187..210
XX FT /note= "extracellular loop-2 (Claim 19)"
XX FT Domain 194..219

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FT      /label= V
FT      /note= "transmembrane domain"
FT      238..258
FT      /label= VI
FT      /note= "transmembrane domain"
FT      261..276
FT      /note= "extracellular loop-3 (Claim 19)"
FT      277..300
FT      /label= VII
FT      /note= "transmembrane domain"
FT      XX
FN      WO9745543-A2.
XX      04-DEC-1997.
FD      28-MAY-1997; 97WO-US009586.
PF      28-MAY-1996; 96US-0018508P.
PR      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX      Combadriere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
XX      Broder CC, Kennedy PE;
XX      WPI; 1998-032650/03.
XX      N-PSDB; AAT76920.
XX      CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
XX      between HIV and a target cell.
XX      Claim 68; Fig 1C; 70pp; English.
XX      This protein sequence comprises of a novel human macrophage-selective CC
XX      chemokine receptor that has been designated CCR5. The sequence was
XX      deduced from an isolated cDNA clone (see AAT76920). An Ala271Leu variant
XX      (see W238340 of CCR5 was also identified. The susceptibility of human
XX      macrophages to HIV infection depends on cell surface expression of CD4
XX      and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
XX      protein coupled cell surface molecules. It plays an essential role in the
XX      membrane fusion step of infection by some HIV isolates. The establishment
XX      of stable, non-human cell lines and transgenic mammals having cells that
XX      coexpress human CD4 and CCR5 provides valuable tools for research of HIV
XX      infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
XX      agents capable of blocking membrane fusion between HIV and target cells
XX      represent potential anti-HIV therapeutics for macrophage tropic strains
XX      of HIV
XX      SQ      Sequence 352 AA;
XX      Query Match      100.0%; Score 118; DB 2; Length 352;
XX      Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX      Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 APYNIIVLLNTFQEPFGLNCS 22
DB      249 APYNIIVLLNTFQEPFGLNCS 270
RESULT 10
AAW88232
ID      AAW88232 standard; protein; 352 AA.
XX      AAW88232;
XX      15-MAR-1999 (first entry)
XX      HIV-1 co-receptor CCR5.
XX      HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
XX      gene therapy; human.
XX      Homo sapiens.
XX      XX

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FH      Key      Location/Qualifiers
FT      Domain    32..56
FT      /note= "transmembrane domain 1"
FT      Domain    67..87
FT      /note= "transmembrane domain 2"
FT      Misc-difference 101
FT      /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA
FT      (stop) in CCR5m303"
FT      Domain    103..124
FT      /note= "transmembrane domain 3"
FT      Domain    142..167
FT      /note= "transmembrane domain 4"
FT      Domain    200..223
FT      /note= "transmembrane domain 5"
FT      Domain    236..260
FT      /note= "transmembrane domain 6"
FT      Domain    275..301
FT      /note= "transmembrane domain 7"
XX      WO9854317-A1.
XX      03-DEC-1998.
XX      29-MAY-1998; 98WO-EP003437.
XX      30-MAY-1997; 97US-0048057P.
XX      (WOND-) FOND MONDIALE RECH & PREVENTION SIDA.
XX      Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
XX      WPI; 1999-059835/05.
XX      N-PSDB; AAV84126.
XX      New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
XX      resistance of CCR5-expressing cells to HIV-1 infection.
XX      Disclosure; Page 34-35; 55pp; English.
XX      This is the amino acid sequence of wild-type human CCR5, which serves as
XX      a co-receptor for infection by macrophage-tropic (M-tropic) strains of
XX      HIV-1. The invention relates to the identification of a CCR5 variant (see
XX      AAW8231), designated CCR5m303, comprising the first two transmembrane
XX      domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
XX      presence of the CCR5m303 variant with the wild type CCR5 allele shows a
XX      positive correlation with resistance to infection with M-tropic HIV-1
XX      strains, and may indicate slower progression of the disease. The
XX      detection of CCR5 variants may be used to identify individuals at lower
XX      risk of infection relative to the general population who, if infected,
XX      may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
XX      36) are provided for use in diagnostic methods for detecting the presence
XX      of such variants. A method is provided for inhibiting HIV-1 infection of
XX      a cell expressing the CCR5 receptor. This involves introducing a nucleic
XX      acid encoding a CCR5 variant into the cell, thereby reducing the number
XX      of functional CCR5 molecules present on the cell surface
XX      SQ      Sequence 352 AA;
XX      Query Match      100.0%; Score 118; DB 2; Length 352;
XX      Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX      Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 APYNIIVLLNTFQEPFGLNCS 22
DB      249 APYNIIVLLNTFQEPFGLNCS 270
RESULT 11
AAW80128
ID      AAY80128 standard; protein; 352 AA.
XX      AAY80128;
XX      Homo sapiens.
XX      XX

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DT 19-MAY-2000 (first entry)
 XX Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
 DE Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;
 XX diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
 KW tumour; infection; leukaemia; psoriasis; allergy;
 KW T-cell mediated autoimmune disease; atherogenesis; anaphylaxis;
 KW inflammation; allergic reaction; silicosis; sarcoidosis;
 KW rheumatoid arthritis; hyper-eosinophilia syndrome.
 XX Homo sapiens.
 OS
 XX US6025154-A.
 FN
 XX 15-FEB-2000.
 PD
 XX 06-JUN-1995; 95US-00466343.
 PF
 XX 06-JUN-1995; 95US-00466343.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Li Y, Ruben SM;
 PI
 XX WPI; 2000-181807/16.
 XX N-PSDB; AAZ91481.
 DR
 XX Isolated nucleic acid encoding human G-protein chemokine receptor useful
 PT for diagnostic assays, scientific research and screening for compounds
 PT which bind to and activate or inhibit activation of the receptor
 PT polypeptides.
 XX Claim 1; Fig 1; 22pp; English.
 PS
 XX The present sequence represents a human G-protein chemokine receptor
 CC designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
 CC screening for compounds which bind to and either: (1) activate the
 CC HDGNR10 polypeptides causing stimulation of haematopoiesis, wound
 CC healing, coagulation, and angiogenesis; treatment of solid tumours,
 CC chronic infections, leukaemia, T-cell mediated autoimmune diseases,
 CC parasitic infections, psoriasis, and to stimulate growth factor activity;
 CC or (2) inhibit activation of the HDGNR10 polypeptides which is useful for
 CC preventing and/or treating allergy, atherogenesis, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
 CC E-mediated allergic reactions, prostaglandin-independent fever, bone
 CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
 CC hyper-eosinophilia syndrome. The polynucleotides are also useful for
 CC diagnostic assays for detecting diseases related to mutations in the
 CC nucleic acid sequences encoding the polypeptides and for detecting an
 CC altered level of the soluble form of the receptor polypeptides. The
 CC polynucleotides are also useful for in vitro purposes related to
 CC scientific research, synthesis of DNA and manufacture of DNA vectors
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLNTFQBFGLNCS 22
 DB 249 APYNIVLLNTFQBFGLNCS 270
 RESULT 12
 AAG79089
 ID AAG79089 standard; protein; 352 AA.
 XX
 AC AAG79089;
 XX
 DT 10-DEC-2001 (first entry)
 XX

DE Amino acid sequence of human CCR5 protein.
 XX
 KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
 KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
 XX Homo sapiens.
 OS
 XX WO200164752-A2.
 PN
 XX 07-SEP-2001.
 PD
 XX 28-FEB-2001; 2001WO-US006322.
 PF
 XX 02-MAR-2000; 2000US-00517605.
 PR
 XX (UYNV) UNIV NEW YORK STATE.
 PA (UYNV-) UNIV NIJMEGEN.
 XX
 PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
 XX WPI; 2001-602565/68.
 DR
 XX An antibody for the treatment or prevention of HIV-infection comprises a
 PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of
 PT DC-SIGN due to concomitant conformational change.
 XX Disclosure; Page 118-119; 131pp; English.
 PS
 XX The specification describes an antibody which is specific for an
 CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
 CC is exposed upon gp120 binding of DC-SIGN due to concomitant
 CC conformational change. DC-SIGN is a receptor that is specifically
 CC expressed on dendritic cells and facilitates infection of T lymphocytes
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
 CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
 CC with high affinity. The antibody of the invention inhibits the trans
 CC enhancement of HIV entry into a T cell or macrophage facilitated by
 CC dendritic cells. The antibody is useful to treat or prevent HIV
 CC infection. The present sequence represents a human CCR5 protein, which is
 CC a translocation promoting agent that interacts with CD4. This receptor
 CC functions in HIV-1 entry into cells
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLNTFQBFGLNCS 22
 DB 249 APYNIVLLNTFQBFGLNCS 270
 RESULT 13
 AAE07046
 ID AAE07046 standard; protein; 352 AA.
 XX
 AC AAE07046;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; neurotropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; immune disorder; Addison's disease;
 KW gastrointestinal tract; lung; liver; diabetes mellitus; allergy;
 KW haemolytic anaemia; autoimmune thyroiditis; Crohn's disease; wound healing;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX

OS XX Homo sapiens.

FT FH Key Location/Qualifiers

FT FT Domain 1..36 /label= Extracellular_domain

FT FT Domain 37..305 /label= Transmembrane_domain

FT FT Domain 37..58 /label= Transmembrane_domain

FT FT Domain 59..67 /label= Transmembrane_domain

FT FT Domain 68..88 /label= Intracellular_loop_1

FT FT Domain 89..102 /label= Transmembrane_domain

FT FT Domain 103..124 /label= Transmembrane_domain

FT FT Domain 125..141 /label= Transmembrane_domain

FT FT Domain 142..166 /label= Transmembrane_domain

FT FT Domain 167..195 /label= Transmembrane_domain

FT FT Domain 196..223 /label= Transmembrane_domain

FT FT Domain 224..235 /label= Transmembrane_domain

FT FT Domain 236..260 /label= Transmembrane_domain

FT FT Domain 261..274 /label= Transmembrane_domain

FT FT Domain 287..305 /label= Transmembrane_domain

FT FT Domain 306..352 /label= Transmembrane_domain

FT FT Domain /label= Intracellular_domain

XX WO200158916-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US004153.

XX PR 09-FEB-2000; 2000US-0181258P.

XX PR 09-MAR-2000; 2000US-0187999P.

XX PR 22-SEP-2000; 2000US-0234336P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488966/53.

XX DR N-PSDB; AAD13282.

XX DR Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

XX PS Claim 102; Fig 1; 518pp; English.

XX CC The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemia) and wound healing. The present sequence is human CCR5 HDGNR10 protein

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNI VLLNTFQEF FGLNCS 22
|||||

DB 249 APYNI VLLNTFQEF FGLNCS 270
|||||

RESULT 14

AAE07048

ID AAE07048 standard; protein; 352 AA.

XX AAE07048;

XX 16-OCT-2001 (first entry)

XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnary;

XX cytostatic; immunosuppressive; neutropic; neuroprotective; gene therapy;

XX neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;

XX rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;

XX gastrointestinal tract; lung; liver; immune disorder; Addison's disease;

XX haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;

XX multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;

XX cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX WO200158916-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004153.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488966/53.

XX DR N-PSDB; AAD13299.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

XX Claim 102; Fig 1; 518pp; English.

XX CC The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemia) and wound healing. The present sequence is human CCR5 HDGNR10 protein

PS Example 40; Page 504-505; 519pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5)

CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are

CC useful for treating, preventing or ameliorating a disease or disorder

CC associated with inflammation, defective or aberrant chemotaxis of immune

CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's

CC sarcoma) or defective or aberrant T-cell antigen presenting cell

CC interaction. The disease or disorder may also be an infectious disease

CC (e.g. a viral infection such as an early stage HIV infection, a

CC cytomegalovirus infection, or a poxvirus infection), an autoimmune

CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The

CC disease or disorder may be associated with aberrant CCR5 expression, lack

CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand

CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful

CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,

CC protein, antibodies, agonists and antagonists are also useful in the

CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal

CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,

CC urogenital); immune disorders (Addison's disease, allergies, autoimmune

CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's

CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)

CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The

CC present sequence is human CCR5 HDGNR10 protein

XX Sequence 352 AA;

XX Query Match 100.0%; Score 118; DB 4; Length 352;

XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;

XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22

DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 15

AAAG80111

ID AAG80111 standard; protein; 352 AA.

AC AAG80111;

DT 17-JAN-2002 (first entry)

XX Human CCR5 protein.

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;

XX inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;

XX chronic bowel inflammation; rheumatoid arthritis; cytostatic;

XX antiinflammatory; antiasthmatic; immunosuppressive; dermatological;

XX antirheumatic; antiarthritic.

XX Homo sapiens.

XX WO200172830-A2.

XX 04-OCT-2001.

XX 02-APR-2001; 2001WO-EP003708.

XX 31-MAR-2000; 2000DE-01016013.

XX (IPFP-) IPF PHARM GMBH.

XX (FORS/) FORSMANN U.

XX Forssmann W, Adermann K, Heitland A, Spodsborg N;

XX WPI; 2001-626256/72.

XX Diagnostic agent containing two or more receptor-specific ligands, useful

XX for detecting tumors, inflammation etc., also therapeutic use of ligand

XX inhibitors.

XX Disclosure; Page 10; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least

CC two different ligands (I) for receptors (II) that are implicated in

CC disease. (A) are used for the diagnosis of tumors (especially colorectal

CC or prostatic), organ rejection, inflammation and autoimmune diseases.

CC Also inhibitors of (I) are used therapeutically against tumors (and their

CC metastases), inflammation (particularly bronchial asthma or chronic bowel

CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),

CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,

CC endocrine, motor or urogenital systems or skin are affected, and bone

CC marrow diseases. The products of the invention are chemokine derivatives

CC which have cytostatic, antiinflammatory, antiasthmatic,

CC immunosuppressive, dermatological, antirheumatic, antiarthritic.

CC Chemokines act on specific tumor and inflammatory cells through a

CC constellation of chemokine receptors (CR), which control migration and

CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine

CC fragments used to illustrate the method of the invention

XX Sequence 352 AA;

XX Query Match 100.0%; Score 118; DB 4; Length 352;

XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;

XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22

DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 16

AAE04321

ID AAE04321 standard; protein; 352 AA.

AC AAE04321;

XX 04-SEP-2001 (first entry)

XX Human chemokine receptor (CKR), CC-CKR-5 related protein #2.

XX Human; transformed mammalian cell; CD4; reporter gene; translocation;

XX human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;

XX chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor;

XX CC-CKR-5; envelope glycoprotein; anti-HIV.

XX Homo sapiens.

XX US6258527-B1.

XX 10-JUL-2001.

XX 21-MAY-1997; 97US-00861105.

XX 20-MAY-1996; 96US-0017157P.

XX 19-JUN-1996; 96US-0020043P.

XX 19-MAY-1997; 97US-00858660.

XX (AAFO-) AARON DIAMOND AIDS RES CENT.

XX (UNY) UNIV NEW YORK STATE.

XX Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;

XX WPI; 2001-417127/44.

XX N-PSDB; AAD08577.

XX Transformed mammalian cell (I) that contains a CD4 gene, reporter gene

XX and HIV LTR for identification of drugs and antibodies for treatment of

XX HIV.

XX Disclosure; Col 47-50; 37pp; English.

XX The present invention relates to a transformed mammalian cell that

CC contains a gene encoding CD4, a construct encoding a reporter gene under
 CC the regulation of an human immuno deficiency virus (HIV) long terminal
 CC repeat (LTR) and that has been transduced with a vector encoding a human
 CC chemokine receptor (CCR) where the CD4 and the CCR are present on the
 CC cell surface of transformed mammalian cell. The invention is useful for
 CC identifying drugs or antibodies that interfere with the translocation of
 CC HIV into transformed mammalian cell or for identifying a human chemokine
 CC receptor that facilitates the infection of a particular HIV strain into
 CC the transformed mammalian cell. Compounds identified can be used to treat
 CC cellular dysfunction and to prevent or combat HIV infection. The present
 CC sequence is a human chemokine receptor (CCR), CC-CR-5 related protein.
 CC CC-CR-5 is the principal cofactor for entry mediated by the envelope
 CC glycoproteins of primary macrophage-tropic strains of HIV-1
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 APYNIIVLLNTFOEFFGLNCS 22
 |||||
 Db 249 APYNIIVLLNTFOEFFGLNCS 270

RESULT 17
 AAE07037
 ID AAE07037 standard; protein; 352 AA.

XX AAE07037;

DT 16-OCT-2001 (first entry)

DE Human G-protein chemokine receptor (CCRS) HDGNR10 protein #1.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
 KW cytostatic; immunosuppressive; neutropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Domain 1..36
 FT /label= Extracellular_domain
 FT Domain 37..305
 FT /label= Transmembrane_domain
 FT Domain 37..58
 FT /label= Transmembrane_domain
 FT /note= "Segment 1"
 FT Domain 59..67
 FT /label= Intracellular_loop_1
 FT Domain 68..88
 FT /label= Transmembrane_domain
 FT /note= "Segment 2"
 FT Domain 89..102
 FT /label= Extracellular_loop_1
 FT Domain 103..124
 FT /label= Transmembrane_domain
 FT /note= "Segment 3"
 FT Domain 125..141
 FT /label= Intracellular_loop_2
 FT Domain 142..166
 FT /label= Transmembrane_domain
 FT /note= "Segment 4"
 FT Domain 167..195
 FT /label= Extracellular_loop_2
 FT Domain 196..223

FT /label= Transmembrane_domain
 FT /note= "Segment 5"
 FT Domain 224..235
 FT /label= Intracellular_loop_3
 FT Domain 236..260
 FT /label= Transmembrane_domain
 FT /note= "Segment 6"
 FT Domain 261..274
 FT /label= Extracellular_loop_3
 FT Domain 287..305
 FT /label= Transmembrane_domain
 FT /note= "Segment 7"
 FT Domain 306..352
 FT /label= Intracellular_domain

XX WO200158915-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004152.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUYA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488965/53.

XX N-PSDB; AAD13181.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor

(CCRS) HDGNR10 polypeptide useful for preventing or treating autoimmune

diseases e.g. rheumatoid arthritis, hyperproliferative disorders and

neurodegenerative disorders.

XX Claim 102; Fig 1; 495pp; English.

XX The present sequence is human G-protein chemokine receptor (CCRS) HDGNR10
 CC protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5
 CC HDGNR10 antibodies are useful for treating, preventing or ameliorating a
 CC disease or disorder associated with inflammation, defective or aberrant
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen
 CC presenting cell interaction. The disease or disorder may also be an
 CC infectious disease (e.g. a viral infection such as an early stage HIV
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative
 CC disorder. The disease or disorder may be associated with aberrant CCR5
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or
 CC lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food
 CC additive or preservative to increase or decrease storage capabilities.
 CC CCR5 HDGNR10 DNA are useful for chromosome identification and in gene
 CC therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists
 CC are also useful in the diagnosis, treatment and prevention of cancer
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,
 CC liver, lung, urogenital); immune disorders (Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis); cardiovascular disorders (myocardial ischaemias) and wound
 CC healing

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. NO. 2.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 APYNIIVLLNTFOEFFGLNCS 22

Db 249 APYNIIVLLNTFOEFFGLNCS 270

RESULT 18
AAE07039
ID AAE07039 standard; protein; 352 AA.
XX AC AAE07039;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
XX
XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
XX human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
XX cytosolic; immunosuppressive; nontropic; neuroprotective; gene therapy;
XX neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
XX rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
XX gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
XX haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
XX multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
XX cardiovascular disorder; myocardial ischaemia.
XX
OS Homo sapiens.
XX
XX WO200158915-A2.
XX
XX 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US0004152.
XX
XX 09-FEB-2000; 2000US-0181258P.
XX
XX 09-MAR-2000; 2000US-0187999P.
XX
XX 22-SEP-2000; 2000US-0234336P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Roschke V, Li Y, Ruben SM;
XX
XX WPI; 2001-488965/53.
XX
XX N-PSDB; AAD13198.
XX
XX Isolated nucleic acid encoding a human G-protein chemokine receptor
XX (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
XX diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
XX neurodegenerative disorders.
XX
XX Example 40; Page 486-487; 495pp; English.
XX
XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
XX protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or
XX ameliorating a disease or disorder associated with inflammation,
XX defective or aberrant chemotaxis of immune cells, HIV infection (such as
XX Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
XX aberrant T-cell antigen presenting cell interaction. The disease or
XX disorder may also be an infectious disease (e.g. a viral infection such
XX as an early-stage HIV infection, a cytomegalovirus infection, or a
XX poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
XX a neurodegenerative disorder. The disease or disorder may be associated
XX with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
XX ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
XX is used as a food additive or preservative to increase or decrease
XX storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
XX identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
XX antibodies, agonists and antagonists are also useful in the diagnosis,
XX treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
XX bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
XX disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
XX autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
XX sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular
XX disorders (myocardial ischaemia) and wound healing
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 118; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNIVLLNTFOBPFGLNCS 22
DB 249 APYNIVLLNTFOBPFGLNCS 270
RESULT 19
AAB46858
ID AAB46858 standard; protein; 352 AA.
XX
XX AAB46858;
XX
XX 16-AUG-2001 (revised)
DT 02-AUG-2001 (revised)
DT 04-MAY-2001 (first entry)
XX
XX Human HDGNR10 protein.
XX
XX HDGNR10; human; G-protein chemokine receptor; antiinflammatory;
XX immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
XX cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;
XX vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
XX angiogenesis; solid tumour; infection; leukemia; growth factor activity;
XX T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
XX anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;
XX immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
XX prostaglandin-independent fever; bone marrow failure; sarcoidosis;
XX hyper-ecsinophilic syndrome; vulnerary.
XX
XX Homo sapiens.
XX
XX OS
XX US2001000241-A1.
XX
XX 12-APR-2001.
XX
XX 29-NOV-2000; 2000US-00725285.
XX
XX 06-JUN-1995; 95US-00466343.
XX
XX 18-NOV-1998; 98US-00195662.
XX
XX 25-JUN-1999; 99US-00339912.
XX
XX (LIYY/) LI Y.
XX (RUBE/) RUBEN S M.
XX
XX Li Y, Ruben SM;
XX
XX WPI; 2001-226317/23.
XX
XX N-PSDB; AAF26390.
XX
XX New human G-protein chemokine receptor polypeptides and polynucleotides,
XX useful for identifying (ant)agonists to the G-protein chemokine receptor.
XX
XX Claim 1a; Page 15; 22pp; English.
XX
XX This invention describes a novel receptor polypeptide (I) selected from
XX (i) a fully defined 329 amino acid sequence (ii) fully disclosed in the
XX specification; and (ii) a polypeptide encoded by the cDNA contained in a
XX plasmid, and fragments, analogs and derivatives of the polypeptide. The
XX products of the invention have antiinflammatory, immunomodulatory
XX anticoagulant, antiallergic, immunosuppressive, vulnerary, cytostatic,
XX antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic
XX activity and can be used for gene therapy. The G-protein chemokine
XX receptors, HDGNR10, (I) are useful for screening for compounds which
XX activate or inhibit activation of (I). The products of the invention can
XX also be used for stimulating haematopoiesis, wound healing, coagulation,
XX angiogenesis, treating solid tumours, chronic infections, leukemia, T-
XX cell mediated autoimmune diseases, parasitic infections, psoriasis, and
XX stimulating growth factor activity. HDGNR10 is useful for treating
XX allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
XX inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
XX reactions, prostaglandin-independent fever, bone marrow failure,

CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
 CC errors in the keyword formatting)

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
 |||||
 DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 20

ABB56342
 ID ABB56342 standard; protein; 352 AA.

XX AC ABB56342;

DT 18-FEB-2002 (first entry)

XX DE Non-endogenous human GPCR protein, SEQ ID NO: 477.

XX KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 XX constitutively activated GPCR; agonist; disease.

XX OS Homo sapiens.

XX CS Synthetic.

XX PN WO200177172-A2.

XX PD 18-OCT-2001.

XX PF 05-APR-2001; 2001WO-US011098.

XX PR 07-APR-2000; 2000US-0195747P.

XX PA (AREN-) ARENA PHARM INC.

XX PI Lehmann-Bruinsma K, Liaw CW, Lin I;

XX DR WPI; 2001-648759/74.

XX DR N-PSDB; AB197978.

XX PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 XX disease treatment, comprises contacting candidate compounds with versions
 XX of GPCRs.

XX PS Claim 1; Page 277-278; 394pp; English.

XX CC The invention relates to G protein-coupled receptors (GPCRs) for which
 XX the endogenous ligand has been identified. Non-endogenous constitutively
 XX activated versions of known GPCRs are used in the invention for the
 XX direct identification of candidate compounds as receptor agonists,
 XX inverse agonists or partial agonists. Such agonists are useful as
 XX therapeutic agents for diseases or disorders associated with GPCRs. The
 XX present sequence is a non-endogenous version of a known human GPCR

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
 |||||
 DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 21

AAB83354

ID AAB83354 standard; protein; 352 AA.

XX AC AAB83354;

XX DT 09-OCT-2001 (first entry)

XX DE Human CCR5 protein sequence.

XX KW Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
 XX human immunodeficiency virus; anti-inflammatory disease; human.

XX OS Homo sapiens.

XX PN EP1118858-A2.

XX PD 25-JUL-2001.

XX PF 03-JAN-2001; 2001EP-00300020.

XX PR 12-JAN-2000; 2000GB-00000659.

XX PR 12-JAN-2000; 2000GB-00000661.

XX PR 12-JAN-2000; 2000GB-00000663.

XX PA (PFIZ) PFIZER LTD.

XX PA (PFIZ) PFIZER INC.

XX PI Dobbs S, Perros M, Rickett GA;

XX DR WPI; 2001-477088/52.

XX DR N-PSDB; AAF87099.

XX PT Determining if an agent can modulate CCR5-gp120 interaction, comprises

XX incubating the agent with CCR5 and gp120 and determining if the agent

XX modulates the interaction.

XX PS Claim 1; Page 110; 113pp; English.

XX CC This sequence represents the human CCR5 protein sequence. The invention
 XX relates to a method for determining whether an agent is capable of
 XX modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
 XX with gp120, comprising incubating the agent with CCR5 and gp120 and
 XX determining whether the agent modulates the interaction, where gp120 is
 XX associated with CD4, and where the interaction is a low affinity binding.
 XX The method is used to identify an agent capable of modulating the
 XX interaction of CCR5 with gp120. An agent identified by the method is used
 XX to prepare a pharmaceutical composition for the treatment of a disease or
 XX condition associated with CCR5 and gp120 interaction, to treat a subject
 XX with a disease or condition associated with CCR5 and gp120 interaction,
 XX and for preparing a pharmaceutical for treating human immunodeficiency
 XX virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
 XX is commercially useful, amenable to high throughput screening, and
 XX detects interaction of gp120 with cells expressing only CCR5

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
 |||||
 DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 22

AAB82948

ID AAB82948 standard; protein; 352 AA.

XX AC AAB82948;

XX DT 21-DEC-2001 (first entry)

XX DE Human HIV-1 co-receptor CCR5.

RESULT 23	
AAU97150	
ID AAU97150 standard; protein; 352 AA.	
XX	
AAU97150;	
AC	
XX	
DT 13-AUG-2002 (first entry)	
XX	
DE Human G-protein chemokine receptor (CCR5) HDGNR10 #1.	
XX	

RESULT 24	
AAU97152	
ID	AAU97152 standard; protein; 352 AA.
XX	
XX	AAU97152;
XX	
DT	13-AUG-2002 (first entry)

DE Human G-protein chemokine receptor (CCR5) HDGMR10 #2.
 XX Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation;
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 KW hyperproliferative disease; neurological disease; receptor.
 XX
 OS Homo sapiens.

XX US2002048786-A1.

XX 25-APR-2002.

XX 09-FEB-2001; 2001US-00779879.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (ROSE/) ROSEN C A.

XX (ROSC/) ROSCHKE V.

XX (LIYY/) LI Y.

XX (RUBE/) RUBEN S M.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2002-434754/46.

XX N-PSDB; ABK51970.

XX New nucleic acid encoding an antibody specific for the G-protein
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 PT inflammation.

XX Disclosure; Page 165-166; 180pp; English.

XX The present invention relates to the isolation of a novel human G-protein
 CC chemokine receptor (CCR5) designated HDGMR10, and polynucleotide
 CC sequences encoding it. The invention also describes antibodies that bind
 CC human G-protein chemokine receptor (CCR5) HDGMR10 and polynucleotide
 CC sequences encoding the antibodies. The antibodies are useful for treating
 CC or preventing inflammation, defective or aberrant chemotaxis of immune
 CC cells and T-cell/antigen-presenting cell interactions, infections and
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 CC infections (especially early-stage human immune deficiency virus (HIV),
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 CC associated with aberrant or deficient expression of the CCR5 receptor or
 CC its ligands. The antibodies are also useful to determine CCR5 expression,
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other
 CC hyperproliferative diseases. The polynucleotide sequences encoding human
 CC G-protein chemokine receptor (CCR5) HDGMR10 can be used to produce the
 CC recombinant receptor, and in the treatment of a wide range of diseases
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 CC present sequence represents human G-protein chemokine receptor (CCR5)
 CC HDGMR10 #2

XX Sequence 352 AA;

Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTQEPFGLNCS 22
 DB 249 APYNIVLLNTQEPFGLNCS 270

RESULT 25
 AAM52829

ID AAM52829 standard; protein; 352 AA.

XX AC AAM52829;

XX

DT 22-FEB-2002 (first entry)
 XX Human CCR5 Gln 55 variant.
 XX CCR5; CC chemokine receptor 5; human; HIV infection;
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
 KW drug screening; identification; variant.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 55

XX /note= "Glu replaces wild-type Leu; encoded by CTG"

XX Misc-difference 58

XX /note= "Encoded by AGC"

XX WO200171346-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009155.

XX 21-MAR-2000; 2000US-0190946P.

XX 21-MAR-2000; 2000US-0190989P.

XX 21-MAR-2000; 2000US-0191299P.

XX 20-MAR-2001; 2001US-00813448.

XX 20-MAR-2001; 2001US-00813651.

XX 20-MAR-2001; 2001US-00813653.

XX (CONS-) CONSENSUS PHARM INC.

XX Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;

XX WPI; 2002-010610/01.

XX N-PSDB; ABA02318.

XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,
 PT comprises binding a molecule from library to a molecule having binding
 PT property corresponding to CCR5 and identifying bound molecule.

XX Example 3; Fig 4B; 50pp; English.

XX The invention relates to a method for identifying a binding compound for
 CC chemokine receptor 5 (CCR5). The method involves screening a library
 CC of test molecules (particularly peptides) with immobilised CCR5, and then
 CC identifying those molecules which bind. The invention also relates to
 CC CCR5-binding molecules identified using the method of the invention, a
 CC methods for identifying consensus motifs for CCR5-binding peptides, a
 CC transfer vector encoding tagged CCR5, a computer-aided methods for
 CC determining the relative binding affinity of a test molecule to CCR5 and
 CC a computer aided drug screening assay that utilises the three-dimensional
 CC structure of CCR5. Compounds identified using the methods of the
 CC invention are useful for treating or preventing HIV (human
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
 CC syndrome) in a patient. The methods of the invention may also be used to
 CC identify agonists or antagonists of the interaction of CCR5 with its
 CC natural ligand, and to determine a binding motif for CCR5. The present
 CC sequence represents a naturally occurring variant of human CCR5 in which
 CC there is a glutamine, rather than a leucine, at position 55

XX Sequence 352 AA;

Query Match 100.0%; Score 118; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTQEPFGLNCS 22
 DB 249 APYNIVLLNTQEPFGLNCS 270

RESULT 26
 AAM52828

ID XX AAM52828 standard; protein; 352 AA.
XX AC AAM52828;
XX DE 22-FEB-2002 (first entry)
XX DT Human CC chemokine receptor 5 (CCR5).
XX DE CCR5; CC chemokine receptor 5; human; HIV infection;
XX KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
XX KW drug screening; identification.
XX OS Homo sapiens.
XX FN WO200171346-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009155.
XX PR 21-MAR-2000; 2000US-0190946P.
XX PR 21-MAR-2000; 2000US-0190996P.
XX PR 21-MAR-2000; 2000US-0191299P.
XX PR 20-MAR-2001; 2001US-00813448.
XX PR 20-MAR-2001; 2001US-00813651.
XX PR 20-MAR-2001; 2001US-00813653.
XX FA (CONS-) CONSENSUS PHARM INC.
XX PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX PT WPI; 2002-010610/01.
XX DR N-PSDB; ABA02317.
XX DR Identifying CC chemokine receptor 5 binding compound for treating AIDS,
XX PT comprises binding a molecule from library to a molecule having binding
XX PT property corresponding to CCR5 and identifying bound molecule.
XX PS Example 3; Fig 4A; 50pp; English.
XX CC The invention relates to a method for identifying a binding compound for
XX CC CC chemokine receptor 5 (CCR5). The method involves screening a library
XX CC of test molecules (particularly peptides) with immobilised CCR5, and then
XX CC identifying those molecules which bind. The invention also relates to
XX CC CCR5-binding molecules identified using the method of the invention,
XX CC methods for identifying consensus motifs for CCR5-binding peptides, a
XX CC transfer vector encoding tagged CCR5, a computer-aided method for
XX CC determining the relative binding affinity of a test molecule to CCR5 and
XX CC structure of CCR5. Compounds identified using the methods of the
XX CC invention are useful for treating or preventing HIV (human
XX CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
XX CC syndrome) in a patient. The methods of the invention may also be used to
XX CC identify agonists or antagonists of the interaction of CCR5 with its
XX CC natural ligand, and to determine a binding motif for CCR5. The present
XX CC sequence represents human CCR5
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 118; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. NO. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNIVLLNTTFOFFGLNCS 22
Db 249 APYNIVLLNTTFOFFGLNCS 270
RESULT 27
ABG70597
ID ABG70597 standard; protein; 352 AA.
XX AC ABG70597;

XX 03-DEC-2002 (first entry)
XX DE Human G-protein chemokine receptor, HDGNR10.
XX DE Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;
XX KW haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour;
XX KW chronic infection; leukaemia; T-cell mediated autoimmune disease;
XX KW parasitic infection; psoriasis; growth factor activity; allergy;
XX KW atherogenesis; anaphylaxis; malignancy; inflammation; histamine;
XX KW immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis;
XX KW prostaglandin-independent fever; bone marrow failure; shock;
XX KW rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic;
XX KW immunosuppressive; antiparasitic; antipsoriatic; antiallergic;
XX KW antiarteriosclerotic; antiinflammatory; antirheumatic; antiarthritic;
XX KW antipyretic; receptor.
XX OS Homo sapiens.
XX PF US2002099176-A1.
XX PD 25-JUL-2002.
XX PF 25-JUN-1999; 99US-00339912.
XX PR 06-JUN-1995; 95US-00466343.
XX FA (LIYY/) LI Y.
XX PA (RUBE/) RUBEN S M.
XX PI Li Y, Ruben SM;
XX DR WPI; 2002-690494/74.
XX DR N-PSDB; ABS54272.
XX PT Novel human G-protein chemokine receptor polypeptide useful for
XX PT identifying modulators for stimulating hematopoiesis, wound healing,
XX PT leukemia, for treating allergy, rheumatoid arthritis, shock and as
XX PT research agents.
XX PS Claim 7; Fig 1; 22pp; English.
XX CC The present invention relates to the isolation of human G-protein
XX CC chemokine receptor, HDGNR10 (CCR5 receptor), and the polynucleotide
XX CC sequence encoding it. HDGNR10 polypeptide and polynucleotide sequences
XX CC are or useful for diagnosing a disease or a susceptibility to a disease
XX CC related to underexpression of HDGNR10. They are useful for identifying
XX CC modulators for stimulating haematopoiesis, wound healing, coagulation,
XX CC angiogenesis, to treat solid tumours, chronic infections, leukaemia, or
XX CC cell mediated autoimmune diseases, parasitic infections, psoriasis, or
XX CC for stimulating growth factor activity. The sequences are also useful for
XX CC preventing and/or treating allergy, atherogenesis, anaphylaxis,
XX CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
XX CC E (IgE)-mediated allergic reactions, prostaglandin-independent fever,
XX CC bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-
XX CC eosinophilic syndrome. Polynucleotide sequences encoding HDGNR10 can be
XX CC used in gene therapy to treat conditions related to underexpression of
XX CC HDGNR10. The present sequence represents human G-protein chemokine
XX CC receptor, HDGNR10
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 118; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. NO. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNIVLLNTTFOFFGLNCS 22
Db 249 APYNIVLLNTTFOFFGLNCS 270
RESULT 28
ABG92883

ID ABG92883 standard; protein; 352 AA.
 AC ABG92883;
 DT 19-NOV-2002 (first entry)
 XX Human immunoglobulin variable heavy domain #1.
 DE
 XX Immunoglobulin; variable heavy chain; variable light chain; human;
 KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
 KW lymphocytopenia.
 XX Homo sapiens.
 OS
 XX WO200264612-A2.
 PN
 XX 22-AUG-2002.
 PD
 XX 08-FEB-2002; 2002WO-US003634.
 PF
 XX 09-FEB-2001; 2001US-00779880.
 PR
 XX 09-FEB-2001; 2001WO-US004153.
 PR
 XX 12-JUN-2001; 2001US-0297257P.
 PR
 XX 08-AUG-2001; 2001US-0310458P.
 PR
 XX 12-OCT-2001; 2001US-0328447P.
 PR
 XX 21-DEC-2001; 2001US-0341725P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Roschke V, Rosen CA, Ruben SM;
 PI
 XX WPI; 2002-643455/69.
 DR
 XX N-PSDB; ABS68606.
 DR
 XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for
 PT treating, preventing, ameliorating or monitoring diseases or disorders
 PT associated with aberrant expression of HDGNR10 e.g. cancer.
 XX Example 55; Fig 4; 562pp; English.
 PS
 XX The invention describes an isolated polynucleotide encoding a first
 CC antibody at least 95-100% identical to a second antibody consisting of an
 CC amino acid sequence comprising at least one, two or three CDR regions of
 CC a variable heavy (VH) or variable light (VL) domain of the antibody
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF27/28.7D5, XF27/28.18B5,
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
 CC is useful treating, preventing, ameliorating, prognosing or monitoring
 CC cancers or other diseases or disorders e.g. immunologic deficiency
 CC syndromes such as blood protein disorders and ataxia telangiectasia,
 CC inflammation associated disorders such as endotoxin lethality, nephritis
 CC and inflammatory bowel disease, conditions associated with an increase in
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
 CC an infectious disease, an autoimmune disease such as Addison's disease,
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
 CC poxvirus infection, a Pneumocystis carni infection, Kaposi's sarcoma,
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
 CC disease or disorder associated with aberrant expression of novel human G-
 CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
 CC sequence of human immunoglobulin sequence associated with the antibodies
 CC against HDGNR10
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLINTQEPFFGLNCS 22
 DB 249 APYNIVLLINTQEPFFGLNCS 270
 RESULT 29
 ABG92880
 ID ABG92880 standard; protein; 352 AA.
 XX
 AC ABG92880;
 DT 19-NOV-2002 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
 XX
 KW Immunoglobulin; variable heavy chain; variable light chain; human;
 KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
 KW lymphocytopenia.
 XX Homo sapiens.
 OS
 XX WO200264612-A2.
 PN
 XX 22-AUG-2002.
 PD
 XX 08-FEB-2002; 2002WO-US003634.
 PF
 XX 09-FEB-2001; 2001US-00779880.
 PR
 XX 09-FEB-2001; 2001WO-US004153.
 PR
 XX 12-JUN-2001; 2001US-0297257P.
 PR
 XX 08-AUG-2001; 2001US-0310458P.
 PR
 XX 12-OCT-2001; 2001US-0328447P.
 PR
 XX 21-DEC-2001; 2001US-0341725P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Roschke V, Rosen CA, Ruben SM;
 PI
 XX WPI; 2002-643455/69.
 DR
 XX N-PSDB; ABS68606.
 DR
 XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for
 PT treating, preventing, ameliorating or monitoring diseases or disorders
 PT associated with aberrant expression of HDGNR10 e.g. cancer.
 XX Example 55; Fig 4; 562pp; English.
 PS
 XX The invention describes an isolated polynucleotide encoding a first
 CC antibody at least 95-100% identical to a second antibody consisting of an
 CC amino acid sequence comprising at least one, two or three CDR regions of
 CC a variable heavy (VH) or variable light (VL) domain of the antibody
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF27/28.7D5, XF27/28.18B5,
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
 CC is useful treating, preventing, ameliorating, prognosing or monitoring
 CC cancers or other diseases or disorders e.g. immunologic deficiency
 CC syndromes such as blood protein disorders and ataxia telangiectasia,
 CC inflammation associated disorders such as endotoxin lethality, nephritis
 CC and inflammatory bowel disease, conditions associated with an increase in
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
 CC an infectious disease, an autoimmune disease such as Addison's disease,
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
 CC poxvirus infection, a Pneumocystis carni infection, Kaposi's sarcoma,
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
 CC disease or disorder associated with aberrant expression of novel human G-
 CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
 CC sequence of human immunoglobulin sequence associated with the antibodies
 CC against HDGNR10
 XX Sequence 352 AA;
 SQ

CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
CC disease or disorder associated with aberrant expression of novel human G-
CC protein chemokine receptor (CCR5) HDGNR10. This is an amino acid sequence
CC of Human G-protein chemokine receptor (CCR5) HDGNR10 #1
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
DB 249 APYNIVLLNTFOEFFGLNCS 270
|||||

RESULT 30
AAE25808
ID AAE25808 standard; protein; 352 AA.
XX
AC AAE25808;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human G-protein chemokine receptor (CCR5), HDGNR10 #1.
XX
KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
KW inflammation; viral infection; autoimmune disease; neurodegeneration;
KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
KW hyperproliferative disease; receptor.
XX
OS Homo sapiens.
XX
PN US2002061834-A1.
XX
PD 23-MAY-2002.
XX
PF 09-FEB-2001; 2001US-00779880.
XX
PR 09-FEB-2000; 2000US-0181258P.
PR 09-MAR-2000; 2000US-0187999P.
PR 22-SEP-2000; 2000US-0234336P.
XX
PA (ROSE/) ROSEN C A.
PA (ROSC/) ROSCHKE V.
PA (LIYY/) LI Y.
PA (RUBE/) RUBEN S M.
XX
PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX
DR WPI: 2002-499674/53.
DR N-PSDB; AAD42409.
XX
PT New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,
PT useful for treatment, prevention and diagnosis of e.g. cancer, also
XX related antibodies.
PS Claim 61; Page 163-164; 186pp; English.
XX
CC The invention relates to human G-protein chemokine receptor (CCR5), CCR5
CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
CC antibodies are used for the treatment or prevention of inflammation,
CC defective or aberrant chemotaxis of immune cells or T cell antigen-
CC presenting cell interaction, viral infections (specifically human immune
CC deficiency (including its early stages), cytomegalovirus or pox viruses),
CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
CC carinii infection, Kaposi's sarcoma or any condition associated with the
CC aberrant expression of CCR5 or their ligands. They are also used for the
CC detection, diagnosis, prognosis and monitoring of cancers or other
CC hyperproliferative diseases. The present sequence is human G-protein
CC chemokine receptor (CCR5), HDGNR10 DNA
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC chemokine receptor (CCR5), HDGNR10 DNA
SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
DB 249 APYNIVLLNTFOEFFGLNCS 270
|||||

RESULT 31
AAE25811
ID AAE25811 standard; protein; 352 AA.
XX
AC AAE25811;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human G-protein chemokine receptor (CCR5), HDGNR10 #2.
XX
KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
KW inflammation; viral infection; autoimmune disease; neurodegeneration;
KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
KW hyperproliferative disease; receptor.
XX
OS Homo sapiens.
XX
PN US2002061834-A1.
XX
PD 23-MAY-2002.
XX
PF 09-FEB-2001; 2001US-00779880.
XX
PR 09-FEB-2000; 2000US-0181258P.
PR 09-MAR-2000; 2000US-0187999P.
PR 22-SEP-2000; 2000US-0234336P.
XX
PA (ROSE/) ROSEN C A.
PA (ROSC/) ROSCHKE V.
PA (LIYY/) LI Y.
PA (RUBE/) RUBEN S M.
XX
PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX
DR WPI: 2002-499674/53.
DR N-PSDB; AAD42426.
XX
PT New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,
PT useful for treatment, prevention and diagnosis of e.g. cancer, also
XX related antibodies.
PS Disclosure; Page 170; 186pp; English.
XX
CC The invention relates to human G-protein chemokine receptor (CCR5), CCR5
CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
CC antibodies are used for the treatment or prevention of inflammation,
CC defective or aberrant chemotaxis of immune cells or T cell antigen-
CC presenting cell interaction, viral infections (specifically human immune
CC deficiency (including its early stages), cytomegalovirus or pox viruses),
CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
CC carinii infection, Kaposi's sarcoma or any condition associated with the
CC aberrant expression of CCR5 or their ligands. They are also used for the
CC detection, diagnosis, prognosis and monitoring of cancers or other
CC hyperproliferative diseases. The present sequence is human G-protein
CC chemokine receptor (CCR5), HDGNR10 DNA
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQFFGLNCS 270

RESULT 32
ABB81054
ID ABB81054 standard; protein; 352 AA.
XX
AC ABB81054;
XX
XX 05-NOV-2002 (first entry)
XX
XX G-protein chemokine receptor, HDGNR10.
XX
XX 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10;
KW G-protein chemokine receptor; haematopoietic; immunosuppressant;
KW antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic;
KW antirheumatic; antiarthritic; gene therapy; human; receptor.
XX
OS Homo sapiens.
XX
XX US2002076745-A1.
XX
XX 20-JUN-2002.
XX
XX 18-NOV-1998; 98US-00195662.
XX
XX 06-JUN-1995; 95US-00466343.
XX
XX (LIYY/) LI Y.
XX (RUBE/) RUBEN S M.
XX
XX Li Y, Ruben SM;
XX
XX WPI; 2002-598724/64.
XX
XX N-PSDB; ABB86542.
XX
XX New polynucleotide encoding a human G protein chemokine receptor HDGNR10,
XX useful e.g. for treating tumors.
XX
XX Claim 7; Fig 1; 22pp; English.
XX
XX The invention relates to a novel human 7-transmembrane receptor, HDGNR10,
XX which has been identified as a G-protein chemokine receptor. The GPCR
XX HDGNR10 polypeptide can be expressed by standard recombinant methodology.
XX Compounds that activate or inhibit the receptor polypeptide, optionally
XX expressed from DNA in gene therapy vectors, are used to treat diseases
XX that require: (a) activation of the receptor (e.g. stimulation of
XX haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune
XX diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the
XX receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis
XX etc). The present sequence represents the human HDGNR10 receptor
XX polypeptide
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 118; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQFFGLNCS 270

RESULT 33
ABB08343
ID ABB08343 standard; protein; 352 AA.
XX
XX ABB08343;
XX

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XX 18-JUN-2002 (first entry)
XX
XX Human chemokine (C-C motif) receptor 5 polypeptide.
XX
XX Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;
KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;
KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;
KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;
XX chromosome 3p21.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 55 /label= Leu, Gln
XX Misc-difference 182 /label= Phe, Leu
XX Misc-difference 223 /label= Arg, Gln
XX
XX WO200177125-A2.
XX
XX 18-OCT-2001.
XX
XX 04-APR-2001; 2001WO-US010708.
XX
XX 05-APR-2000; 2000US-0194361P.
XX
XX (GENA-) GENAISANCE PHARM INC.
XX
XX Choi JY, Klieem SE, Koshiy B;
XX
XX WPI; 2002-041282/05.
XX
XX N-PSDB; ABA97318, ABA97319.
XX
XX New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful
XX to diagnose and treat diseases associated with its abnormal expression or
XX function, including human immunodeficiency virus-1 infection.
XX
XX Claim 29; Fig 3; 61pp; English.
XX
XX The present sequence is that of a polypeptide encoded by the human
XX chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see
XX ABA97318, ABA97319). The specification describes haplotyping the CCR5
XX gene of an individual by determining if the individual has one of the
XX CCR5 haplotypes or haplotype pairs fully defined in the specification.
XX The specification also describes an isolated polynucleotide comprising a
XX nucleotide sequence which is a polymorphic variant of the reference CCR5
XX gene sequence and comprises an isogene defined by a haplotype described
XX in the specification and its encoded polypeptide. The methods of the
XX invention are useful to diagnose and develop treatment for diseases
XX associated with abnormal expression or function of the gene. The CCR5
XX isogenes and the screened compounds are useful for treating human
XX immunodeficiency virus (HIV)-1 infection and the progression to acquired
XX immunodeficiency syndrome (AIDS). The invention has antiviral
XX applications. The specification describes genotyping the CCR5 gene of an
XX individual; predicting a haplotype pair for the CCR5 gene of an
XX individual; identifying an association between a trait and a haplotype or
XX haplotype pair of the CCR5 gene. The specification describes a
XX composition comprising a genotyping oligonucleotide for detecting a CCR5
XX polymorphism; a recombinant non-human organism transformed with CCR5
XX polynucleotide expressing a CCR5 protein encoded by the variant sequence;
XX an isolated antibody specific for the CCR5 polypeptide and a method for
XX screening drugs targeting the CCR5 polypeptide
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 118; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22

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DB 249 APYNIVLLNTFQEFFGLNCS 270
|||||
RESULT 34
ID ABG75540
AC ABG75540; 352 AA.
DT 16-APR-2003 (first entry)
DE Human G-protein chemokine receptor, HDGNR10, protein.
KW Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor;
KW HDGNR10; signal transduction; gene therapy; haematopoiesis;
KW wound healing; coagulation; angiogenesis; tumour; chronic infection;
KW leukaemia; T-cell mediated auto-immune disease; parasitic infection;
KW psoriasis; growth factor; allergy; atherogenesis; anaphylaxis;
KW malignancy; inflammation; histamine; IgE-mediated;
KW prostaglandin-independent fever; bone marrow failure; silicosis;
KW sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.
OS Homo sapiens.
PN US2002132269-A1.
XX 19-SEP-2002.
XX 11-FEB-2000; 2000US-00502783.
XX 06-JUN-1995; 95US-00466343.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Li Y, Ruben SM;
XX WPI; 2003-208944/20.
XX N-PSDB; ABX10635.
XX Novel human G-protein chemokine receptor polypeptide useful for
XX diagnostic purposes and for identifying modulators of the polypeptide
XX useful for treating leukemia, autoimmune diseases, psoriasis and allergic
XX reactions.
XX Claim 7; Fig 1; 22pp; English.
XX The invention discloses a G-protein chemokine receptor (sometimes
XX referred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the
XX polynucleotide encoding it. G-protein chemokine receptors are involved in
XX signal transduction pathways. The polynucleotide and polypeptide can be
XX used to identify compounds which activate or inhibit activation of the
XX protein and these compounds are useful for treating a patient having need
XX to activate or inhibit a G-protein chemokine receptor. The compound is
XX administered by providing to the patient DNA encoding the agonist or
XX antagonist and expressing them in vivo (gene therapy). The
XX polynucleotides and polypeptide are also useful for diagnosing a
XX disease or susceptibility to a disease related to an under-expression of
XX the protein, for chromosome identification or as immunogens for producing
XX antibodies. Agonists are useful in stimulating haematopoiesis, wound
XX healing, coagulation, angiogenesis, to treat solid tumours, chronic
XX infections, leukaemia, T-cell mediated auto-immune diseases, parasitic
XX infections, psoriasis and to stimulate growth factor activity.
XX Antagonists are useful in the prevention and treatment of allergy,
XX atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation,
XX histamine and IgE-mediated allergic reactions, prostaglandin-independent
XX fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis,
XX shock and hyper-eosinophilic syndrome. The sequence presented is the
XX human HDGNR10 protein
XX Sequence 352 AA;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNIVLLNTFQEFFGLNCS 22
DB 249 APYNIVLLNTFQEFFGLNCS 270
|||||
RESULT 35
ABR58602
ID ABR58602 standard; protein; 352 AA.
XX
AC ABR58602;
XX
DT 09-JUL-2003 (first entry)
DE Human cancer related protein SEQ ID NO:259.
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
PN WO2003025138-A2.
XX
PD 27-MAR-2003.
XX 17-SEP-2002; 2002WO-US029560.
XX 17-SEP-2001; 2001US-0323469P.
XX 20-SEP-2001; 2001US-0323887P.
XX 13-NOV-2001; 2001US-0350666P.
XX 08-FEB-2002; 2002US-0355145P.
XX 08-FEB-2002; 2002US-0355257P.
XX 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
XX Zlotnik A;
XX WPI; 2003-354600/33.
XX N-PSDB; ACC72740.
XX New genes that are up-regulated or down-regulated in cancers, useful as
XX markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX therapeutic targets for screening drugs for treating these diseases.
XX Claim 12; Page 745; 767pp; English.
XX The present invention describes an isolated nucleic acid molecule, which
XX comprises the sequence of any of the genes that are up-regulated or down-
XX regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX related gene nucleotide sequences which encode the proteins given in
XX ABR58521 to ABR58709. Also described: (1) determining the presence or
XX absence of a pathological cell in a patient; (2) an expression vector
XX comprising a nucleic acid molecule described above; (3) a host cell
XX comprising the vector; (4) an isolated polypeptide, which is encoded by
XX the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX of (4); (6) specifically targeting a compound to a pathological cell in a
XX patient by administering to the patient the antibody above; and (7) a
XX drug screening assay. The nucleic acid is useful as diagnostic markers or
XX therapeutic targets. In particular, the nucleic acid is useful for
XX diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
XX atherosclerosis and endometriosis. The nucleic acid is also useful in
XX drug screening, particularly for identifying agents for treating these
XX pathologies
XX Sequence 352 AA;

```

Query Match      100.0%; Score 118; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APYNIIVLLNTFOEFFGLNCS 22
    |||||
Db 249 APYNIIVLLNTFOEFFGLNCS 270

RESULT 36
AAO29514
ID AAO29514 standard; protein; 352 AA.
XX
AC AAO29514;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human C-C chemokine receptor type 5 (333) protein.
XX
KW Human; urological disorder; stress urinary incontinence; prostate cancer;
KW benign prostatic hyperplasia; overactive bladder; oversensitive bladder;
KW overflow urinary incontinence; gene therapy; nephrotropic; prostatitis;
KW kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.
XX
OS Homo sapiens.
XX
FN WO2003039475-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US035824.
XX
PR 07-NOV-2001; 2001US-0344552P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Silos-Santiago I;
XX
WPI; 2003-449396/42.
DR N-PSDB; AAL59912.
XX
PT Identifying a compound, capable of treating urological disorder e.g.;
PT benign prostatic hyperplasia, by assaying the ability of the compound to
PT modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or
PT polypeptide activity.
XX
PS Disclosure; Page 81; 87pp; English.
XX
CC The invention relates to a method for treating an urological disorder
CC which comprises assaying the ability of the compound to modulate 313,
CC 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide
CC activity. The method is useful for identifying a compound for treating an
CC urological disorder comprising urinary incontinence e.g., overactive/
CC oversensitive bladder, overflow urinary incontinence, stress urinary
CC incontinence caused by dysfunction of the bladder, urethra or central/
CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,
CC prostate cancer or kidney disorders. It is also used in gene therapy. The
CC present sequence is human C-C chemokine receptor type 5 (CCR5; 333)
CC protein. This sequence is used to illustrate the method of the invention
XX
SQ Sequence 352 AA;

Query Match      100.0%; Score 118; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APYNIIVLLNTFOEFFGLNCS 22
    |||||
Db 249 APYNIIVLLNTFOEFFGLNCS 270

RESULT 37
ABU61654
ID ABU61654 standard; protein; 352 AA.
XX
AC ABU61654;
XX
DT 08-AUG-2003 (first entry)
XX
DE Human G-protein chemokine receptor (HDGNR10) polypeptide.
XX
KW Human; G-protein chemokine receptor; receptor; HDGNR10;
KW 7-transmembrane receptor.
XX
OS Homo sapiens.
XX
FN US2003023044-A1.
XX
PD 30-JAN-2003.
XX
PF 03-SEP-2002; 2002US-00232686.
XX
PR 06-JUN-1995; 95US-00466343.
PR 18-NOV-1998; 98US-00195662.
PR 25-JUN-1999; 99US-00339912.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Li Y, Ruben SM;
XX
WPI; 2003-456307/43.
DR N-PSDB; ACA61721.
XX
PT Producing an antibody, involves immunizing an animal with a polypeptide
PT or with a polypeptide encoded by the human G-protein chemokine receptor
PT clone in ATCC 97183, and recovering the antibody.
XX
PS Claim 1; Fig 1; 23pp; English.
XX
CC The invention relates to a method of producing an antibody, involving
CC immunising an animal with a human G-protein chemokine receptor (HDGNR10)
CC polypeptide (also referred to as a human 7-transmembrane receptor) and
CC recovering an antibody which binds the polypeptide. The method is useful
CC for producing an antibody which binds specifically to the human G-protein
CC chemokine receptor polypeptide. This sequence represents the HDGNR10
CC polypeptide of the invention
XX
SQ Sequence 352 AA;

Query Match      100.0%; Score 118; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APYNIIVLLNTFOEFFGLNCS 22
    |||||
Db 249 APYNIIVLLNTFOEFFGLNCS 270

RESULT 38
ABP97728
ID ABP97728 standard; protein; 352 AA.
XX
AC ABP97728;
XX
DT 28-MAY-2003 (first entry)
XX
DE Amino acid sequence of human chemokine receptor CCR5.
XX
KW Human; chemokine receptor; CCR5; viral infection; surface protein;
KW respiratory virus infection; respiratory syncytial virus infection;
KW RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.
XX
OS Homo sapiens.
XX
FN WO2003014153-A2.
XX

```


PD 20-FEB-2003.
XX
PF 12-AUG-2002; 2002WO-CA001248.
XX
PR 10-AUG-2001; 2001US-0311088P.
XX
PA (TOPI-) TOPIGEN PHARM INC.
XX
PI Renzi P, Zemzoumi K;
XX
PR WPI; 2003-256541/25.
XX
DR N-PSDB; ABZ68881.
XX
XX
PT Modulating viral infection of a cell, for treating or preventing
PT respiratory virus infections, bronchitis, pneumonia or asthma, by
PT modulating a binding interaction between a cell chemokine-receptor and a
PT surface protein of the virus.
XX
PS Disclosure; Page 96-98; 120pp; English.
XX
CC The present sequence represents human chemokine receptor CCR5. The
CC specification describes a method for modulating viral infection of a
CC cell. The method comprises modulating a binding interaction between a
CC cell chemokine-receptor and a surface protein of the virus. The proviso
CC is that the cell chemokine-receptor is not CX3CR1 and that the virus is
CC not HIV. The method is useful for treating or preventing respiratory
CC virus infection in vertebrates, more particularly respiratory syncytial
CC virus (RSV) infections, and related diseases, e.g. bronchiolitis,
CC bronchitis, pneumonia or asthma
XX
SQ Sequence 352 AA;
Query Match 100.0%; Score 118; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270
RESULT 39
ID ABP81933 standard; protein; 352 AA.
XX
AC ABP81933;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human C-C chemokine receptor 5 protein SEQ ID NO:352.
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regenerative-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
XX Homo sapiens.
XX
XX WO200261087-A2.
XX
XX 08-AUG-2002.
XX
XX 19-DEC-2001; 2001WO-US050107.
XX
XX 19-DEC-2000; 2000US-0257144P.
XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burner GC, Roush CL, Brown JP;
XX
XX WPI; 2003-045718/04.
DR N-PSDB; ABZ42781.
XX
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
XX Sequence 352 AA;
Query Match 100.0%; Score 118; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270
RESULT 40
ID ADC03341 standard; protein; 352 AA.
XX
AC ADC03341;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human chemokine receptor 88-C.
XX
XX receptor; human; anti-HIV; virucide; HIV; SIV; 88-C; 88-2B;
KW chemokine receptor; envelope protein; atherosclerosis;
KW rheumatoid arthritis; tumour growth suppression; asthma; viral infection;
KW AIDS; inflammatory condition.
XX
XX Homo sapiens.
XX
XX US2002150888-A1.
XX
XX 17-OCT-2002.
XX
XX 26-MAR-2002; 2002US-00106623.
XX

XX 20-DEC-1995; 95US-00575967.
 PR 07-JUN-1996; 96US-00661393.
 PR 20-DEC-1996; 96US-00771276.
 XX
 PA (GRAY/) GRAY P W.
 PA (SCHW/) SCHWEICKART V L.
 PA (RAFO/) RAFOU C J.
 XX
 PI Gray PW, Schweickart VL, Raport CJ;
 XX
 XX WPI; 2003-182491/18.
 DR N-PSDB; ADC03340.
 XX
 XX Screening for a modulator of HIV and SIV infection utilizing
 PT polynucleotides that encode the 88C or 88-2B chemokine receptors, useful
 PT for diagnosing and treating disorders such as atherosclerosis, arthritis,
 PT AIDS and asthma.
 XX
 PS Claim 2; Page 17-18; 29pp; English.
 XX
 CC The invention relates to screening for a modulator of human
 CC immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV)
 CC infection, comprising contacting a first composition having an human
 CC (ADC03341) or macaque (ADC03359) 88C chemokine receptor polypeptide with
 CC a second composition having an HIV or SIV envelope protein in the
 CC presence or absence of a compound. Also included are screening for a
 CC modulator of HIV infection, detecting HIV infection of cells (comprising
 CC contacting a cell that has been recombinantly modified to express at
 CC least one of human chemokine receptors 88C and 88-2B with HIV, and
 CC detecting HIV infection in the cell) and inhibiting HIV infection of
 CC cells (comprising contacting cells with an antibody to at least one of
 CC human chemokine receptors 88C and 88-2B with HIV, and detecting HIV
 CC infection of the cell after the contacting step). The methods and
 CC compositions of the present invention are useful for the diagnosis and
 CC treatment of disorders associated with the aberrant expression or
 CC activity of 88C or 88-2B chemokine receptors, such as atherosclerosis,
 CC rheumatoid arthritis, tumour growth suppression, asthma, viral infection,
 CC AIDS and other inflammatory conditions. The genes for human 88-C and 88-
 CC 2B are located on chromosome 3p21. The present sequence represents human
 CC chemokine receptor 88-C.
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 7; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
 Db 249 APYNIVLLNTFOEFFGLNCS 270

Search completed: September 28, 2004, 09:03:38
 Job time : 52.525 secs

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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:00:23 ; Search time 19.8 Seconds
(without alignments)
57.362 Million cell updates/sec

Title: US-10-084-813-14
Perfect score: 118
Sequence: 1 APYNVLLNTQEFFGLNCS 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	352	3	US-08-466-343D-2
2	118	100.0	352	3	US-09-087-232A-13
3	118	100.0	352	3	US-08-861-105-14
4	118	100.0	352	3	US-08-575-867A-2
5	118	100.0	352	3	US-09-045-583-52
6	118	100.0	352	4	US-09-517-605-5
7	118	100.0	352	4	US-09-534-185-52
8	118	100.0	352	4	US-08-833-752-5
9	118	100.0	352	4	US-09-502-783A-2
10	118	100.0	352	4	US-08-796-202-1
11	108	91.5	354	4	US-08-724-884A-2
12	103	87.3	329	4	US-09-502-783A-9
13	103	87.3	344	3	US-08-466-343D-9
14	103	87.3	347	1	US-08-461-244-3
15	103	87.3	360	1	US-08-450-393A-4
16	103	87.3	360	3	US-08-446-669-4
17	103	87.3	360	3	US-09-045-583-50
18	103	87.3	360	4	US-09-534-185-50
19	103	87.3	360	4	US-09-534-185-51
20	103	87.3	360	4	US-08-833-752-7
21	103	87.3	360	4	US-09-131-827A-2
22	103	87.3	360	4	US-09-131-827A-20
23	103	87.3	360	5	PCT-US95-00476-4
24	103	87.3	374	1	US-08-450-393A-2
25	103	87.3	374	3	US-08-446-669-2
26	103	87.3	374	3	PCT-US95-00476-2
27	103	87.3	374	5	PCT-US95-00476-2

28	70	59.3	344	3	US-08-681-192-2	Sequence 2, Appli
29	61	51.7	25	3	US-09-087-232A-22	Sequence 22, Appli
30	56	47.5	355	1	US-08-012-988A-2	Sequence 2, Appli
31	56	47.5	355	1	US-08-450-393A-5	Sequence 5, Appli
32	56	47.5	355	3	US-08-446-669-5	Sequence 5, Appli
33	56	47.5	355	4	US-09-239-938-1	Sequence 1, Appli
34	56	47.5	355	4	US-09-886-319A-14	Sequence 14, Appli
35	56	47.5	355	5	PCT-US95-00476-5	Sequence 5, Appli
36	55	46.6	355	4	US-08-833-752-8	Sequence 8, Appli
37	54	45.8	355	4	US-08-833-752-9	Sequence 9, Appli
38	53	44.9	170	3	US-08-875-573-6	Sequence 6, Appli
39	53	44.9	360	3	US-08-875-573-20	Sequence 20, Appli
40	53	44.9	360	3	US-09-232-878-2	Sequence 2, Appli
41	53	44.9	360	3	US-09-045-583-55	Sequence 55, Appli
42	53	44.9	360	4	US-09-534-185-55	Sequence 55, Appli
43	53	44.9	360	4	US-08-939-107-34	Sequence 34, Appli
44	52	44.1	105	2	US-08-103-170-12	Sequence 12, Appli
45	52	44.1	317	1	US-08-118-270-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-466-343D-2

Query Match 100.0%; Score 118; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTQEFFGLNCS 22
|||
Db 249 APYNVLLNTQEFFGLNCS 270
|||

RESULT 2

```

US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087.232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-13
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Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 3
US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 NI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-861-105-14
Query Match 100.0%; Score 118; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 4
US-08-575-967A-2
; Sequence 2, Application US/08575967A
; Patent No. 6285184
; GENERAL INFORMATION:
; APPLICANT: Gray et al.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,967A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6285184and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32918
; TELECOMMUNICATION INFORMATION:

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TELEPHONE:	206-485-1900				
TELEFAX:	206-485-1662				
INFORMATION FOR SEQ ID NO:	2;				
SEQUENCE CHARACTERISTICS:					
LENGTH:	352 amino acids				
TYPE:	amino acid				
TOPOLOGY:	linear				
MOLECULE TYPE:	protein				
FEATURE:					
NAME/KEY:	misc feature				
OTHER INFORMATION:	/= "89C amino acid sequence"				
US-08-575-967A-2					
Query Match	100.0%; Score 118; DB 3; Length 352;				
Best Local Similarity	100.0%; Pred. No. 4.1e-12;				
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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RESULT 5					
US-09-045-583-52					
Sequence 52, Application US/09045583					
Patent No. 6287805					
GENERAL INFORMATION:					
APPLICANT: Graham, Gerard J. et al.					
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled					
NUMBER OF SEQUENCES: 56					
CORRESPONDENCE ADDRESS:					
ADDRESSEE: LAHIVE & COCKFIELD, LLP					
STREET: 48 State Street					
CITY: Boston					
STATE: Massachusetts					
COUNTRY: USA					
ZIP: 02109					
COMPUTER READABLE FORM:					
MEDIUM TYPE: Floppy disk					
COMPUTER: IBM PC compatible					
OPERATING SYSTEM: PC-DOS/MS-DOS					
SOFTWARE: Patent In Release #1.0, Version #1.25					
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APPLICATION NUMBER: US/09/045,583					
FILING DATE: 20-MAR-98					
CLASSIFICATION: 435					
PRIOR APPLICATION DATA:					
APPLICATION NUMBER:					
FILING DATE:					
ATTORNEY/AGENT INFORMATION:					
NAME: Mandragouras, Amy E.					
REGISTRATION NUMBER: 36,207					
REFERENCE/DOCKET NUMBER: MNI-044					
TELECOMMUNICATION INFORMATION:					
TELEPHONE: (617)227-7400					
TELEFAX: (617)742-4214					
INFORMATION FOR SEQ ID NO: 52:					
SEQUENCE CHARACTERISTICS:					
LENGTH: 352 amino acids					
TYPE: amino acid					
TOPOLOGY: linear					
MOLECULE TYPE: peptide					
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US-09-045-583-52					
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QY	1 APYNIVLLNTQEFFGLNCS 22				
Db	249 APYNIVLLNTQEFFGLNCS 270				
RESULT 6					
US-09-517-605-5					
Sequence 5, Application US/09517605					
Patent No. 6391567					
GENERAL INFORMATION:					
APPLICANT: Littman, Dan R.					
APPLICANT: Kwon, Douglas S.					
APPLICANT: van Kooyk, Yvette					
APPLICANT: Geijtenbeek, Ineo					
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO					
FILE REFERENCE: 1049-1-017					
CURRENT APPLICATION NUMBER: US/09/517,605					
CURRENT FILING DATE: 2000-03-02					
NUMBER OF SEQ ID NOS: 17					
SOFTWARE: Patent In Ver. 2.0					
SEQ ID NO 5					
LENGTH: 352					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-09-517-605-5					
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Best Local Similarity	100.0%; Pred. No. 4.1e-12;				
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QY	1 APYNIVLLNTQEFFGLNCS 22				
Db	249 APYNIVLLNTQEFFGLNCS 270				
RESULT 7					
US-09-534-185-52					
Sequence 52, Application US/09534185					
Patent No. 6403767					
GENERAL INFORMATION:					
APPLICANT: Graham, Gerard J. et al.					
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled					
Heptahelical Receptor Superfamily and Uses					

```
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

Query Match      100.0%; Score 118; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQFFGLNCS 270

RESULT 8
US-08-833-752-5
; Sequence 5, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: FARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CG-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-752-5

Query Match      100.0%; Score 118; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQFFGLNCS 270

RESULT 9
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CRS
; TITLE OF INVENTION: HDGR10
; FILE REFERENCE: 1488.1150006
```

```
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match      100.0%; Score 118; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQFFGLNCS 270

RESULT 10
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match      100.0%; Score 118; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQFFGLNCS 270

RESULT 11
US-08-724-984A-2
; Sequence 2, Application US/08724984A
; Patent No. 6388055
; GENERAL INFORMATION:
; APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
; TITLE OF INVENTION: NO. 6388055el Mouse Genomic Clone of the CC-
; TITLE OF INVENTION: CCR5 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,984A
; FILING DATE: October 3, 1996
```

```
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-724-984A-2

Query Match 91.5%; Score 108; DB 4; Length 354;
Best Local Similarity 95.2%; Pred. No. 2.1e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PYNIVILLNTFQEPFGLNCS 22
Db 252 PYNIVLLTTTQEPFGLNCS 272

RESULT 12
US-09-502-783A-9
; Sequence 9, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-502-783A-9

Query Match 87.3%; Score 103; DB 4; Length 329;
Best Local Similarity 90.0%; Pred. No. 1.4e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PYNIVLLNTFQEPFGLNCS 21
Db 226 PYNIVLLNTFQEPFGLSNC 245

RESULT 13
US-08-466-343D-9
; Sequence 9, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
```

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; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-466-343D-9

Query Match 87.3%; Score 103; DB 3; Length 344;
Best Local Similarity 90.0%; Pred. No. 1.4e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PYNIVLLNTFQEPFGLNCS 21
Db 241 PYNIVLLNTFQEPFGLSNC 260

RESULT 14
US-08-461-244-3
; Sequence 3, Application US/08461244
; Patent No. 5776729
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESS: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,244
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
```

```
;
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-244-3

Query Match      87.3%; Score 103; DB 1; Length 347;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 PYNIVLLNTQEFPGFLNLC 21
Db      245 PYNIVLLNTQEFPGFLSNC 264

RESULT 15
US-08-450-393A-4
; Sequence 4, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserz, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-4

Query Match      87.3%; Score 103; DB 1; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 PYNIVLLNTQEFPGFLNLC 21
Db      258 PYNIVLLNTQEFPGFLSNC 277

RESULT 16
US-08-446-669-4
; Sequence 4, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-4

Query Match      87.3%; Score 103; DB 3; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 PYNIVLLNTQEFPGFLNLC 21
Db      258 PYNIVLLNTQEFPGFLSNC 277

RESULT 17
US-09-045-583-50
; Sequence 50, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
```



```

; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-045-583-50

Query Match      87.3%; Score 103; DB 3; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PYNIVLLNTQFFFGSLNC 21
Db 258 PYNIVLLNTQFFFGSLNC 277

RESULT 18
; US-09-045-583-51
; Sequence 51, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-045-583-51

Query Match      87.3%; Score 103; DB 3; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PYNIVLLNTQFFFGSLNC 21
Db 258 PYNIVLLNTQFFFGSLNC 277

```

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RESULT 19
; US-09-534-185-50
; Sequence 50, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; THEREFOR
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
; US-09-534-185-50

Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PYNIVLLNTQFFFGSLNC 21
Db 258 PYNIVLLNTQFFFGSLNC 277

RESULT 20
; US-09-534-185-51
; Sequence 51, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; THEREFOR
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

```

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-534-185-51

Query Match 87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFPGLSNC 21
||||:|||||:|||||:
Db 258 PYNIVLLNTQEFPGLSNC 277

RESULT 21
US-08-833-752-7
Sequence 7, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 360 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6448375e
US-08-833-752-7

Query Match 87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFPGLSNC 21
||||:|||||:|||||:
Db 258 PYNIVLLNTQEFPGLSNC 277

RESULT 22
US-09-131-827A-2
Sequence 2, Application US/09131827A
Patent No. 6600030
GENERAL INFORMATION:
APPLICANT: Dean, Michael
APPLICANT: O'Brien, Stephen J.
APPLICANT: Smith, Michael
APPLICANT: Carrington, Mary
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
FILE REFERENCE: 14014.0333
CURRENT APPLICATION NUMBER: US/09/131,827A
CURRENT FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/055,659
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-131-827A-2

Query Match 87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFPGLSNC 21
||||:|||||:|||||:
Db 258 PYNIVLLNTQEFPGLSNC 277

RESULT 23
US-09-131-827A-20
Sequence 20, Application US/09131827A
Patent No. 6600030
GENERAL INFORMATION:
APPLICANT: Dean, Michael
APPLICANT: O'Brien, Stephen J.
APPLICANT: Smith, Michael
APPLICANT: Carrington, Mary
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
FILE REFERENCE: 14014.0333
CURRENT APPLICATION NUMBER: US/09/131,827A
CURRENT FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/055,659
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 20
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-131-827A-20

```

Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PYNIVLLNTFQEPFGLNCC 21
Db      258 PYNIVLLNTFQEPFGLSNC 277

RESULT 24
PCT-US95-00476-4
; Sequence 4, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-00476-4

Query Match      87.3%; Score 103; DB 5; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PYNIVLLNTFQEPFGLNCC 21
Db      258 PYNIVLLNTFQEPFGLSNC 277

RESULT 25
US-08-450-393A-2
; Sequence 2, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California

Query Match      87.3%; Score 103; DB 1; Length 374;
Best Local Similarity 90.0%; Pred. No. 1.6e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PYNIVLLNTFQEPFGLNCC 21
Db      258 PYNIVLLNTFQEPFGLSNC 277

RESULT 26
US-08-446-669-2
; Sequence 2, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CcoleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-2

Query Match      87.3%; Score 103; DB 1; Length 374;
Best Local Similarity 90.0%; Pred. No. 1.6e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PYNIVLLNTFQEPFGLNCC 21
Db      258 PYNIVLLNTFQEPFGLSNC 277

RESULT 27
US-08-446-669-2
; Sequence 2, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CcoleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-2

```

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-2
Query Match 87.3%; Score 103; DB 3; Length 374;
Best Local Similarity 90.0%; Pred. No. 1.6e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 2 PYNIVLLNTQEPFFGLNLC 21
Db 258 PYNIVLLNTQEPFFGLSNC 277

```

```

RESULT 27
PCT-US95-00476-2
; Sequence 2, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berlinet, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-00476-2

```

```

Query Match 87.3%; Score 103; DB 5; Length 374;
Best Local Similarity 90.0%; Pred. No. 1.6e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 2 PYNIVLLNTQEPFFGLNLC 21
Db 258 PYNIVLLNTQEPFFGLSNC 277

```

```

RESULT 28
US-08-681-192-2
; Sequence 2, Application US/08681192
; Patent No. 6287801
; GENERAL INFORMATION:
; APPLICANT: BERGMA, DEREK
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: SARAU, HENRY
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNFD578

```

```

; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,192
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: ATG50014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5031
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-681-192-2

```

```

Query Match 59.3%; Score 70; DB 3; Length 344;
Best Local Similarity 57.1%; Pred. No. 0.00063;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

```

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QY 1 APYIVLLNTQEPFFGLNLC 21
Db 252 APYNTAFLLSTKEHFLSDC 272

```

```

RESULT 29
US-09-087-232A-22
; Sequence 22, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A

```

FILING DATE: 28 MAY 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: AP 31115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2628
TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-087-232A-22

Query Match 51.7%; Score 61; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTF 12
Db 14 APYNVLLNTF 25

RESULT 30
US-08-012-988A-2
Sequence 2, Application US/08012988A
Patent No. 5652133
GENERAL INFORMATION:
APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Cloning and Expression of Human
TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
TITLE OF INVENTION: alpha)/RANTES Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,988A
FILING DATE: 19930128
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-012-988A-2

Query Match 47.5%; Score 56; DB 1; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNVLLNTFOEFFGLNNC 21
Db 254 PYNLTILISVFQDFLFTHEC 273

RESULT 31
US-08-450-393A-5
Sequence 5, Application US/08450393A
Patent No. 5707815
GENERAL INFORMATION:
APPLICANT: Charo, Israel
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-450-393A-5

Query Match 47.5%; Score 56; DB 1; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNVLLNTFOEFFGLNNC 21
Db 254 PYNLTILISVFQDFLFTHEC 273

RESULT 32
US-08-446-669-5
Sequence 5, Application US/08446669
Patent No. 6132987
GENERAL INFORMATION:
APPLICANT: Charo, Israel
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto

```
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-446-669-5
```

```
Query Match 47.5%; Score 56; DB 3; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 2 PYNIVLLNTFOEFFGLNLC 21
Db 254 PYNLTILISVQDFLFTHEC 273
```

```
RESULT 33
US-09-239-938-1
; Sequence 1, Application US/09239938
; Patent No. 6329510
; GENERAL INFORMATION:
; APPLICANT: Qln, Shixin
; APPLICANT: Newman, Walter
; APPLICANT: Kassam, Nasim
; APPLICANT: Leukosite, Inc.
; TITLE OF INVENTION: ANTI-CCR1 ANTIBODIES AND METHODS OF USE
; FILE REFERENCE: LKS97-13
; CURRENT APPLICATION NUMBER: US/09/239,938
; CURRENT FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-239-938-1
```

```
Query Match 47.5%; Score 56; DB 4; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 2 PYNIVLLNTFOEFFGLNLC 21
Db 254 PYNLTILISVQDFLFTHEC 273
```

```
RESULT 34
US-09-886-319A-14
; Sequence 14, Application US/09886319A
```

```
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jörn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886,319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-319A-14
```

```
Query Match 47.5%; Score 56; DB 4; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 2 PYNIVLLNTFOEFFGLNLC 21
Db 254 PYNLTILISVQDFLFTHEC 273
```

```
RESULT 35
PCT-US95-00476-5
; Sequence 5, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```

```
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-00476-5

Query Match 47.5%; Score 56; DB 5; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEPFGLNNC 21
Db 254 PYNLTILISVQDFLFTHC 273

RESULT 36
US-08-833-752-8
; Sequence 8, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: FARMETIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/08/833.752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6448375e
US-08-833-752-9

Query Match 45.8%; Score 54; DB 4; Length 355;
Best Local Similarity 35.0%; Pred. No. 0.35;
Matches 7; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEPFGLNNC 21
Db 254 PYNLTILISVQDFLFTHC 273

RESULT 38
US-08-875-573-6
; Sequence 6, Application US/08875573
; Patent No. 6150132
; GENERAL INFORMATION:
; APPLICANT: Wells, Timothy N.C.
; APPLICANT: Power, Christine A.
; TITLE OF INVENTION: A CHEMOKINE RECEPTOR ABLE TO BIND TO
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 No. 6150132th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/875.573
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CB96/00143
; FILING DATE: 24-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9501683.8
; FILING DATE: 27-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
```

NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-172
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-573-6

Query Match 44.9%; Score 53; DB 3; Length 170;
Best Local Similarity 52.4%; Pred. No. 0.22; Mismatches 2; Indels 8; Gaps 0;
Matches 11; Conservative 2; Mismatches 2; Indels 8; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNCS 22
Db 122 PYNIVLFLETLVEVLQDCT 142

RESULT 39
US-08-875-573-20
Sequence 20, Application US/08875573
Patent No. 6150132
GENERAL INFORMATION:
APPLICANT: Wells, Timothy N.C.
APPLICANT: Power, Christine A.
TITLE OF INVENTION: A CHEMOKINE RECEPTOR ABLE TO BIND TO
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6150132th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875.573
FILING DATE: 31-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/00143
FILING DATE: 24-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9501683.8
FILING DATE: 27-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-172
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-573-20

Query Match 44.9%; Score 53; DB 3; Length 360;
Best Local Similarity 52.4%; Pred. No. 0.53;
Matches 11; Conservative 2; Mismatches 2; Indels 8; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNCS 22
Db 257 PYNIVLFLETLVEVLQDCT 277

RESULT 40
US-09-232-878-2
Sequence 2, Application US/09232878
Patent No. 6245332
GENERAL INFORMATION:
APPLICANT: Butcher, Eugene
APPLICANT: Campbell, James
APPLICANT: Rottman, James
APPLICANT: Wu, Lijian
TITLE OF INVENTION: Modulation of Systemic Memory T cell Trafficking
FILE REFERENCE: SUN-110PRV
CURRENT APPLICATION NUMBER: US/09/232,878
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 360
TYPE: PRT
ORGANISM: H. sapiens
US-09-232-878-2

Query Match 44.9%; Score 53; DB 3; Length 360;
Best Local Similarity 52.4%; Pred. No. 0.53;
Matches 11; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNCS 22
Db 257 PYNIVLFLETLVEVLQDCT 277

Search completed: September 28, 2004, 09:21:33
Job time : 20.8 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:06:23 ; Search time 72.875 Seconds
(without alignments)
97.074 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APYNIVLLNTFQFFGLNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	22	14	US-10-084-813-14
2	118	100.0	332	14	US-10-095-876A-2
3	118	100.0	352	9	US-09-725-285-2
4	118	100.0	352	9	US-09-759-841-2
5	118	100.0	352	9	US-09-779-879A-2
6	118	100.0	352	9	US-09-779-879A-22
7	118	100.0	352	9	US-09-779-880A-2
8	118	100.0	352	9	US-09-779-880A-22
9	118	100.0	352	9	US-09-813-653-15
10	118	100.0	352	9	US-09-813-653-17
11	118	100.0	352	9	US-09-796-202-1
12	118	100.0	352	9	US-09-195-662A-2
13	118	100.0	352	9	US-09-339-912A-2
14	118	100.0	352	9	US-09-938-719-5
15	118	100.0	352	9	US-09-939-226-5

16	118	100.0	352	9	US-09-938-703-5	Sequence 5, Appli
17	118	100.0	352	9	US-09-502-783A-2	Sequence 2, Appli
18	118	100.0	352	10	US-09-734-221A-14	Sequence 14, Appl
19	118	100.0	352	11	US-09-826-509-477	Sequence 477, App
20	118	100.0	352	12	US-10-151-274-5	Sequence 5, Appli
21	118	100.0	352	13	US-10-106-623-2	Sequence 2, Appli
22	118	100.0	352	13	US-10-106-623-20	Sequence 20, Appl
23	118	100.0	352	14	US-10-232-886-2	Sequence 2, Appli
24	118	100.0	352	14	US-10-086-814-1	Sequence 1, Appli
25	118	100.0	352	14	US-10-067-800-2	Sequence 2, Appli
26	118	100.0	352	14	US-10-067-800-22	Sequence 22, Appl
27	118	100.0	352	14	US-10-230-058A-6	Sequence 6, Appli
28	118	100.0	352	14	US-10-225-567A-352	Sequence 352, App
29	118	100.0	352	14	US-10-323-314-1	Sequence 1, Appli
30	118	100.0	352	14	US-10-072-301-1	Sequence 1, Appli
31	118	100.0	352	14	US-10-164-849-52	Sequence 52, Appl
32	118	100.0	352	14	US-10-071-866-1	Sequence 1, Appli
33	118	100.0	352	14	US-10-135-839-2	Sequence 2, Appli
34	118	100.0	352	14	US-10-135-839-22	Sequence 22, Appl
35	118	100.0	352	14	US-10-239-423-67	Sequence 67, Appl
36	118	100.0	352	14	US-10-439-845-2	Sequence 2, Appli
37	118	100.0	352	14	US-10-439-845-4	Sequence 4, Appli
38	118	100.0	352	15	US-10-360-828-1	Sequence 1, Appli
39	118	100.0	352	16	US-10-661-798-5	Sequence 5, Appli
40	118	100.0	352	16	US-10-791-905-2	Sequence 2, Appli
41	118	100.0	352	16	US-10-612-791-5	Sequence 5, Appli
42	103	87.3	329	9	US-09-725-285-9	Sequence 9, Appli
43	103	87.3	329	9	US-09-195-662A-9	Sequence 9, Appli
44	103	87.3	329	9	US-09-339-912A-9	Sequence 9, Appli
45	103	87.3	329	9	US-09-502-783A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-10-084-813-14
; Sequence 14, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 14
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-14

Query Match 100.0%; Score 118; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
DB 1 APYNIVLLNTFQFFGLNCS 22

RESULT 2

US-10-095-876A-2
; Sequence 2, Application US/10095876A
; Publication No. US20030148294A1

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: GENERAL INFORMATION:
: APPLICANT: Au-Young, Janice; Bandman, Olga
: APPLICANT: Coleman, Roger; Wilde, Craig G.
: TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
: FILE REFERENCE: PF-0060-1 CON
: CURRENT APPLICATION NUMBER: US/10/095,876A
: PRIORITY FILING DATE: 2002-03-11
: PRIOR APPLICATION NUMBER: US 08/638,081
: PRIORITY FILING DATE: 1996-04-26
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PERL Program
: SEQ ID NO 2
: LENGTH: 332
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
: US-10-095-876A-2

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Query Match      100.0%; Score 118; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. NO. 1.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYXIVLLNTFQFFGLNNCS 22
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DB 229 APYXIVLLNTFQFFGLNNCS 250
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RESULT 3
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

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Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. NO. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  APYNIVLLINTFQFFPFLNNC 22
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Db      249  APYNIVLLINTFQFFPFLNNC 270

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RESULT 4
US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan

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, APPLICANT: Perros, Manoussos
, TITLE OF INVENTION: Array Method
, FILE REFERENCE: FC1034GAPME
, CURRENT APPLICATION NUMBER: US/09/759,841
, CURRENT FILING DATE: 2001-01-12
, PRIOR APPLICATION NUMBER: GB 0000561.9
, PRIOR FILING DATE: 2000-01-12
, PRIOR APPLICATION NUMBER: GB 0000563.5
, PRIOR FILING DATE: 2000-01-12
, PRIOR APPLICATION NUMBER: GB 0000569.3
, PRIOR FILING DATE: 2000-01-12
, NUMBER OF SEQ ID NOS: 6
, SOFTWARE: PatentIn ver. 2.1
, SEQ ID NO 2
, LENGTH: 352
, TYPE: PRT
, ORGANISM: Homo sapiens
, US-09-759-841-2

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Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      249  APYNIIVLLNLTFOEFFGLNNCS  270

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RESULT 5
US-09-779-879A-2
; Sequence 2, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-2

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Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APYIVILLNTFOEFFGLNACS 22
Db      249 APYIVILLNTFOEFFGLNACS 270

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RESULT 6
US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.

; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-22

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 7
US-09-779-880A-2
; Sequence 2, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGMR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-2

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 8
US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGMR10

; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-22

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 9
US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-15

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 10
US-09-813-653-17
; Sequence 17, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005

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; CURRENT APPLICATION NUMBER: US/09/813.653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-17

Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 11
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 12
US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGMR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.115002
; CURRENT APPLICATION NUMBER: US/09/195.662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
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; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 13
US-09-339-912A-2
; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; FILE REFERENCE: 1488.115003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2

Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 14
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
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; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5
Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 15
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5
Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 16
US-09-938-703-5
; Sequence 5, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5
Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 17
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. US2002013269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
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; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
|||||
DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 18

US-09-734-221A-14
; Sequence 14, Application US/09734221A
; Publication No. US20030096221A1
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.

; DENG, HONGKUI
; ELLMEIER, WILFRIED
; LANDAU, NATHANIEL R.
; LIU, RONG

; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/734,221A

FILING DATE: 11-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/666,020

FILING DATE: 19-JUN-1996

APPLICATION NUMBER: US 08/227,319

FILING DATE: 13-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1049-1-004 N2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-734-221A-14

Query Match 100.0%; Score 118; DB 10; Length 352;

Best Local Similarity 100.0%; Pred. No. 2e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22

|||||

DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 19

US-09-826-509-477

; Sequence 477, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

; FILE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 477

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-826-509-477

Query Match 100.0%; Score 118; DB 11; Length 352;

Best Local Similarity 100.0%; Pred. No. 2e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22

|||||

DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 20

US-10-151-274-5

; Sequence 5, Application US/10151274

; Publication No. US20030064071A1

; GENERAL INFORMATION:

; APPLICANT: Littman, Dan R.

; APPLICANT: Kwon, Douglas S.

; APPLICANT: van Kooyk, Yvette

; APPLICANT: Geijtenbeek, Theo

; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

; TITLE OF INVENTION: INTO

; FILE REFERENCE: 1049-1-017

; CURRENT APPLICATION NUMBER: US/10/151,274

; CURRENT FILING DATE: 2002-05-20

; PRIOR APPLICATION NUMBER: US/09/517,605

; PRIOR FILING DATE: 2000-03-02

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-151-274-5

Query Match 100.0%; Score 118; DB 12; Length 352;

Best Local Similarity 100.0%; Pred. No. 2e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 APYNIVLLNTFQFFGLNCS 22
Db      249 APYNIVLLNTFQFFGLNCS 270

RESULT 21
US-10-106-623-2
; Sequence 2, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; Report, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-106-623-20
;
; Query Match      100.0%; Score 118; DB 13; Length 352;
; Best Local Similarity 100.0%; Pred. No. 2e-10;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 APYNIVLLNTFQFFGLNCS 22
Db      249 APYNIVLLNTFQFFGLNCS 270

RESULT 23
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2
;
; Query Match      100.0%; Score 118; DB 14; Length 352;
; Best Local Similarity 100.0%; Pred. No. 2e-10;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 APYNIVLLNTFQFFGLNCS 22
Db      249 APYNIVLLNTFQFFGLNCS 270

RESULT 22
US-10-106-623-20
; Sequence 20, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; Report, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
```


; Sequence 352, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Christine L.
; APPLICANT: Roush, Antigenic Peptides and Antibodies for G Protein-Coupled Receptors
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-225-567A-352

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 29
US-10-323-314-1
; Sequence 1, Application US/10323314
; Publication No. US20030139571A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010-1/JFW/WAF/DJK
; CURRENT APPLICATION NUMBER: US/10/323,314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
; US-10-323-314-1

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 30
US-10-072-301-1
; Sequence 1, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-072-301-1

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 31
US-10-164-649-52
; Sequence 52, Application US/10164649
; Publication No. US20030162943A1
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/164,649
; FILING DATE: 07-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-164-649-52

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 32
US-10-071-866-1
; Sequence 1, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:


```

; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-10-439-845-2

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 37
US-10-439-845-4
; Sequence 4, Application US/10439845
; Publication No. US20030195348A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-10-439-845-2

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 38
US-10-360-828-1
; Sequence 1, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-360-828-1

Query Match 100.0%; Score 118; DB 15; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 39
US-10-661-798-5
; Sequence 5, Application US/10661798
; Publication No. US20040110127A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; APPLICANT: Frederic, Libert
; TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV Ent
; FILE REFERENCE: 9409/2023F
; CURRENT APPLICATION NUMBER: US/10/661,798
```

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/ CURRENT FILING DATE: 2003-09-12
/ PRIOR APPLICATION NUMBER: 09/938,703
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: 09/626,939
/ PRIOR FILING DATE: 2000-07-27
/ PRIOR APPLICATION NUMBER: 08/833,752
/ PRIOR FILING DATE: 1997-04-09
/ PRIOR APPLICATION NUMBER: 08/810,028
/ PRIOR FILING DATE: 1997-03-03
/ PRIOR APPLICATION NUMBER: EP 96870021.1
/ PRIOR FILING DATE: 1996-03-01
/ PRIOR APPLICATION NUMBER: EP 96870102.9
/ PRIOR FILING DATE: 1996-08-06
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-661-738-5

Query Match      100.0%; Score 118; DB 16; Length 352;
Best Local Similarity 100.0%; Pred.No.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
DB 249 APYNIVLLNTFQFFGLNCS 270
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RESULT 40
US-10-791-905-2
/ Sequence 2, Application US/10791905
/ Publication No. US20040151719A1
/ GENERAL INFORMATION:
/ APPLICANT: Li, Yi
/ APPLICANT: Ruben, Steven, M.
/ TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CORS) HDGRL0
/ FILE REFERENCE: 1488.115000P
/ CURRENT APPLICATION NUMBER: US/10791,905
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 10/127,764
/ PRIOR FILING DATE: 2002-04-23
/ PRIOR APPLICATION NUMBER: 09/502,783
/ PRIOR FILING DATE: 2000-02-11
/ PRIOR APPLICATION NUMBER: 09/339,912
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 09/195,662
/ PRIOR FILING DATE: 1998-11-18
/ PRIOR APPLICATION NUMBER: 08/466,343
/ PRIOR FILING DATE: 1995-06-06
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-791-905-2
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Query Match      100.0%; Score 118; DB 16; Length 352;
Best Local Similarity 100.0%; Pred.No.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
DB 249 APYNIVLLNTFQFFGLNCS 270
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Search completed: September 28, 2004, 09:44:42
Job time : 73.875 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:57:36 ; Search time 11.925 Seconds
(without alignments)
178.961 Million cell updates/sec

Title: US-10-084-813-14
Perfect score: 118
Sequence: 1 APYNIVLLNTFFQEFGLNCS 22
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	118	100.0	352	2 A43113	chemokine (C-C) re
2	103	87.3	360	2 JC2443	chemokine (C-C) re
3	103	87.3	374	2 I38450	chemokine (C-C) re
4	70	59.3	344	2 JC5942	chemokine receptor
5	56	47.5	355	2 A45177	chemokine (C-C) re
6	54.5	46.2	1075	2 T07448	probable DNA-direc
7	53	44.9	360	2 A57160	chemokine (C-C) re
8	52	44.1	355	2 G02436	chemokine (C-C) re
9	52	44.1	360	2 JC4587	chemokine (C-C) re
10	52	44.1	383	2 S55394	G protein-coupled
11	52	44.1	466	2 JH0597	muscarinic acetyl
12	52	44.1	466	2 S10126	muscarinic acetyl
13	52	44.1	466	2 S10856	muscarinic acetyl
14	52	44.1	466	2 A27386	muscarinic acetyl
15	51	43.2	589	2 A29476	muscarinic acetyl
16	50	42.4	490	2 A35546	muscarinic acetyl
17	48	40.7	294	2 AG2937	hypothetical prote
18	48	40.7	300	2 F98344	histidinol-phospha
19	48	40.7	342	2 G69502	MIP-1 alpha recept
20	48	40.7	359	2 I49341	muscarinic acetyl
21	48	40.7	589	2 A48557	muscarinic acetyl
22	48	40.7	589	2 B29514	muscarinic acetyl
23	48	40.7	590	2 S10128	muscarinic acetyl
24	48	40.7	590	2 S01114	muscarinic acetyl
25	48	40.7	590	2 S47572	muscarinic acetyl
26	48	40.7	639	2 A55019	muscarinic acetyl
27	47	39.8	352	2 B69901	fatty-acid desatur
28	47	39.8	478	2 C29514	muscarinic acetyl
29	47	39.8	479	2 S10127	muscarinic acetyl

RESULT 1

A43113
chemokine (C-C) receptor 5 - human
N:Alternate names: C-C CKR-5; CCR5
C:Species: Homo sapiens (man)
C>Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000
C:Accession: A43113; S71808; A58834; A58832; G02653; A58833
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A:Title: Molecular cloning and functional expression of a new human CC-chemokine receptor:
A:Reference number: A43113; MUID:96241590; PMID:8639485
A:Accession: A43113
A:Molecule type: mRNA
A:Residues: 1-352 <SAM1>
A:Cross-references: GB:X91492; NID:G1262810; PID:CAA62796.1; PID:G1262811
R:Samson, M.; Libert, P.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pau
Nature 382, 722-725, 1996
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of
A:Reference number: S71808; MUID:96345670; PMID:8751444
A:Accession: S71808
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206; 207-230 <SAM2>
A:Accession: A58834
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184, 'IKDSHLGAGPAAACHGLILGNPKNSASVSK' <SAM3>
A:Cross-references: GB:X99393; NID:G1524062; PID:CAA67767.1; PID:G1524063
A:Note: this frameshift mutation results in a non-functional receptor but confers a degra
nd may have had a selective advantage by conferring resistance to Yersinia plague infecti
R:Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec
A:Reference number: A58832; MUID:96295970; PMID:8699119
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:G1502408; PID:AA17071.1; PID:G1502409
R:Experimental source: Clone 8, endotoxin-stimulated peripheral blood monocytes
submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89, 'L', 91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine
A:Reference number: A58833; MUID:96291862; PMID:8663314

ALIGNMENTS

A;Accession: A58833
 A;Molecule type: mRNA
 A;Residues: 1-352 <RAP>
 A;Cross-references: GB:U54994; NID:gl1457945; PIDN:AAC50598.1; PID:gl1457946
 C;Comment: This is a receptor for chemokines MIP-lambda (see PIR:A30574), MIP-lbeta (see PIR:A30575) and dual-tropic strains of HIV-1 bind to a complex of chemokine (C-C) receptor 2 and dual-tropic strains of HIV-1 bind to a complex of chemokine (C-C) receptor 2.
 C;Genetics:
 A;Gene: GDB:CMKBR5; CCR5; CCR-5; CC-CCR-5; CCR5; ChemR13
 A;Cross-references: GDB:1230510; OMIM:601373
 A;Map position: 3p21-3p21
 C;Function:
 A;Description: G protein-coupled receptor for chemokines MIP-lambda, MIP-lbeta and RANTES.
 A;Note: probably acts to control granulocyte proliferation and differentiation
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;132-56/Domain: transmembrane #status predicted <TM1>
 F;167-87/Domain: transmembrane #status predicted <TM2>
 F;103-124/Domain: transmembrane #status predicted <TM3>
 F;142-166/Domain: transmembrane #status predicted <TM4>
 F;193-218/Domain: transmembrane #status predicted <TM5>
 F;236-257/Domain: transmembrane #status predicted <TM6>
 F;285-300/Domain: transmembrane #status predicted <TM7>
 F;20-269,101-178/disulfide bonds: #status predicted
 F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
 F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 118; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.5e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVILLNTFOEFGFLNCS 22
 DB 249 APYIVILLNTFOEFGFLNCS 270

RESULT 2
 Jc2443
 chemokine (C-C) receptor 2, splice form B - human
 N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine receptor
 C;Species: Homo sapiens (man)
 C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
 A;Accession: Jc2443; I38463
 R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
 Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
 A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor
 A;Reference number: Jc2443; MUID:94324942; PMID:8048929
 A;Accession: Jc2443
 A;Molecule type: mRNA
 A;Residues: 1-360 <YAM>
 A;Cross-references: DBJ:J29984; NID:g531246; PIDN:BA06253.1; PID:g531247
 R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A;Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins 1 and 2
 A;Reference number: A53477; MUID:94195821; PMID:8146186
 A;Accession: I38463
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-360 <RES>
 A;Cross-references: EMBL:U03905; NID:9472557; PIDN:AAA19120.1; PID:g472558
 C;Genetics:
 A;Gene: GDB:CMKBR2
 A;Cross-references: GDB:337364; OMIM:601267
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
 F;43-70/Domain: transmembrane #status predicted <TM1>
 F;81-100/Domain: transmembrane #status predicted <TM2>
 F;115-136/Domain: transmembrane #status predicted <TM3>
 F;154-178/Domain: transmembrane #status predicted <TM4>
 F;207-226/Domain: transmembrane #status predicted <TM5>
 F;244-268/Domain: transmembrane #status predicted <TM6>
 F;287-309/Domain: transmembrane #status predicted <TM7>

F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;113-190/disulfide bonds: #status predicted

Query Match 87.3%; Score 103; DB 2; Length 360;
 Best Local Similarity 90.0%; Pred. No. 9.3e-09;
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVILLNTFOEFGFLNCS 21
 DB 258 PYNIVILLNTFOEFGFLNCS 277

RESULT 3
 I38450

chemokine (C-C) receptor 2, splice form A - human
 N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine receptor
 C;Species: Homo sapiens (man)
 C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
 C;Accession: I38450
 R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A;Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins 1 and 2
 A;Reference number: A53477; MUID:94195821; PMID:8146186
 A;Accession: I38450
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-374 <RES>
 A;Cross-references: EMBL:U03882; NID:9472555; PIDN:AAA19119.1; PID:g472556
 C;Genetics:
 A;Gene: GDB:CMKBR2
 A;Cross-references: GDB:337364; OMIM:601267
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
 F;44-68/Domain: transmembrane #status predicted <TM1>
 F;79-99/Domain: transmembrane #status predicted <TM2>
 F;115-136/Domain: transmembrane #status predicted <TM3>
 F;154-178/Domain: transmembrane #status predicted <TM4>
 F;208-226/Domain: transmembrane #status predicted <TM5>
 F;244-268/Domain: transmembrane #status predicted <TM6>
 F;292-309/Domain: transmembrane #status predicted <TM7>
 F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;32-277,113-190/disulfide bonds: #status predicted

Query Match 87.3%; Score 103; DB 2; Length 374;
 Best Local Similarity 90.0%; Pred. No. 9.6e-09;
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVILLNTFOEFGFLNCS 21
 DB 258 PYNIVILLNTFOEFGFLNCS 277

RESULT 4
 Jc5942

chemokine receptor - human
 C;Species: Homo sapiens (man)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C;Accession: Jc5942
 R;Pan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
 Biochem. Biophys. Res. Commun. 243, 264-268, 1998
 A;Title: Cloning and characterization of a novel human chemokine receptor.
 A;Reference number: Jc5942; MUID:98139902; PMID:9473515
 A;Accession: Jc5942
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-344 <PAN>
 A;Cross-references: GB:U97123; NID:g2897070; PIDN:AAC39595.1; PID:g2897071
 C;Superfamily: vertebrate rhodopsin

Query Match 59.3%; Score 70; DB 2; Length 344;
 Best Local Similarity 57.1%; Pred. No. 0.0018;
 Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

```

Qy  1 APYNVLLNTFOEFFGLNNC 21
      |||||  |::|  |::|
Db  252 APYNIAPFLSTFKHEFSLSDC 272

RESULT 5
A45177
Chemokine (C-C) receptor 1 - human
N/Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C/Accession: A45177; I55671
R/Note, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 77, 415-425, 1993
A/Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor
A/Reference number: A45177; MUID:93161416; PMID:7679328
A/Accession: A45177
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-355 <NEO>
A/Cross-references: GB:L10918; NID:G292416; PIDN:AAA36543.1; PID:G292417
A/Experimental source: HL60 cells
A/Note: sequence extracted from NCBI backbone (NCBIP:124876)
R/Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A/Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
A/Reference number: I55671; MUID:93240122; PMID:7683036
A/Accession: I55671
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-355 <RES>
A/Cross-references: GB:L10918; NID:G292416; PIDN:AAA36543.1; PID:G292417
C/Genetics:
A/Gene: GDB:CMKBR1; CMKR-1
A/Cross-references: GDB:I38446; OMIM:601159
A/Map position: 3p21-3p21
C/Superfamily: vertebrate rhodopsin
P/36-60/Domain: transmembrane #status predicted <TM1>
P/61-91/Domain: transmembrane #status predicted <TM2>
P/108-129/Domain: transmembrane #status predicted <TM3>
P/147-171/Domain: transmembrane #status predicted <TM4>
P/205-223/Domain: transmembrane #status predicted <TM5>
P/240-264/Domain: transmembrane #status predicted <TM6>
P/288-305/Domain: transmembrane #status predicted <TM7>
P/5/Binding site: carbohydrate (Asn) (covalent) #status predicted
P/24-273,106-183/Disulfide bonds: #status predicted
P/345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 47.5%; Score 56; DB 2; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.33;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy  2 PYNIVLLNTFOEFFGLNNC 21
      |||||  |::|  |::|
Db  254 PYNLTILISVQDFLFTHEC 273

RESULT 6
T07448
Probable DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Japanese black pine chloroplast
C/Species: Chloroplast Pinus thunbergiana (Japanese black pine)
C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 18-Aug-2000
C/Accession: T07448
R/Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A/Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome
A/Reference number: Z16030; MUID:95024047; PMID:7937893
A/Accession: T07448
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1075 <WAK>

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A;Cross-references: EMBL:D17510; NID:g529643; PIDN:BAA04326.1; PID:g1262609
C;Genetics:
A;Gene: rpoB
A;Genome: chloroplast
C;Superfamily: DNA-directed RNA polymerase beta chain
C;Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 45.2%; Score 54.5; DB 2; Length 1075;
Best Local Similarity 63.2%; Pred. No.1.8;
Matches 12; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 2 PYNIV---LLNLTRQEPPG 17
| | | | |
Db 355 PQNLVTSTLLKNTFDFFG 373

RESULT 7
A57160
chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: A57160
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Wé
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDN
A;Reference number: A57160; MURD:95370289; PMID:7642634
A;Accession: A57160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: GB:X85740; NID:g1370103; PIDN:CAS59743.1; PID:g971452
A;Note: source clone KS-5
C;Genetics:
A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F;76-97/Domain: transmembrane #status predicted <TM1>
F;740-65/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;151-175/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;23-276,110-187/Disulfide bonds: #status predicted
F;745/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;132/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

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Query Match          44.9%; Score 53; DB 2; Length 360;
Best Local Similarity 52.4%; Pred. No. 1;
Matches 11; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy      2 PYNIVLLNTFFQFFGLNNGS 22
      ||||| | | | | | : | :
Db      257 PYNIVLFLETLVEVLQDCT 277

RESULT 8
G02436
chemokine (C-C) receptor 3 - human
N:Alternate names: C-C CKR-3
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
C:Accession: G02436; A57237
R:Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A:Reference number: H01272
A:Accession: G02436
A:Status: translated from GB/EMBL/DBJ

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A:Molecule type: DNA
A:Residues: 1-355 <PON>
A:Cross-references: ENBL:U49727; NID:gl477560; PIDN:AAB09726.1; PID:gl477561
C:Combadriere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
A:Reference number: A57237; MUID:95348056; PMID:7622448
A:Accession: A57237
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>
A:Cross-references: GB:U28694; NID:gl199579; PIDN:AAC50469.1; PID:gl199580
A>Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.
C:Genetics:
A:Gene: GDB:CMKBR3
A:Cross-references: GDB:579624; OMIM:601268
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-261/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:24-273, 106-183/disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 44.1%; Score 52; DB 2; Length 355;
Best Local Similarity 40.0%; Pred. No. 1.4;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQFPGLNLC 21
||||:||||:|
DB 254 PYNVAILSSVQSLIFGND 273

RESULT 9
JC4587
chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-Mar-1995 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: JC4587
R:Hogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A:Reference number: JC4587; MUID:96136324; PMID:8573157
A:Accession: JC4587
A:Molecule type: mRNA
A:Residues: 1-360 <HO>
A:Cross-references: ENBL:X90862; NID:gl167851; PIDN:CAA62372.1; PID:gl167852
A:Experimental source: thymus
C:Genetics:
A:Gene: cc ckr-4
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
F:2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:2,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
F:145/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 44.1%; Score 52; DB 2; Length 360;
Best Local Similarity 47.6%; Pred. No. 1.5;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQFPGLNLC 22
||||:||||:|
DB 257 PYNVVLFTLVEVLQDCT 277

RESULT 10
S55594

G protein-coupled receptor E1 - equine herpesvirus 2
C:Species: equine herpesvirus 2
C>Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C:Accession: S55594
R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A:Title: The DNA sequence of equine herpesvirus 2.
A:Reference number: S55594; MUID:95302501; PMID:7783207
A:Accession: S55594
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-383 <TEL>
A:Cross-references: GB:U20824; NID:ig695172; PIDN:AAC13788.1; PID:ig695173
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 44.1%; Score 52; DB 2; Length 383;
Best Local Similarity 50.9%; Pred. No. 1.6;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12
||||:||||:|
DB 293 PYNIVLLSTF 303

RESULT 11
JH0197
muscarinic acetylcholine receptor M2 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 24-Nov-1999
C:Accession: JH0197; D37121
R:Lai, J.; Bloom, J.W.; Yamamura, H.I.; Roeske, W.R.
Life Sci. 47, 1001-1013, 1990
A:Title: Amplification of the rat m2 muscarinic receptor gene by the polymerase chain re
A:Reference number: JH0197; MUID:91041524; PMID:2172674
A:Accession: JH0197
A:Molecule type: DNA
A:Residues: 1-466 <LA>
R:Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invol
A:Reference number: A37121; MUID:90337982; PMID:2380182
A:Accession: D37121
A>Status: preliminary
A:Molecule type: protein
A:Residues: 60-122 <KUR>
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmem
F:23-48/Domain: transmembrane #status predicted <TM1>
F:61-85/Domain: transmembrane #status predicted <TM2>
F:98-119/Domain: transmembrane #status predicted <TM3>
F:139-162/Domain: transmembrane #status predicted <TM4>
F:184-207/Domain: transmembrane #status predicted <TM5>
F:389-409/Domain: transmembrane #status predicted <TM6>
F:421-442/Domain: transmembrane #status predicted <TM7>

Query Match 44.1%; Score 52; DB 2; Length 466;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTF 12
||||:||||:|
DB 401 APYNVVLNTF 412

RESULT 12
S10126
muscarinic acetylcholine receptor M2 - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Nov-1999
C:Accession: S10126
R:Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capor, D.J.
EMBO J. 6, 3923-3929, 1987

A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of muscarinic acetylcholine receptors in the rat brain
A;Reference number: S04326; MUID:88166632; PMID:3443095
A;Accession: S10126
A;Molecule type: DNA
A;Residues: 1-466 <PER>
A;Cross-references: EMBL:X15264; NID:g32319; PIDN:CAA33335.1; PID:g32320
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C
F;23-48/Domain: transmembrane #status predicted <TM1>
F;60-89/Domain: transmembrane #status predicted <TM2>
F;98-119/Domain: transmembrane #status predicted <TM3>
F;139-162/Domain: transmembrane #status predicted <TM4>
F;184-207/Domain: transmembrane #status predicted <TM5>
F;389-409/Domain: transmembrane #status predicted <TM6>
F;421-442/Domain: transmembrane #status predicted <TM7>
F;2,6,9/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.1%; Score 52; DB 2; Length 466;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNYVLLNTF 12
||||:|:|:|
Db 401 APYNYVLLNTF 412

RESULT 13
S10856
muscarinic acetylcholine receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999
C;Accession: S10856
F;Gocayne, J.; Robinson, D.A.; FitzGerald, M.G.; Chung, F.Z.; Kurlav, A.R.; Lentes, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 8296-8300, 1987
A;Title: Primary structure of rat cardiac beta-adrenergic and muscarinic cholinergic receptors
A;Reference number: S10855; MUID:88068581; PMID:2825184
A;Accession: S10856
A;Molecule type: mRNA
A;Residues: 1-466 <GCG>
A;Cross-references: EMBL:J03025; NID:g203461; PIDN:AAA40926.1; PID:g203462
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C
F;23-48/Domain: transmembrane #status predicted <TM1>
F;61-85/Domain: transmembrane #status predicted <TM2>
F;98-119/Domain: transmembrane #status predicted <TM3>
F;139-162/Domain: transmembrane #status predicted <TM4>
F;184-207/Domain: transmembrane #status predicted <TM5>
F;389-409/Domain: transmembrane #status predicted <TM6>
F;421-442/Domain: transmembrane #status predicted <TM7>

Query Match 44.1%; Score 52; DB 2; Length 466;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNYVLLNTF 12
||||:|:|:|
Db 401 APYNYVLLNTF 412

RESULT 14
A27386
muscarinic acetylcholine receptor, cardiac - pig
N;Alternate names: muscarinic acetylcholine receptor M2
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2000
C;Accession: A27386; A25656
R;Peralta, E.G.; Winslow, J.W.; Peterson, G.L.; Smith, D.H.; Ashkenazi, A.; Ramachandran
Science 236, 600-605, 1987
A;Title: Primary structure and biochemical properties of an M-2 muscarinic receptor.
A;Reference number: A27386; MUID:87206169; PMID:3107123
A;Accession: A27386
A;Molecule type: DNA; mRNA
A;Residues: 1-466 <PER>

A;Cross-references: GB:M16331; NID:g164311; PIDN:AAA30986.1; PID:g164313
A;Experimental source: atrial muscle
A;Note: the protein sequence derived from the mRNA clones differs from that of the genomic
R;Castro, J.
FEBS Lett. 209, 367-372, 1986
A;Title: Primary structure of porcine cardiac muscarinic acetylcholine receptor deduced from
A;Reference number: A25656; MUID:87080790; PMID:3792556
A;Accession: A25656
A;Molecule type: mRNA
A;Residues: 1-329, 'K', 331-466 <KUB>
A;Cross-references: GB:X04708; NID:g1859; PIDN:CAA28413.1; PID:g1860
C;Superfamily: vertebrate rhodopsin
C;Keywords: cardiac muscle; G protein-coupled receptor; glycoprotein; heart; neurotransmitter
F;23-48/Domain: transmembrane #status predicted <TM1>
F;61-85/Domain: transmembrane #status predicted <TM2>
F;98-119/Domain: transmembrane #status predicted <TM3>
F;139-162/Domain: transmembrane #status predicted <TM4>
F;184-207/Domain: transmembrane #status predicted <TM5>
F;389-409/Domain: transmembrane #status predicted <TM6>
F;421-442/Domain: transmembrane #status predicted <TM7>

Query Match 44.1%; Score 52; DB 2; Length 466;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNYVLLNTF 12
||||:|:|:|
Db 401 APYNYVLLNTF 412

RESULT 15
A29476
muscarinic acetylcholine receptor M4 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Feb-2000
C;Accession: A29476
R;Braun, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 149, 125-132, 1987
A;Title: A novel subtype of muscarinic receptor identified by homology screening.
A;Reference number: A29476; MUID:88077068; PMID:3120722
A;Accession: A29476
A;Molecule type: mRNA
A;Residues: 1-589 <BRA>
A;Cross-references: GB:M18086; NID:g202657; PIDN:AAA40659.1; PID:g202658
C;Experimental source: brain
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane
F;67-90/Domain: transmembrane #status predicted <TM1>
F;104-124/Domain: transmembrane #status predicted <TM2>
F;142-163/Domain: transmembrane #status predicted <TM3>
F;184-206/Domain: transmembrane #status predicted <TM4>
F;230-251/Domain: transmembrane #status predicted <TM5>
F;492-512/Domain: transmembrane #status predicted <TM6>
F;527-545/Domain: transmembrane #status predicted <TM7>

Query Match 43.2%; Score 51; DB 2; Length 589;
Best Local Similarity 61.5%; Pred. No. 3.5;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFQ 14
||||:|:|:|:|
Db 505 PYNIVLLNTFQ 517

RESULT 16
A35546
muscarinic acetylcholine receptor M4 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 21-Jul-2000
A;Reference number: A35546
A;Accession: A35546
R;Tietje, K.M.; Goldman, P.S.; Nathanson, N.M.
J. Biol. Chem. 265, 2828-2834, 1990

A:Residues: 1-300 <KUR>
A/Cross-references: GB:AE007870; FIDN:AAK90282.1; PID:g15160307; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L 3415
A:Map position: linear chromosome
C:Superfamily: inner membrane protein ugpa

Query Match 40.7%; Score 48; DB 2; Length 300;
Best Local Similarity 52.4%; Pred. No. 5.4;
Matches 11; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 2 PYN--IVLLANTFOEFFGLNN 20
|:| | | | | :| | | | |
Db 248 PFNSSFVLLKVIREFAFQLNN 268

RESULT 19
HG9502
histidinol-phosphate aminotransferase (hisC-2) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C:Accession: G69502
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: G69502
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-342 <LE>
A/Cross-references: GB:AS000963; GB:AS000782; NID:G2689286; PIDN:AB89229.1; PID:g2648510
C:Superfamily: probable histidinol-phosphate transaminase

Query Match 40.7%; Score 48; DB 2; Length 342;
Best Local Similarity 50.0%; Pred. No. 6.1;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 YNIVLLNTFOEFFGL 18
|:| | | | | :| | | | |
Db 195 YNIVLVRSFSKFFGL 210

RESULT 20
I49341
Mip-1 alpha receptor like-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
C:Accession: I49341
R:Gao, J.L.; Murphy, P.M. J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemok A:Reference number: I49339; MUID:95340546; PMID:7542241
A:Accession: I49341
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <RES>
A/Cross-references: EMBL:U28406; NID:g881551; PID:g881552
C:Superfamily: vertebrate rhodopsin

Query Match 40.7%; Score 48; DB 2; Length 359;
Best Local Similarity 45.0%; Pred. No. 6.4;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNNC 21
|:| | | | | :| | | | |
Db 258 PYNIVLVFSAFHSTFLETSC 277

RESULT 21

S48657
 muscarinic acetylcholine receptor MR - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C:Accession: S48657; S24948
 R;Hererra, L.; Carvallo, P.; Antonelli, M.; Olate, J.
 FEBS Lett. 352, 175-179, 1994
 A:Title: Cloning of a Xenopus laevis muscarinic receptor encoded by an intronless gene.
 A:Reference number: S48657; MUID:95010703; PMID:7925970
 A:Accession: S48657
 A:Molecule type: mRNA
 A:Residues: 1-484 <HER>
 A:Cross-references: GB:X65865; NID:G64900; PIDN:CAA46694.1; PID:G64901
 R;Olate, J.
 submitted to the EMBL Data Library, April 1992
 A:Reference number: S24948
 A:Accession: S24948
 A:Molecule type: mRNA
 A:Residues: 1-131, 'X', 133-484 <OLA>
 A:Cross-references: EMBL:X65865; NID:G64900; PID:G64901
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane
 F:71-95/Domain: transmembrane #status predicted <TM1>
 F:108-129/Domain: transmembrane #status predicted <TM2>
 F:149-172/Domain: transmembrane #status predicted <TM3>
 F:194-217/Domain: transmembrane #status predicted <TM4>
 F:407-427/Domain: transmembrane #status predicted <TM5>
 F:439-460/Domain: transmembrane #status predicted <TM7>
 Query Match 40.7%; Score 48; DB 2; Length 484;
 Best Local Similarity 63.6%; Pred. No. 8.7;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PYNIVLLNTF 12
 DB 420 PYNWMLNTF 430
 RESULT 22
 B29514
 muscarinic acetylcholine receptor M3 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Feb-2000
 C:Accession: B94518; B94293; B37121; B29514
 R;Bonner, T.I.
 submitted to GenBank, July 1987
 A:Reference number: A94518
 A:Accession: B94518
 A:Molecule type: mRNA
 A:Residues: 1-589 <BO1>
 R;Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
 Science 237, 527-532, 1987
 A:Title: Identification of a family of muscarinic acetylcholine receptor genes.
 A:Reference number: A94293; MUID:87263421; PMID:3037705
 A:Accession: B94293
 A:Molecule type: mRNA
 A:Residues: 1-269,463-589 <BO2>
 A:Experimental source: cerebral cortex
 A:Note: only a part of the protein translation is given; none of the nucleotide sequence
 R;Kurbanach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
 J. Biol. Chem. 265, 13702-13708, 1990
 A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues inv
 A:Reference number: A37121; MUID:90337982; PMID:2380182
 A:Accession: B37121
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 104-166 <KUR>
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane
 F:67-90/Domain: transmembrane #status predicted <TM1>
 F:104-124/Domain: transmembrane #status predicted <TM2>
 F:142-163/Domain: transmembrane #status predicted <TM3>

F:184-206/Domain: transmembrane #status predicted <TM4>
 F:230-251/Domain: transmembrane #status predicted <TM5>
 F:492-512/Domain: transmembrane #status predicted <TM6>
 F:527-545/Domain: transmembrane #status predicted <TM7>
 F:6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 40.7%; Score 48; DB 2; Length 589;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PYNIVLLNTF 12
 DB 505 PYNIMVLNTF 515
 RESULT 23
 S10128
 muscarinic acetylcholine receptor M4 - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Feb-2000
 C:Accession: S10128
 R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
 EMBO J. 6, 3923-3929, 1987
 A:Title: Distinct primary structures, ligand-binding properties and tissue-specific expre
 A:Reference number: S04336; MUID:89166632; PMID:3443095
 A:Accession: S10128
 A:Molecule type: DNA
 A:Residues: 1-590 <PER>
 A:Cross-references: EMBL:X15266; NID:G32323; PIDN:CAA33337.1; PID:G32324
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmem
 F:105-131/Domain: transmembrane #status predicted <TM1>
 F:143-164/Domain: transmembrane #status predicted <TM2>
 F:185-207/Domain: transmembrane #status predicted <TM3>
 F:231-252/Domain: transmembrane #status predicted <TM4>
 F:493-513/Domain: transmembrane #status predicted <TM5>
 F:525-546/Domain: transmembrane #status predicted <TM7>
 F:5,6,15,41/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 40.7%; Score 48; DB 2; Length 590;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PYNIVLLNTF 12
 DB 506 PYNIMVLNTF 516
 RESULT 24
 S01114
 muscarinic acetylcholine receptor M2, glandular - pig
 N:Alternate names: muscarinic acetylcholine receptor III
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Feb-2000
 C:Accession: S01114
 R;Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.
 FEBS Lett. 235, 257-261, 1988
 A:Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonis
 A:Reference number: S01114; MUID:88296835; PMID:3402600
 A:Accession: S01114
 A:Molecule type: DNA
 A:Residues: 1-590 <AKT>
 A:Cross-references: EMBL:X12712; NID:G1861; PIDN:CAA31215.1; PID:G1862
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmem
 F:105-125/Domain: transmembrane #status predicted <TM1>
 F:143-164/Domain: transmembrane #status predicted <TM2>
 F:185-207/Domain: transmembrane #status predicted <TM3>
 F:231-253/Domain: transmembrane #status predicted <TM4>
 F:493-513/Domain: transmembrane #status predicted <TM5>
 F:528-546/Domain: transmembrane #status predicted <TM7>

Query Match 40.7%; Score 48; DB 2; Length 590;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12
 |||:|:|:|
 Db 506 PYNIMVLVNTF 516

RESULT 25
 S47572
 muscarinic acetylcholine receptor m3 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Feb-2000
 C:Accession: S47572
 R:Lee, P.H.K.; Hodges, P.K.; Glickman, P.; Chang, K.J.
 Biochim. Biophys. Acta 1223, 151-154, 1994
 A:Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 re
 A:Reference number: S47572; MUID:94339178; PMID:8061048
 A:Accession: S47572
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-590 <LE>
 A:Cross-references: EMBL:U08286; NID:9520465; PIDN:AAA51866.1; PID:9520466
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 40.7%; Score 48; DB 2; Length 590;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12
 |||:|:|:|
 Db 506 PYNIMVLVNTF 516

RESULT 26
 A55019
 muscarinic acetylcholine receptor, M3 isoform - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 21-Jul-2000
 C:Accession: A55019
 R:Gadbut, A.P.; Galper, J.B.
 J. Biol. Chem. 269, 25823-25829, 1994
 A:Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and
 A:Reference number: A55019; MUID:95014393; PMID:7929287
 A:Accession: A55019
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-639 <GAD>
 A:Cross-references: GB:LI0617; NID:9530097; PIDN:AAA65961.1; PID:9530098
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 40.7%; Score 48; DB 2; Length 639;
 Best Local Similarity 72.7%; Pred. No. 12;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12
 |||:|:|:|
 Db 556 PYNIMVLVNTF 566

RESULT 27
 B69901
 fatty-acid desaturase homolog yocE - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 C:Accession: B69901
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.;
 Koether, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauviel,
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Saco, T.; Scanlon,
 A:Authors: Schleith, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9364377
 A:Accession: B69901
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-352 <KUN>
 A:Cross-references: GB:Z99114; GB:AL009126; NID:92634230; PIDN:CAB13810.1; PID:92634311
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yocE
 C:Superfamily: omega-3 fatty acid desaturase

Query Match 39.8%; Score 47; DB 2; Length 352;
 Best Local Similarity 60.0%; Pred. No. 9.1;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 NIVLLNTQEEFGL 18
 :|:|:|:|:|
 Db 28 SLIQLLNTFIPFGL 42

RESULT 28
 C29514
 muscarinic acetylcholine receptor M4 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999
 C:Accession: C94518; C94293; E37121; C29514
 R:Bonner, T.I.
 submitted to GenBank, July 1987
 A:Reference number: A94518
 A:Accession: C94518
 A:Molecule type: mRNA
 A:Residues: 1-478 <BO1>
 R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
 Science 237, 527-532, 1987
 A:Title: Identification of a family of muscarinic acetylcholine receptor genes.
 A:Reference number: A94293; MUID:87263421; PMID:3037705
 A:Accession: C94293
 A:Molecule type: mRNA
 A:Residues: 1-233;373-478 <BO2>
 A:Experimental source: cerebral cortex
 A:Note: only a part of the protein translation is given; none of the nucleotide sequence
 R:Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
 J. Biol. Chem. 265, 13702-13708, 1990
 A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invol
 A:Reference number: A37121; MUID:90337982; PMID:2380182
 A:Accession: E37121
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 68-130 <KUR>
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
 F:31-56/Domain: transmembrane #status predicted <TM1>
 F:99-127/Domain: transmembrane #status predicted <TM2>
 F:106-127/Domain: transmembrane #status predicted <TM3>
 F:147-170/Domain: transmembrane #status predicted <TM4>
 F:192-215/Domain: transmembrane #status predicted <TM5>
 F:401-421/Domain: transmembrane #status predicted <TM6>
 F:433-454/Domain: transmembrane #status predicted <TM7>
 F:8,13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.8%; Score 47; DB 2; Length 478;
 Best Local Similarity 60.0%; Pred. No. 9.1;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 NIVLLNTQEEFGL 18
 :|:|:|:|:|
 Db 28 SLIQLLNTFIPFGL 42

RESULT 28
 C29514
 muscarinic acetylcholine receptor M4 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999
 C:Accession: C94518; C94293; E37121; C29514
 R:Bonner, T.I.
 submitted to GenBank, July 1987
 A:Reference number: A94518
 A:Accession: C94518
 A:Molecule type: mRNA
 A:Residues: 1-478 <BO1>
 R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
 Science 237, 527-532, 1987
 A:Title: Identification of a family of muscarinic acetylcholine receptor genes.
 A:Reference number: A94293; MUID:87263421; PMID:3037705
 A:Accession: C94293
 A:Molecule type: mRNA
 A:Residues: 1-233;373-478 <BO2>
 A:Experimental source: cerebral cortex
 A:Note: only a part of the protein translation is given; none of the nucleotide sequence
 R:Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
 J. Biol. Chem. 265, 13702-13708, 1990
 A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invol
 A:Reference number: A37121; MUID:90337982; PMID:2380182
 A:Accession: E37121
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 68-130 <KUR>
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
 F:31-56/Domain: transmembrane #status predicted <TM1>
 F:99-127/Domain: transmembrane #status predicted <TM2>
 F:106-127/Domain: transmembrane #status predicted <TM3>
 F:147-170/Domain: transmembrane #status predicted <TM4>
 F:192-215/Domain: transmembrane #status predicted <TM5>
 F:401-421/Domain: transmembrane #status predicted <TM6>
 F:433-454/Domain: transmembrane #status predicted <TM7>
 F:8,13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNVILLNTF 12
||||:|:|:|
Db 414 PYNVMVLVNTF 424

RESULT 29
S10127
muscarinic acetylcholine receptor M3 - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Nov-1999
C:Accession: S10127
R:Paralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1987
A:Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of three human muscarinic acetylcholine receptor subtypes
A:Reference number: S04326; MUID:8816632; PMID:3443095
A:Accession: S10127
A:Molecule type: DNA
A:Residues: 1-479 <PER>
A:Cross-references: EMBL:X15265; NID:g32321; PIDN:CAA33336.1; PID:g32322
C:Superfamily: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatidylinositol 3-OH kinase activator
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatidylinositol 3-OH kinase activator
F:32-57/Domain: transmembrane #status predicted <TM1>
F:70-94/Domain: transmembrane #status predicted <TM2>
F:106-128/Domain: transmembrane #status predicted <TM3>
F:148-171/Domain: transmembrane #status predicted <TM4>
F:192-216/Domain: transmembrane #status predicted <TM5>
F:401-422/Domain: transmembrane #status predicted <TM6>
F:433-456/Domain: transmembrane #status predicted <TM7>
F:3,8,13/Binding site: carbohydrate (Asn) #status predicted

Query Match 39.8%; Score 47; DB 2; Length 479;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNVILLNTF 12
||||:|:|:|
Db 415 PYNVMVLVNTF 425

RESULT 30
S33776
muscarinic acetylcholine receptor m4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 24-Nov-1999
C:Accession: S33776; S33135
R:van Koppen, C.J.; Lenz, W.; Nathanson, N.M.
Biochim. Biophys. Acta 1173, 342-344, 1993
A:Title: Isolation, sequence and functional expression of the mouse m4 muscarinic acetylcholine receptor cDNA
A:Reference number: S33776; MUID:93305731; PMID:7916637
A:Accession: S33776
A:Molecule type: DNA
A:Residues: 1-479 <KOP>
A:Cross-references: EMBL:X63473; NID:g296913; PIDN:CAA45071.1; PID:g296914
C:Superfamily: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatidylinositol 3-OH kinase activator
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatidylinositol 3-OH kinase activator
F:31-56/Domain: transmembrane #status predicted <TM1>
F:69-93/Domain: transmembrane #status predicted <TM2>
F:106-127/Domain: transmembrane #status predicted <TM3>
F:147-170/Domain: transmembrane #status predicted <TM4>
F:192-215/Domain: transmembrane #status predicted <TM5>
F:402-422/Domain: transmembrane #status predicted <TM6>
F:434-455/Domain: transmembrane #status predicted <TM7>

Query Match 39.8%; Score 47; DB 2; Length 479;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNVILLNTF 12
||||:|:|:|
Db 415 PYNVMVLVNTF 425

RESULT 31
T01844
Probable sugar transport protein PSD12.9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Sep-1999
C:Accession: T01844
R:Murray, J.; Langston, Y.; Ahrens, C.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of Arabidopsis thaliana F9D12.
A:Reference number: Z14444
A:Accession: T01844
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-507 <MUR>
A:Cross-references: EMBL:AF077407; NID:g3319339; PIDN:AAC26232.1; PID:g3319343
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Introns: 44/1; 150/3; 359/3
A:Note: F9D12.9
C:Superfamily: glucose transport protein
C:Keywords: sugar transport; transmembrane protein
Query Match 39.8%; Score 47; DB 2; Length 507;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 PYNVILLNTFQBFGLN 19
|:|:|:|:|:|:|
Db 280 PFVIGMLQFFQFTGIN 297

RESULT 32
T31013
hypothetical protein 87 - Sulfolobus sp. plasmid pNOB8
C:Species: Sulfolobus sp.
C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C:Accession: T31013
R:She, Q.; Phan, H.; Garrett, R.A.; Albers, S.V.; Stedman, K.M.; Zillig, W.
Extremophiles 2, 417-425, 1998
A:Title: Genetic profile of pNOB8 from Sulfolobus: the first conjugative plasmid from an extremophile
A:Reference number: Z20959; MUID:9044580; PMID:9827331
A:Accession: T31013
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-87 <SHE>
A:Cross-references: EMBL:AJ010405; NID:el351926; PID:el351935; PIDN:CAA09119.1
A:Experimental source: strain NOB8H2
C:Genetics:
A:Genome: plasmid pNOB8

Query Match 39.4%; Score 46.5; DB 2; Length 87;
Best Local Similarity 47.4%; Pred. No. 2.6;
Matches 9; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 3 XNIVLL-LNTFOFFGLNN 20
|:|:|:|:|:|:|
Db 18 XNILLHISNFIQLGLNN 36

RESULT 33
E69633
glutamine ABC transporter (membrane protein) glmM - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: E69633
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Eppington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron, akuch, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:9804033; PMID:9384377
A:Accession: E69633
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-216 <KNU>
A:Cross-references: GB:Z99117; GB:Z99118; GB:AL009126; NID:G2635200; PIDN:CAB14703.1; PI
A:Experimental source: strain 168
C:Genetics:
A:Gene: glmM
C:Superfamily: histidine permease protein M

Query Match 39.0%; Score 46; DB 2; Length 216;
Best Local Similarity 64.7%; Pred. No. 8;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 4 NIVLLNTFQPFGLNN 20
DB 62 NIPLLLITFVFGUPN 78
RESULT 34
I49339
macrophage inflammatory protein-1 alpha receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
R:Accession: I49339
R:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
A:Reference number: I49339; MUID:95340546; PMID:7542241
A:Accession: I49339
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <RES>
A:Cross-references: EMBL:U28404; NID:9881547; PIDN:AAA89153.1; PID:9881548
C:Superfamily: vertebrate rhodopsin

Query Match 39.0%; Score 46; DB 2; Length 355;
Best Local Similarity 35.0%; Pred. No. 13;
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 2 PYNLVSVFVSFAQDVLFTNQ 273
DB 254 PYNLVSVFVSFAQDVLFTNQ 273
RESULT 35
S42628
G protein-coupled receptor Gpcr6 - mouse
N:Alternate names: interleukin-8 receptor homolog; muBLR1 protein
C:Species: Mus musculus (house mouse)
C>Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 21-Jul-2000
R:Accession: S42628; C48909
R:Kaiser, E.; Foerster, R.; Wolf, I.; Ebensperger, C.; Kuehl, W.M.; Lipp, M.
Eur. J. Immunol. 23, 2532-2539, 1993
A:Title: The G protein-coupled receptor BLR1 is involved in murine B cell differentiation
A:Reference number: S42628; MUID:94009211; PMID:8405054
A:Accession: S42628
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-374 <KAI>
A:Cross-references: EMBL:X71788; NID:92598563; PIDN:CAA50673.1; PID:9433947
R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.

Genomics 18, 175-184, 1993
A:Title: Identification, chromosomal location, and genome organization of mammalian G-pr
A:Reference number: A48909; MUID:94116980; PMID:8288218
A:Accession: C48909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 151-269 <WTL>
A:Cross-references: GB:I20332; NID:9438798; PIDN:AAA16852.1; PID:9438799
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 39.0%; Score 46; DB 2; Length 374;
Best Local Similarity 25.6%; Pred. No. 14;
Matches 11; Conservative 6; Mismatches 4; Indels 22; Gaps 1;

QY 1 APYNIIVLLNTFQ-----EFFGLNLC 21
DB 275 SPYHIVFDLTLERLKVNSCELSGYLSVAITLCEFLGLAHC 317

RESULT 36
S32785
G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999
C:Accession: S32785
R:Kouba, M.; Vanetti, M.; Wang, X.; Schaefer, M.; Hoell, V.
FEBS Lett. 321, 173-178, 1993
A:Title: Cloning of a novel putative G-protein-coupled receptor (NLR) which is expressed
A:Reference number: S32785; MUID:93238948; PMID:8386678
A:Accession: S32785
A:Molecule type: mRNA
A:Residues: 1-374 <KOU>
A:Cross-references: GB:X71463; GB:S59748; NID:9599926; PIDN:CAA50582.1; PID:9599927
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 39.0%; Score 46; DB 2; Length 374;
Best Local Similarity 25.6%; Pred. No. 14;
Matches 11; Conservative 6; Mismatches 4; Indels 22; Gaps 1;

QY 1 APYNIIVLLNTFQ-----EFFGLNLC 21
DB 275 SPYHIVFDLTLERLKVNSCELSGYLSVAITLCEFLGLAHC 317

RESULT 37
T28952
hypothetical protein F28A12.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T28952
R:Sammons, L.; Murray, J.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of *C. elegans* cosmid F28A12.
A:Reference number: Z20547
A:Accession: T28952
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-613 <SAM>
A:Cross-references: EMBL:U64851; PIDN:AAC47987.1; GSPDB:GN00023; CESP:F28A12.1
A:Experimental source: strain Bristol N2; clone F28A12
C:Genetics:
A:Gene: CESP:F28A12.1
A:Map position: 5
A:Introns: 41/1, 92/3, 159/1, 302/3, 358/1, 382/1, 433/2, 464/1, 512/3, 567/3

Query Match 39.0%; Score 46; DB 2; Length 613;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 LINTQPEFFGLN 19
:||||:||||

Db 459 ILTNFKIFGLN 470

RESULT 38

C29959

DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - spinach chloroplast

C;Species: chloroplast Spinacia oleracea (spinach)

C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 18-Jun-1999

C;Accession: C29959

R;Hudson, G.S.; Holton, T.A.; Whitfield, P.R.; Bottomley, W.

J. Mol. Biol. 200, 639-654, 1988

A;Title: Spinach chloroplast rpoBC genes encode three subunits of the chloroplast RNA po

A;Reference number: A29959; PMID:88316931; PMID:3045324

A;Accession: C29959

A;Molecule type: DNA

A;Residues: 1-1070 <HUD>

A;Cross-references: GB:M55297; NID:G295119; PIDN:AAA84637.1; PID:G295121

C;Genetics:

A;Gene: rpoB

A;Genome: chloroplast

C;Superfamily: DNA-directed RNA polymerase beta chain

C;Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 38.6%; Score 45.5; DB 2; Length 1070;

Best Local Similarity 45.8%; Pred. No. 50;

Matches 11; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

Qy 2 PYNIVL---LLNTQEFEGGLNCS 22

Db 352 PQNLVTSTPLTTTFESFGLHPLS 375

RESULT 39

T25510

hypothetical protein C04E6.10 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Jun-2000

C;Accession: T25510

R;Bentley, D.; Gattung, S.

submitted to the EMBL Data Library, April 1997

A;Description: The sequence of C. elegans cosmid C04E6.

A;Reference number: 220043

A;Accession: T25510

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-312 <BEN>

A;Cross-references: EMBL:U97012; PIDN:AAB52330.1; GSPDB:GN00023; CESP:C04E6.10

A;Experimental source: strain Bristol N2; clone C04E6

C;Genetics:

A;Gene: CESP:C04E6.10

A;Map position: 5

A;Introns: 68/2; 97/2; 148/3; 241/3; 263/1

C;Superfamily: Caenorhabditis hypothetical protein C49G7.2

Query Match 38.1%; Score 45; DB 2; Length 312;

Best Local Similarity 44.4%; Pred. No. 17;

Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 5 IVLLNTQEFEGGLNCS 22

Db 78 ITYILNGFCTVGLSTCA 95

RESULT 40

I58186

probable G protein-coupled receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

C;Accession: I58186

R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.

Neurosci. Lett. 169, 85-89, 1994

A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and b

A;Reference number: I58186; PMID:94323113; PMID:8047298

A;Accession: I58186

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-354 <RES>

A;Cross-references: EMBL:U04808; NID:G2558635; PIDN:AAB87093.1; PID:G439861

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 38.1%; Score 45; DB 2; Length 354;

Best Local Similarity 58.8%; Pred. No. 19;

Matches 10; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Qy 2 PYNIVLLNT--FOEFF 16

Db 247 PYNIVIFLETLKFNFF 263

Search completed: September 28, 2004, 09:07:10

Job time : 13.075 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:55:11 ; Search time 6.875 Seconds
(without alignments)
166.624 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APYNIVLLNTQEPFGLNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118	100.0	352	1 CCR5_CERAE	P56493 cercopithec
2	118	100.0	352	1 CCR5_CERAE	O62742 cercopithec
3	118	100.0	352	1 CCR5_CERAE	O62742 cercopithec
4	118	100.0	352	1 CCR5_GORGO	P56439 gorilla gor
5	118	100.0	352	1 CCR5_HUMAN	P51681 homo sapien
6	118	100.0	352	1 CCR5_HYLL	O97883 hylobates l
7	118	100.0	352	1 CCR5_HYLL	O95nc0 hylobates m
8	118	100.0	352	1 CCR5_HYLL	O95nc5 hylobates s
9	118	100.0	352	1 CCR5_MACMU	P72436 macaca mula
10	118	100.0	352	1 CCR5_PANTR	P56440 pan troglod
11	118	100.0	352	1 CCR5_PAFHA	P56441 papio hamad
12	118	100.0	352	1 CCR5_PONPY	O97881 pongo pygma
13	118	100.0	352	1 CCR5_PYGNI	O97880 pygathrix b
14	118	100.0	352	1 CCR5_PYGNE	O97882 pygathrix n
15	118	100.0	352	1 CCR5_TRAPR	O97878 trachypithe
16	118	100.0	352	1 CCR5_TRAPH	O97879 trachypithe
17	108	91.5	354	1 CCR5_MOUSE	P51682 mus musculu
18	105	89.0	354	1 CCR5_RAT	O08556 rattus norv
19	103	87.3	360	1 CCR2_MACMU	O18793 macaca mula
20	103	87.3	374	1 CCR2_HUMAN	P41597 homo sapien
21	87	73.7	373	1 CCR2_RAT	O5193 rattus norv
22	79	66.9	373	1 CCR2_MOUSE	P51683 mus musculu
23	56	47.5	355	1 CCR1_HUMAN	P32246 homo sapien
24	54.5	46.2	1075	1 RPOB_FINTH	P41607 pinus thunb
25	53	44.9	360	1 CCR4_HUMAN	P51679 homo sapien
26	52	44.1	355	1 CCR3_HUMAN	P51677 homo sapien
27	52	44.1	359	1 CCR3_RAT	O54814 rattus norv
28	52	44.1	360	1 CCR4_MOUSE	P51680 mus musculu
29	52	44.1	440	1 ACM2_PANTR	O9n247 pan troglod
30	52	44.1	466	1 ACM2_HUMAN	O9n172 homo sapien
31	52	44.1	466	1 ACM2_MOUSE	O9er24 mus musculu
32	52	44.1	466	1 ACM2_PIG	P06199 sus scrofa
33	52	44.1	466	1 ACM2_RAT	P10980 rattus norv

ALIGNMENTS

RESULT 1

ID	CCR5_CERAE	STANDARD;	PRT;	352 AA.
AC	P56493;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (CCR5).			
GN	CCR5 OR CMKBR5.			
OS	Cercopithecus aethiops (Green monkey) (Grivet).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
OC	Cercopithecinae; Cercopithecus.			
OX	NCBI_TaxID=9534;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=980011387; PubMed=9343222;			
RA	Kuhmann S.B., Platt E.J., Kozak S.L., Kabat D.;			
RT	"Polymorphisms in the CCR5 genes of African green monkeys and mice			
RT	implicate specific amino acids in infections by simian and human			
RT	immunodeficiency viruses.";			
RL	J. Virol. 71:8642-8656(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Murayama Y., Matsunaga S., Inoue-Murayama M.;			
RT	"cDNA sequence of African green monkey CCR-5 chemokine receptor			
RT	gene.";			
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,			
CC	MIP-1-beta and RANTES and subsequently transduces a signal by			
CC	increasing the intracellular calcium ions level. May play a role			
CC	in the control of granulocytic lineage proliferation or			
CC	differentiation.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U83324; AAC51795.1; -			
DR	EMBL; U83325; AAC51796.1; -			
DR	EMBL; AB015944; EAA31328.1; -			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm.1; 1.			
DR	PRINTS; PR00237; GPCRHHODPSN.			
DR	PROSITE; PS00237; G PROTEIN RECEPTOR F1_1; 1.			
DR	PROSITE; PS00362; G-PROTEIN RECEPTOR F1_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;			
KW	Polymorphism.			
FT	DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).			

34	51.5	43.6	355	1	CCR3_CERAE	P56492 cercopithec
35	51.5	43.6	355	1	CCR3_MACMU	P56483 macaca mula
36	51	43.2	355	1	CCR1_MACMU	P56482 macaca mula
37	50	42.4	490	1	ACM4_CHICK	P17200 gallus gall
38	48	40.7	342	1	H182_ARCFU	O28255 archaeoglob
39	48	40.7	359	1	CCR3_MOUSE	P51678 mus musculu
40	48	40.7	484	1	ACM4_XENLA	P30544 xenopus lae
41	48	40.7	589	1	ACM3_MOUSE	O9er23 mus musculu
42	48	40.7	589	1	ACM3_RAT	P08483 rattus norv
43	48	40.7	590	1	ACM3_BOVIN	P41984 bos taurus
44	48	40.7	590	1	ACM3_GORGO	O9n2a3 gorilla gor
45	48	40.7	590	1	ACM3_HUMAN	P20309 homo sapien

FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 FT VARIANT 14 14 N -> Y.
 FT VARIANT 352 352 F -> L.
 SQ SEQUENCE 352 AA; 40561 MW; 7528690C72BC29A CRC64;
 Query Match 100.0%; Score 118; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 4.7e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYINVLNLTQFFFGLNCS 22
 DB 249 APYINVLNLTQFFFGLNCS 270
 RESULT 2
 CKR5_CERY
 ID CKR5_CERY STANDARD; PRT; 352 AA.
 AC Q9TV42.
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCRS).
 GN CCR5 OR CXCR5.
 OS Cercopithecus pygerythrus (Vervet monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=60710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=100;
 EX MEDLINE=99335215; PubMed=10408730;
 RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,
 RA Diop O., Rigoulet J., Haire-Sinoussi F., Fomsgaard A.;
 RT "Mutations in CCR5-coding sequences are not associated with HIV
 RT carrier status in African nonhuman primates."
 RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC -----
 DR EMBL; AF035222; AAD44015.1; --
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00337; G-PROTEIN RECEPTOR_F1_1; 1.
 DR PROSITE; PS00362; G-PROTEIN RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40558 MW; EF17D67C8CC3DB0 CRC64;
 Query Match 100.0%; Score 118; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 4.7e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYINVLNLTQFFFGLNCS 22
 DB 249 APYINVLNLTQFFFGLNCS 270
 RESULT 3
 CKR5_CERTO
 ID CKR5_CERTO STANDARD; PRT; 352 AA.
 AC Q62743; Q62744; Q62745; Q62746;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCRS).
 GN CCR5 OR CXCR5.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Isolate 079; 085, 087, and 089;
 RX MEDLINE=98321155; PubMed=9656999;
 RA Chen Z., Gettiffe A., Ho D.D., Marx P.A.;
 RT "Primary HIV isolates use the CCR5 coreceptor from sooty mangabeys
 RT naturally infected in west Africa: a comparison of coreceptor usage
 RT of primary HIV-1 and HIV-2, and HIVmac."
 RL Virology 246:113-124(1998).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC -----
 DR EMBL; AF035222; AAD44015.1; --
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.

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DR EMBL; AF051902; AAC39830.1; -.
DR EMBL; AF051903; AAC39831.1; -.
DR EMBL; AF051904; AAC39832.1; -.
DR EMBL; AF051905; AAC39833.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT VARIANT 2 2
FT VARIANT 3 3
FT VARIANT 25 25
FT VARIANT 100 100
FT VARIANT 107 107
FT VARIANT 134 134
FT VARIANT 146 146
FT VARIANT 340 340
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;
Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270
RESULT 4
CKR5_GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).
GN CKR5 OR CMKCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
```

```
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF005659; AAB62553.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS00262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT SEQUENCE 352 AA; 40515 MW; D0B6FCB9FE5EAC84 CRC64;
Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270
RESULT 5
CKR5_HUMAN STANDARD; PRT; 352 AA.
AC P51581; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
AC O14708; O15538; Q9UFA4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCRS)
DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
GN CKR5 OR CMKCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96241590; PubMed=8639485;
RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
RT "Molecular cloning and functional expression of a new human
```

CC-chemokine receptor gene.";
 RA Biochemistry 35:3362-3367(1996).
 [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96291862; PubMed=8663314;
 RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
 RA "Molecular cloning and functional characterization of a novel human
 RA CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";
 RA J. Biol. Chem. 271:17161-17166(1996).
 [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96295970; PubMed=8699119;
 RA Conbadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
 RA "Cloning and functional expression of CC CR5, a human monocyte CC
 RA chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
 RA RANTES.";
 RA J. Leukoc. Biol. 60:147-152(1996).
 [4]
 RP SEQUENCE FROM N.A.
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
 RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
 RA Ghoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
 RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
 RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
 RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
 RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
 RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98001387; PubMed=9343222;
 RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RA "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RA implicate specific amino acids in infections by simian and human
 RA immunodeficiency viruses.";
 RA J. Virol. 71:8642-8656(1997).
 [6]
 RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
 RA MEDLINE=98022612; PubMed=9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Kahn B.,
 RA Ho D.D.;
 RA "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
 RA AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 [7]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98049523; PubMed=9388201;
 RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
 RA "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
 RA with 5'-end heterogeneity, dual promoter usage, and evidence for
 RA polymorphisms within the regulatory regions and noncoding exons.";
 RA J. Biol. Chem. 272:30662-30671(1997).
 [8]
 RP SEQUENCE FROM N.A., AND VARIANT ARG-178.
 RA Magliorowski M., Barre-Sinoussi F., Issatras H., Theodorou I.,
 RA Debre P.;
 RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 [9]
 RP SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RA "cDNA clones of human proteins involved in signal transduction
 RA sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 [10]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RA MEDLINE=96260017; PubMed=8649511;
 RA Deng H., Liu R., Elmeier W., Choe S., Umrtaiz D., Burkhardt M.,
 RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
 RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
 RA "Identification of a major co-receptor for primary isolates of
 RA HIV-1.";
 RA Nature 381:661-666(1996).
 [11]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RA MEDLINE=96260018; PubMed=8649512;
 RP

RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
 RA Nagashima K.A., Cayan C., Maddon P.J., Koup R.A., Moore J.P.,
 RA "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
 RA CC-CKR-5.";
 RA Nature 381:667-673(1996).
 [12]
 RP SULFATION
 RA MEDLINE=99189752; PubMed=10089882;
 RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
 RA "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
 RA entry.";
 RA Cell 96:667-676(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and rantes and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation. Acts as co-receptor with CD4 for primary non-
 CC syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1
 CC virus. It promotes Env-mediated fusion of the virus.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Found in promyelocytic cells.
 CC -!- PTM: Sulfation contributes to the efficiency of HIV-1 entry.
 CC -!- PTM: Modified by O-linked glycosylation, but not by N-linked
 CC glycosylation.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 DR EMBL; X91492; CAA62796.1; -
 DR EMBL; U54994; AAC50598.1; -
 DR EMBL; U57840; AAB17071.1; -
 DR EMBL; U95626; AAB57793.1; -
 DR EMBL; U83326; AAC51797.1; -
 DR EMBL; AF011500; AAB65700.1; -
 DR EMBL; AF011501; AAB65701.1; -
 DR EMBL; AF011502; AAB65702.1; -
 DR EMBL; AF011503; AAB65703.1; -
 DR EMBL; AF011505; AAB65705.1; -
 DR EMBL; AF011506; AAB65706.1; -
 DR EMBL; AF011507; AAB65707.1; -
 DR EMBL; AF011508; AAB65708.1; -
 DR EMBL; AF011509; AAB65709.1; -
 DR EMBL; AF011510; AAB65710.1; -
 DR EMBL; AF011511; AAB65711.1; -
 DR EMBL; AF011512; AAB65712.1; -
 DR EMBL; AF011513; AAB65713.1; -
 DR EMBL; AF011514; AAB65714.1; -
 DR EMBL; AF011515; AAB65715.1; -
 DR EMBL; AF011516; AAB65716.1; -
 DR EMBL; AF011517; AAB65717.1; -
 DR EMBL; AF011518; AAB65718.1; -
 DR EMBL; AF011519; AAB65719.1; -
 DR EMBL; AF011520; AAB65720.1; -
 DR EMBL; AF011521; AAB65721.1; -
 DR EMBL; AF011522; AAB65722.1; -
 DR EMBL; AF011523; AAB65723.1; -
 DR EMBL; AF011524; AAB65724.1; -
 DR EMBL; AF011525; AAB65725.1; -
 DR EMBL; AF011526; AAB65726.1; -
 DR EMBL; AF011527; AAB65727.1; -
 DR EMBL; AF011528; AAB65728.1; -
 DR EMBL; AF011529; AAB65729.1; -
 DR EMBL; AF011530; AAB65730.1; -
 DR EMBL; AF011531; AAB65731.1; -
 DR EMBL; AF011532; AAB65732.1; -

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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
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CC EMBL; AF177899; AAK43382.1; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 2; 1.
 DR PROSITE: PS0262; G-PROTEIN RECEPTOR FL 1; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178
 FT BY SIMILARITY.
 FT MOD RES 3 3
 FT SULFATION (BY SIMILARITY).
 FT MOD RES 10 10
 FT SULFATION (BY SIMILARITY).
 FT MOD RES 14 14
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 SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 4.7e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVLLNTFQFFGLNCS 22
 |||||
 DB 249 APYIVLLNTFQFFGLNCS 270

RESULT 8
 CKR5_HYLSY STANDARD; PRT; 352 AA.
 AC Q95NC5;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
 GN CCR5 OR CXKR5.
 OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=9590;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RA "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC or send an email to license@isb-sib.ch).

CC EMBL; AF177884; AAK43367.1; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 2; 1.
 DR PROSITE: PS0262; G-PROTEIN RECEPTOR FL 1; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178
 FT BY SIMILARITY.
 FT MOD RES 3 3
 FT SULFATION (BY SIMILARITY).
 FT MOD RES 10 10
 FT SULFATION (BY SIMILARITY).
 FT MOD RES 14 14
 FT SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 4.7e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVLLNTFQFFGLNCS 22
 |||||
 DB 249 APYIVLLNTFQFFGLNCS 270

RESULT 9
 CKR5_MACMU STANDARD; PRT; 352 AA.
 AC P79436; O02746;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
 GN CCR5 OR CXKR5.
 OS Macaca mulatta (Rhesus macaque),
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544, 9541, 9545;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP SPECIES=M.mulatta;
 RX MEDLINE=97184592; PubMed=9032394;
 RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
 RA Newman W., Gerard N., Gerard C., Sodroski J.;
 RT "Utilization of C-C chemokine receptor 5 by the envelope
 RT glycoproteins of a pathogenic simian immunodeficiency virus,
 RT SIVmac239.";
 RL J. Virol. 71:2522-2527(1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP SPECIES=M.mulatta; STRAIN=Indian macaque;
 RX MEDLINE=97213934; PubMed=9060623;
 RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;

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Query Match      100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APYNIVLLNTFQFFFLNCS 22
        |||||
        249 APYNIVLLNTFQFFFLNCS 270

Db

RESULT 10
CKRS5_PANTR
ID CKR5_PANTR STANDARD; PRT; 352 AA.
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5) (CCR5).
DE CCR5 OR CMKR5.
GN Pan troglodytes (Chimpanzee).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OC NCBI_TaxID=9598;
OX [1]
RN
RN
RN
SEQUENCE FROM N.A.
RP MEDLINE=97268687; PubMed=9108095;
RP Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RP Sharov M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RP Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RA "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RN
RN
SEQUENCE FROM N.A.
RP Zimmerman P.A., Buckler-White A., Alkhatib G.;
RP Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RN
RN
SEQUENCE FROM N.A.
RP MEDLINE=98022612; PubMed=9359654;
RP Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RP Ho D.D.;
RA "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RT AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [4]
RN
RN
SEQUENCE FROM N.A.
RP MEDLINE=97426118; PubMed=9282822;
RP Zacharova V., Zachar V., Goustin A.S.;
RA "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
RT HIV type 1 host.";
RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
RN [5]
RN
RN
SEQUENCE FROM N.A.
RP MEDLINE=98090115; PubMed=9430250;
RP Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RA "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
RT AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RN [6]
RN
RN
SEQUENCE FROM N.A.
RP Zhang Y., Ryder O.A., Zhang Y.;
RA "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny.";
RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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EMBL; AF005663; AAB62557.1; -
DR EMBL; U94329; AAB58446.1; -
DR EMBL; AF011542; AAB65742.1; -
DR EMBL; U97666; AAC51670.1; -
DR EMBL; AF011540; AAB65740.1; -
DR EMBL; U89797; AAC03717.1; -
DR EMBL; AF177894; AAK43377.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PRINTS; PR00237; GPCR_Rhodpsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT TRANSMEM 353 352
FT DISULFID 101 178
FT MOD RES 3 3
FT MOD RES 10 10
FT MOD RES 14 14
FT MOD RES 15 15
FT MOD RES 268 268
FT CARBOHYD 123 123
FT CONFLICT 123 123
T -> S (IN REF. 1).
SEQUENCE 352 AA; 40539 MW; 4A33B69B80FE34C CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVILLNTFQEFFGLNCS 22
DB 249 APYIVILLNTFQEFFGLNCS 270

RESULT 11
ID_CKRS5_PAPHA STANDARD; PRT; 352 AA.
AC P56441;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CNKBR5
OS Papio hamadryas (Hamadryas baboon), and
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9557, 9555;
[1]

SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.,

RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RX MEDLINE=99210133; PubMed=10195758;
RA Sakseena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
RT "Species-specific changes in the CCR5 gene from African and Asian
RT nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=P.anubis;
RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC 1- FUNCTION: Receptor for a C-C type chemokines. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC 1- SUBCELLULAR LOCATION: Integral membrane protein.
CC 1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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EMBL; AF005658; AAB62552.1; -
DR EMBL; AF105287; AAD20556.1; -
DR EMBL; AF105288; AAD20557.1; -
DR EMBL; AF105289; AAD20558.1; -
DR EMBL; AF105290; AAD20559.1; -
DR EMBL; AF023452; AAC63830.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodpsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD RES 3 3
FT MOD RES 10 10
FT MOD RES 14 14
FT MOD RES 15 15
FT MOD RES 268 268
FT CARBOHYD 123 123
FT CONFLICT 123 123
T -> S (IN REF. 1).
SEQUENCE 352 AA; 40489 MW; 5E15049BA1FE8B2 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVILLNTFQEFFGLNCS 22


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Db 249 APYNVLLNTFQEFFGLNCS 270
RESULT 12
CKR5_PONPY STANDARD; PRT; 352 AA.
AC O9781;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKRS.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OC NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075446; AAD19858.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 219 235
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 302 352
FT BY SIMILARITY.
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;
Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNVLLNTFQEFFGLNCS 22
|||||

Db 249 APYNVLLNTFQEFFGLNCS 270
RESULT 13
CKR5_PYGBI STANDARD; PRT; 352 AA.
AC O9780;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKRS.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OC NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075445; AAD19857.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 219 235
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 302 352
FT BY SIMILARITY.
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;
Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNVLLNTFQEFFGLNCS 22
|||||
```

Db 249 APYNIIVLLNTQEFPLNCS 270
|||||

RESULT 14

ID CKR5 PYGNE STANDARD; PRT; 352 AA.
AC 097882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCRS).
GN Pygathrix nemaeus (Dove langur).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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or send an email to license@sb-sib.ch).

EMBL; AF075448; AAD19860.1;
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCRHOODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 1 30
FT DOMAIN 31 58
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 59 68
FT DOMAIN 69 89
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 90 102
FT DOMAIN 103 124
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 125 141
FT DOMAIN 142 166
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 167 198
FT DOMAIN 199 218
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 219 235
FT DOMAIN 261 277
FT TRANSMEM 261 277
FT DOMAIN 278 301
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT TRANSMEM 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B3E861 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APYNIIVLLNTQEFPLNCS 22
|||||
Db 249 APYNIIVLLNTQEFPLNCS 270
|||||

RESULT 15

ID CKR5 TRAFR STANDARD; PRT; 352 AA.
AC 097878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKBR5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; AF075442; AAD19854.1;
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCRHOODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 1 30
FT DOMAIN 31 58
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 59 68
FT DOMAIN 69 89
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 90 102
FT DOMAIN 103 124
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 125 141
FT DOMAIN 142 166
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 167 198
FT DOMAIN 199 218
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 219 235
FT DOMAIN 261 277
FT TRANSMEM 261 277
FT DOMAIN 278 301
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT TRANSMEM 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
DB 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 16
CKR5 TRAPH STANDARD; PRT; 352 AA.
ID CKR5 TRAPH STANDARD; PRT; 352 AA.
AC Q97879;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF075443; AAD19855.1; -
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm1; 1.
CC PRINTS: PR00237; GPCR_RHODOPSIN.
CC PROSITE: PS00237; G_PROTEIN_RECP_F1_1;
CC PROSITE: PS00262; G_PROTEIN_RECP_F1_2;
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 31 58 1 (POTENTIAL).
FT TRANSMEM 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938F CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
DB 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 17
CKR5 MOUSE STANDARD; PRT; 354 AA.
ID CKR5 MOUSE STANDARD; PRT; 354 AA.
AC P51682; O35313; O35891; P97308; P97405; Q61867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
DE alpha receptor).
GN CKR5 OR CMKBR5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SvJ; TISSUE=Spleen;
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT 1alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9";
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96278910; PubMed=8662890;
RA Meyer A., Coyly A.J., Proudfoot A.E.L., Wells T.N.C., Power C.A.;
RT "Cloning and characterization of a novel murine macrophage
RT inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 271:14445-14451(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=129/Ola;
RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CKR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=129;
RX MEDLINE=97404635; PubMed=9261347;
RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
RT "Two distinct CKR5 domains can mediate coreceptor usage by human
RT immunodeficiency virus type 1.";
RL J. Virol. 71:6305-6314(1997).
RN [6]
RP SEQUENCE FROM N.A.
RA Guo B., Kuno K., Harada A., Matsushima K.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC but not in nonhematopoietic cell lines.

QY 2 PYNIVLLNTFQFFFLNNCS 22
 DB 252 PYNIVLLNTFQFFFLNNCS 272

RESULT 19

CKR2 MACMU STANDARD; PRT; 360 AA.
 AC 018793;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 2 (C-CR-2) (CCR-2) (CCR2)
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
 GN CCR2 OR CMKBR2.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 receptors.";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 CC -1- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level."
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=B; IsoId=O18793-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=O18793-2; Sequence=Not described;
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AF013958; AAD11572.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
 KW Alternative splicing.
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 43 70 1 (POTENTIAL).
 FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 81 100 2 (POTENTIAL).
 FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 115 136 3 (POTENTIAL).
 FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 154 178 4 (POTENTIAL).
 FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 226 5 (POTENTIAL).
 FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 244 268 6 (POTENTIAL).
 FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 286 309 7 (POTENTIAL).
 FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 14 14 N-LINKED (GLCNAC...) (POTENTIAL).
 FT MOD_RES 26 26 SULFATION (BY SIMILARITY).

FT DISULFID 113 190 BY SIMILARITY.
 SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;
 Query Match 87.3%; Score 103; DB 1; Length 360;
 Best Local Similarity 90.0%; Pred. No. 1.1e-08;
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFQFFFLNNC 21
 DB 258 PYNIVLLNTFQFFFLNNC 277

RESULT 20

CKR2 HUMAN STANDARD; PRT; 374 AA.
 AC P41597;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE C-C chemokine receptor type 2 (C-CR-2) (CCR-2) (CCR2)
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
 GN CCR2 OR CMKBR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94195821; PubMed=8146186;
 RA Charo I.F., Myers S.J., Herman A., Francis C., Connolly A.J.,
 RA Coughlin S.R.;
 RT "Molecular cloning and functional expression of two monocyte
 RT chemoattractant protein 1 receptors reveals alternative splicing of
 RT the carboxyl-terminal tails.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94324942; PubMed=8048929;
 RA Yanagani S., Tokuda Y., Ishii K., Tanaka H., Endo N.;
 RT "cDNA cloning and functional expression of a human monocyte
 RT chemoattractant protein 1 receptor.";
 RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97150864; PubMed=8995400;
 RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;
 RT "Organization and differential expression of the human monocyte
 RT chemoattractant protein 1 receptor gene. Evidence for the role of the
 RT carboxyl-terminal tail in receptor trafficking.";
 RL J. Biol. Chem. 272:1038-1045(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
 RA Nham M., Farnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
 RA Gnoj L., la Baside M., Kaplan N., Greco T., Touchman J.,
 RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
 RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
 RA Solinsky K., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
 RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
 RN Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.
 RA Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,
 RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
 RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SULFATION OF TYR-26, AND N-GLYCOSYLATION.
 RX MEDLINE=20501139; PubMed=11046064;
 RA Proebrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
 RA Chakravarty L., Kolattukudy P.E.;
 RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
 RT has tyrosine sulfation in a conserved extracellular N-terminal
 RT region."

RN RP SEQUENCE FROM N.A.
RX MEDLINE=93240122; PubMed=7683036;
RA Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
EA Murphy P.M.;
RT Structure and functional expression of the human macrophage
RL inflammatory protein 1 alpha/FANTES receptor.";
J. Exp. Med. 177:1421-1427(1993).
[3]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Monocytes;
RX MEDLINE=94092629; PubMed=7505609;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT Molecular cloning of cDNAs encoding a LD78 receptor and putative
RL leukocyte chemotactic peptide receptors.";
Int. Immunol. 5:1239-1249(1993).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-
beta or MCP-1 and subsequently transduces a signal by increasing
the intracellular calcium ions level. Responsible for affecting
stem cell proliferation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed in different hematopoietic
cells.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC
EMBL; L09230; AAA58408.1; -
EMBL; L10918; AAA36543.1; -
EMBL; D10925; BAA01723.1; -
PIR; A45177; A45177.
Genew; HGNC:1602; CCR1.
MIM; 601159; -
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004950; P:chemokine receptor activity; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0006935; P:chemotaxis; TAS.
GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.
GO; GO:0006955; P:immune response; TAS.
GO; GO:0006954; P:inflammatory response; TAS.
GO; GO:0007125; P:invasive growth; TAS.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
DR PRINTS; P300237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
FT DOMAIN 61 64 2 (POTENTIAL).
FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD N-LINKED (GLCNAC. .) (POTENTIAL).
[2]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=93240122; PubMed=7683036;
RA Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
EA Murphy P.M.;
RT Structure and functional expression of the human macrophage
RL inflammatory protein 1 alpha/FANTES receptor.";
J. Exp. Med. 177:1421-1427(1993).
[3]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Monocytes;
RX MEDLINE=94092629; PubMed=7505609;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT Molecular cloning of cDNAs encoding a LD78 receptor and putative
RL leukocyte chemotactic peptide receptors.";
Int. Immunol. 5:1239-1249(1993).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-
beta or MCP-1 and subsequently transduces a signal by increasing
the intracellular calcium ions level. Responsible for affecting
stem cell proliferation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed in different hematopoietic
cells.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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send an email to license@isb-sib.ch)
CC
EMBL; L09230; AAA58408.1; -
EMBL; L10918; AAA36543.1; -
EMBL; D10925; BAA01723.1; -
PIR; A45177; A45177.
Genew; HGNC:1602; CCR1.
MIM; 601159; -
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004950; P:chemokine receptor activity; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0006935; P:chemotaxis; TAS.
GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.
GO; GO:0006955; P:immune response; TAS.
GO; GO:0006954; P:inflammatory response; TAS.
GO; GO:0007125; P:invasive growth; TAS.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
DR PRINTS; P300237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
FT DOMAIN 61 64 2 (POTENTIAL).
FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD N-LINKED (GLCNAC. .) (POTENTIAL).
us-10-084-813-14.rsp
Page 16

FT SQ SEQUENCE 360 AA; 41402 MW; 51EBE12AD1FAFABF CRC64; /FTID=VAR_010670.
 Query Match 44.9%; Score 53; DB 1; Length 360;
 Best Local Similarity 52.4%; Pred. No. 0.71;
 Matches 11; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 2 PYNIVLLNTQEFEGNNS 22
 D5 257 PYNIVLFLTLVLEVLQDCT 277

RESULT 26
 CCR3 HUMAN
 ID CCR3 HUMAN STANDARD; PRT: 355 AA.
 AC P51677; Q15748; Q86WD2; Q9ULY8;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-VAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
 DE (CCR3) (Eosinophil eotaxin receptor).
 GN CCR3 OR CCR3
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Monocytes;
 RA MEDLINE=95334056; PubMed=7622448;
 RX Combadere C., Ahuja S.K., Murphy P.M.;
 RT "Cloning and functional expression of a human eosinophil CC chemokine
 receptor.";
 RL J. Biol. Chem. 270:16491-16494(1995).
 [2]
 RP ERRATUM.
 RA Combadere C., Ahuja S.K., Murphy P.M.;
 RL J. Biol. Chem. 270:30235-30235(1995).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96235044; PubMed=8642344;
 RA Daugherty B.L., Siciliano S.J., Demartino J.A., Malkowitz L.,
 RA Sirotna A., Springer M.S.;
 RT "Cloning, expression, and characterization of the human eosinophil
 eotaxin receptor.";
 RL J. Exp. Med. 183:2349-2354(1996).
 [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96281895; PubMed=8676064;
 RA Ponath P.D., Qin S., Post T.W., Wang J., Wu L., Gerard N.P.,
 RA Newman W., Gerard C., Mackay C.R.;
 RT "Molecular cloning and characterization of a human eotaxin receptor
 expressed selectively on eosinophils.";
 RL J. Exp. Med. 183:2737-2748(1996).
 [5]
 RP SEQUENCE FROM N.A.
 RA Xiao L., Weiss S., Oari S., Rudolph D., Hodge T., Lal R.;
 RT "Partial resistance to infection by syncytium-inducing primary HIV-1
 in exposed uninfected individuals homozygous for CCR5 32bp deletion.";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 [6]
 RP SEQUENCE FROM N.A., AND VARIANT SER-218.
 RX MEDLINE=21040311; PubMed=11196669;
 RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
 RA Hirai K., Tokunaga K.;
 RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
 RL Genes Immun. 1:97-104(1999).
 [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22074933; PubMed=12079287;
 RA Vilh S., Dayhoff D.E., Wang C.E., Inam Z., Ehrenberg P.K.,
 RA Michael N.L.;
 RT "Transcription regulation of human chemokine receptor CCR3: evidence

RT for a rare TATA-less promoter structure conserved between Drosophila
 and humans.";
 RL Genomics 80:86-95(2002).
 [8]
 RP SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 [9]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Lung, and Testis;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Bhat N.K.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
 CC eotaxin-3, MCP-3, MCP-4, RANTES and MIP-1 delta. Subsequently
 CC transduces a signal by increasing the intracellular calcium ions
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: In eosinophils as well as trace amounts in
 CC neutrophils and monocytes.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC -----
 CC EMBL: U28694; AAC50469.1; -
 CC EMBL: U51241; AAB16831.1; -
 CC EMBL: U49727; AAB09726.1; -
 CC EMBL: AF026535; AAB82589.1; -
 CC EMBL: AB023887; AAB86964.1; -
 CC EMBL: AF247361; AAL85154.1; -
 CC EMBL: AY221092; AAO65970.2; -
 CC EMBL: BC033514; AAB33514.1; -
 CC F01: G02436; G02436
 CC Genbank; HGNC:1604; CCR3.
 CC MIM: 601268; -
 CC GO: GO:0005887; C: integral to plasma membrane; TAS.
 CC GO: GO:0004950; F: chemokine receptor activity; TAS.
 CC GO: GO:0007155; P: cell adhesion; TAS.
 CC GO: GO:0006968; P: cellular defense response; TAS.
 CC GO: GO:0005935; P: chemotaxis; TAS.
 CC GO: GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
 CC GO: GO:0007188; P: G-protein signaling, coupled to CAMP nucleoside; TAS.
 CC GO: GO:0006954; P: inflammatory response; TAS.
 CC GO: GO:0007125; P: invasive growth; TAS.
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm 1; 1.
 CC PRINTS: PR00237; GPCRHOOPS.
 CC -----

DR PROSITE; PS00237; G PROTEIN RECP Fl_1; 1.
DR PROSITE; PS0262; G PROTEIN RECP Fl_2; 1.
KW G-protein coupled receptor; Transmembrane; Polymorphism.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 62 1 (POTENTIAL).
FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 93 2 (POTENTIAL).
FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT VARIANT 218 218 the population; may show reduced activity.
FT CONFLICT 276 276 S -> T (IN REF. 4 AND 5).
SQ SEQUENCE 355 AA; 41043 MW; E95DCD7A6C643874 CRC64;
Query Match 44.1%; Score 52; DB 1; Length 355;
Best Local Similarity 40.0%; Pred. No. 1;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 2 PYNVILLNLTFOEPPFLNLC 21
|||:||||:|:|:
Db 254 PYNVAILLSSYSILFGNDC 273
RESULT 27
CKR3_RAT STANDARD; PRT; 359 AA.
AC O54814; O55169;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
DE (CKR3).
GN CKR3 OR CMK3R3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=Wistar; TISSUE=Spleen;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafianca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RA "Chemokine receptor expression in cultured glia and rat experimental
RA allergic encephalomyelitis";
RT J. Neuroimmunol. 86:1-12(1998).
RL [2]
SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RX Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in spleen but not in astrocytes or
CC microglia.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF003954; AAC03337.1; -
CC EMBL; Y13400; CRA73830.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOODPSN.
DR PROSITE; PS00237; G PROTEIN RECP Fl_1; 1.
DR PROSITE; PS0262; G PROTEIN RECP Fl_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 64 POTENTIAL.
FT DOMAIN 65 74 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 75 95 POTENTIAL.
FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 113 133 POTENTIAL.
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 POTENTIAL.
FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 227 POTENTIAL.
FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 264 POTENTIAL.
FT DOMAIN 265 288 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 289 309 POTENTIAL.
FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 164 164 F -> L (IN REF. 2).
SQ SEQUENCE 359 AA; 41643 MW; 880F682984F501DA CRC64;
Query Match 44.1%; Score 52; DB 1; Length 359;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 2 PYNVILLNLTFOEPPFLNLC 21
|||:||||:|:|:
Db 258 PYNVILLLSAFHSFLETSC 277
RESULT 28
CKR4_MOUSE STANDARD; PRT; 360 AA.
AC P51880;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 4 (C-C CKR-4) (CC-CKR-4) (CCR-4) (CCR4).
GN CKR4 OR CMK4R4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96136324; PubMed=8573157;
RA Hoogwerf A.J., Black D., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RA "Molecular cloning of murine CC CKR-4 and high affinity binding of
RA chemokines to murine and human CC CKR-4";
RT Biochem. Biophys. Res. Commun. 218:337-343(1996).
RL [2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Cytotoxic T-cell;
RX MEDLINE=97335974; PubMed=9192769;
RA Youn B.-S., Kim S.-H., Lyu M.-S., Kozak C.A., Taub D.D., Kwon B.S.;
RA "Molecular cloning and characterization of a cDNA, CHEM1, encoding a
RA chemokine receptor with a homology to the human C-C chemokine
RA receptor, CCR-4";
RT Blood 89:4448-4460(1997).
RL [3]
FUNCTION.

RX MEDLINE=20273981; PubMed=10811868;
 RA Buser R., Conquet F., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
 RT "A key role for CC chemokine receptor 4 in lipopolysaccharide-induced
 RL endotoxic shock";
 RL J. Exp. Med. 191:1755-1764(2000).
 CC -!- FUNCTION: High affinity receptor for the C-C type chemokines
 CC TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is
 CC mediated by G(i) proteins which activate a phosphatidylinositol-
 CC calcium second messenger system. Could play a role in
 CC lipopolysaccharide (LPS)-induced endotoxic shock. In the CNS,
 CC could mediate hippocampal-neuron survival.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in the thymus, macrophages and T-
 CC and B-cells.
 CC -!- DEVELOPMENTAL STAGE: Low expression at 7.5 dpc and 12.5 dpc in the
 CC yolk sac.
 CC -!- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
 CC PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
 CC BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2 (BY SIMILARITY).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; X90862; CRA62372.1; -;
 DR EMBL; U15208; AAA92582.1; -;
 DR PIR; JC4587; JC4587.
 DR MGD; MGI:107824; Ccr4.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IMP.
 DR GO; GO:006935; P:chemotaxis; IMP.
 DR GO; GO:006954; P:inflammatory response; IMP.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PS00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECF_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation.
 FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 40 67 1 (POTENTIAL).
 FT DOMAIN 68 77 2 (POTENTIAL).
 FT TRANSSEM 78 98 2 (POTENTIAL).
 FT DOMAIN 99 111 3 (POTENTIAL).
 FT TRANSSEM 112 133 3 (POTENTIAL).
 FT DOMAIN 134 150 4 (POTENTIAL).
 FT TRANSSEM 151 175 4 (POTENTIAL).
 FT DOMAIN 176 206 5 (POTENTIAL).
 FT TRANSSEM 207 226 5 (POTENTIAL).
 FT DOMAIN 227 242 6 (POTENTIAL).
 FT TRANSSEM 243 267 6 (POTENTIAL).
 FT DOMAIN 268 284 7 (POTENTIAL).
 FT TRANSSEM 285 308 7 (POTENTIAL).
 FT DOMAIN 309 360 7 (POTENTIAL).
 FT TRANSSEM 343 346 POLY-SER.
 FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 110 187 BY SIMILARITY.
 FT CONFLICT 4 4 T -> I (IN REF. 2).
 FT CONFLICT 145 145 S -> T (IN REF. 2).
 FT CONFLICT 181 181 E -> Q (IN REF. 2).
 FT CONFLICT 205 205 E -> D (IN REF. 2).
 FT CONFLICT 221 221 W -> C (IN REF. 2).
 FT CONFLICT 241 241 V -> L (IN REF. 2).
 FT CONFLICT 246 246 G -> A (IN REF. 2).
 FT CONFLICT 293 293 G -> A (IN REF. 2).
 FT CONFLICT 311 311 F -> S (IN REF. 2).
 SQ SEQUENCE 360 AA; 41462 MW; 97BDB8C96D259AE3 CRC64;

Query Match 44.1%; Score 52; DB 1; Length 360;
 Best Local Similarity 47.6%; Pred. No. 1;
 Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 2 PYNIVLLNTQEFFGLNCS 22
 DB 257 PYNVLFLETLVELEVLQDCT 277
 RESULT 29
 ACM2_PANTR
 ID ACM2_PANTR STANDARD; PRT; 440 AA.
 AC Q9NZAF;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Muscarinic acetylcholine receptor M2 (Fragment).
 GN CHRM2.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 ON NCBI_TaxID=9598;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Isolate 220;
 RA Kitano T., Kobayakawa H., Saitou N.;
 RL "Silver project";
 RT Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
 CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
 CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
 CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS
 CC ADENYLATE CYCLASE INHIBITION.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AB041392; BAA94477.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECF_F1_2; 1.
 DR Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
 KW Phosphorylation; Multigene family; G-protein coupled receptor.
 FT NON_TER 1 1
 FT TRANSSEM <1 19 1 (POTENTIAL).
 FT DOMAIN 20 33 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 34 54 2 (POTENTIAL).
 FT DOMAIN 55 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 72 93 3 (POTENTIAL).
 FT DOMAIN 94 113 4 (POTENTIAL).
 FT TRANSSEM 114 136 4 (POTENTIAL).
 FT DOMAIN 137 158 5 (POTENTIAL).
 FT TRANSSEM 159 181 5 (POTENTIAL).
 FT DOMAIN 182 362 6 (POTENTIAL).
 FT TRANSSEM 363 383 6 (POTENTIAL).
 FT DOMAIN 384 397 7 (POTENTIAL).
 FT TRANSSEM 398 417 7 (POTENTIAL).
 FT DOMAIN 418 440 7 (POTENTIAL).
 FT DISULFID 70 150 BY SIMILARITY.
 FT MOD_RES 420 420 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 424 424 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 439 439 PHOSPHORYLATION (POTENTIAL).
 SQ SEQUENCE 440 AA; 48854 MW; 12B0324E13D37DDF CRC64;

Query Match 44.1%; Score 52; DB 1; Length 440;
Best Local Similarity 66.7%; Pred. No. 1.2;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTF 12
|||:|:|:|:|
Db 375 APYNVMLNTF 386

RESULT 30
ACM2 HUMAN STANDARD; PRT; 466 AA.
ID ACM2_HUMAN
AC P08172; O9P1X9;
DT 01-AUG-1998 (Rel. 08, Created)
DT 01-AUG-1998 (Rel. 08, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Muscarinic acetylcholine receptor M2.
GN CHRM2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87263421; PubMed=3037705;
RA Bonner T.I., Buckley N.J., Young A.C., Brann M.R.;
RT "Identification of a family of muscarinic acetylcholine receptor
genes.";
RL Science 237:527-532 (1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166632; PubMed=3443095;
RA Peralta E.G., Ashkenazi A., Winslow J.W., Smith D.H.,
RA Ramachandran J., Capon D.J.;
RT "Distinct primary structures, ligand-binding properties and tissue-
specific expression of four human muscarinic acetylcholine
receptors.";
RL EMBO J. 6:3923-3929 (1987).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
RT "cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 27-466 FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver project.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE.
CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS
CC ADENYLATE CYCLASE INHIBITION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; M16404; AA51570.1; -.
DR EMBL; X15264; CAA33335.1; -.
DR EMBL; AF498916; AAM18939.1; -.
DR EMBL; AB041391; BAA94476.1; -.
DR PIR; S10126; S10126.
PDB; 1LUB; 19-JUN-02.

Genew; HGNC:1951; CHRM2.
MIM; 118493; -.
GO; GO:0005887; C: integral to plasma membrane; TAS.
GO; GO:0004981; F: muscarinic acetylcholine receptor activity; TAS.
GO; GO:0007188; P: G-protein signaling, coupled to cAMP nucleo. .; TAS.
GO; GO:0007207; P: muscarinic acetyl choline receptor, phospho. .; TAS.
GO; GO:0007339; P: neurogenesis; TAS.
GO; GO:0009405; P: pathogenesis; TAS.
GO; GO:0008016; P: regulation of heart rate; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW Phosphorylation; Multigene family; G-protein coupled receptor;
KW 3D-structure.
FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 23 45 1 (POTENTIAL).
FT DOMAIN 46 59 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 60 80 2 (POTENTIAL).
FT DOMAIN 81 97 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 98 119 3 (POTENTIAL).
FT DOMAIN 120 139 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 162 4 (POTENTIAL).
FT DOMAIN 163 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 207 5 (POTENTIAL).
FT DOMAIN 208 388 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 389 409 6 (POTENTIAL).
FT DOMAIN 410 423 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 424 443 7 (POTENTIAL).
FT DOMAIN 444 466 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 2 2 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 9 9 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 96 176 BY SIMILARITY.
FT MOD_RES 446 446 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 450 450 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 465 465 PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE 466 AA; 51715 MW; 2FC2FD7748C22BEC CRC64;

Query Match 44.1%; Score 52; DB 1; Length 466;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTF 12
|||:|:|:|:|
Db 401 APYNVMLNTF 412

RESULT 31
ACM2 MOUSE STANDARD; PRT; 466 AA.
ID ACM2_MOUSE
AC Q9E3Z4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Muscarinic acetylcholine receptor M2.
GN CHRM2 OR CHRM-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Gomez J., Weiss J.;
RT "Isolation, sequence and functional expression of mouse muscarinic
acetylcholine receptor genes.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS


```
FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 5 (POTENTIAL).
FT TRANSMEM 198 223 6 (POTENTIAL).
FT DOMAIN 224 239 7 (POTENTIAL).
FT TRANSMEM 240 264 8 (POTENTIAL).
FT DOMAIN 265 281 9 (POTENTIAL).
FT TRANSMEM 282 305 10 (POTENTIAL).
FT DOMAIN 306 355 11 (POTENTIAL).
FT CARBOHYD 5 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
SQ SEQUENCE 355 AA; 41198 MW; 41CAEA7CC19D23D4 CRC64;

Query Match 43.2%; Score 51; DB 1; Length 355;
Best Local Similarity 45.0%; Pred. No. 1-4;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQBFQFGLNCC 21
    |||: ||: |||: ||:
Db 254 PYNLTSLISVQBFQFLFHLCC 273

RESULT 37
ACM4 CHICK STANDARD; PRT; 490 AA.
AC P17200;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Muscarinic acetylcholine receptor M4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90153912; PubMed=2154460;
RA Tietje K.M., Goldman P.S., Nathanson N.M.;
RT "Cloning and functional analysis of a gene encoding a novel
muscarinic acetylcholine receptor expressed in chick heart and
brain."
RL J. Biol. Chem. 265:2828-2834 (1990).
CC -!- FUNCTION: The muscarinic acetylcholine receptor mediates various
cellular responses, including inhibition of adenylyl cyclase,
breakdown of phosphoinositides and modulation of potassium
channels through the action of G proteins. Primary transducing
effect is inhibition of adenylyl cyclase. May couple to multiple
functional responses in cell lines.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in heart and brain.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
CC EMBL; J05218; AAA48563.1; -
CC FIR; A35546; A35546.
CC HSP; P02699; 1BOU.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC -----

KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW Phosphorylation; Multigene family; G-protein coupled receptor.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 64 1 (POTENTIAL).
FT DOMAIN 65 78 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 79 99 2 (POTENTIAL).
FT DOMAIN 100 116 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 117 138 3 (POTENTIAL).
FT DOMAIN 139 158 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 159 181 4 (POTENTIAL).
FT DOMAIN 182 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 226 5 (POTENTIAL).
FT DOMAIN 227 412 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 413 433 6 (POTENTIAL).
FT DOMAIN 434 447 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 448 467 7 (POTENTIAL).
FT DOMAIN 468 490 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 115 195 BY SIMILARITY.
SQ SEQUENCE 490 AA; 54937 MW; 2CDFB5FA7D2298E CRC64;

Query Match 42.4%; Score 50; DB 1; Length 490;
Best Local Similarity 61.5%; Pred. No. 2.8;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQBF 14
    |||: ||: |||: ||:
Db 426 PYNVNLINTFCE 438

RESULT 38
HI82_ARCFU STANDARD; PRT; 342 AA.
ID HI82_ARCFU
AC 028255;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histidinol-phosphate aminotransferase 2 (EC 2.6.1.9) (Imidazole
acetol-phosphate transaminase 2).
OS Archaeoglobus fulgidus.
GN HISC2 OR AF2024.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., DiAndrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370 (1997).
CC -!- CATALYTIC ACTIVITY: L-histidinol-phosphate + 2-oxoglutarate = 3-
(imidazol-4-yl)-2-oxopropyl phosphate + L-glutamate.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: Histidine biosynthesis; seventh step.
CC -!- SIMILARITY: Belongs to class-II of pyridoxal-phosphate-dependent
amintotransferases. Histidinol-phosphate aminotransferases
subfamily.
CC -----
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DR EMBL; AF000963; AAB89229.1; --
 DR PIR; G69502; G69502.
 DR HSP; P06986; 1FG7.
 DR TIGR; AF2024; --
 DR HAMAP; MF_01023; --; 1.
 DR InterPro; IPR004839; AminoTrans_I/II.
 DR InterPro; IPR001917; AminoTrans_II.
 DR InterPro; IPR005861; HisP_AminoTrans.
 DR Pfam; PF00155; aminotran_1.2; 1.
 DR TIGRFAMs; TIGR01141; hisC_1.
 DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; FALSE NEG.
 KW Histidine biosynthesis; Transferase; AminoTransferase;
 FT Pyridoxal phosphate; Complete proteome.
 FT BINDING 206 206 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 342 AA; 38941 MW; F71DA0FD66191D80 CRC64;

Query Match 40.7%; Score 48; DB 1; Length 342;
 Best Local Similarity 50.0%; Pred. No. 4.1; Mismatches 3; Indels 0; Gaps 0;
 Matches 8; Conservative 5;

QY 3 YNIVLLNTFOEFFGL 18
 ||::||:|:|:|
 Db 195 YNNLVLSFSKFFGL 210

RESULT 39

CC CRK3_MOUSE
 AC P51678;
 DT 01-OCT-1996 (Rel. 34; Created)
 DT 01-OCT-1996 (Rel. 34; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Probable C-C chemokine receptor type 3 (C-C CRK-3) (CC-CRK-3) (CCR-3)
 DE (CCR3) (Macrophage inflammatory protein-1 alpha receptor-like
 DE 2) (MIP-1 alpha RL2).
 GN CRK3 OR CMKBR3 OR CMKBR1L2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RC MEDLINE=96072806; PubMed=7594543;
 RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
 RA Gerard C.;
 RA "Molecular characterization of two murine eosinophil beta chemokine
 RT receptors.";
 RL J. Immunol. 155:5299-5305(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RC MEDLINE=95340546; PubMed=7542241;
 RA Gao J.-L., Murphy P.M.;
 RA "Cloning and differential tissue-specific expression of three mouse
 RT beta chemokine receptor-like genes, including the gene for a
 RT functional macrophage inflammatory protein-1 alpha receptor.";
 RL J. Biol. Chem. 270:17494-17501(1995).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
 CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Detected in skeletal muscle and in trace
 CC amounts in leukocytes.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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DR EMBL; U29677; AAA86118.1; --
 DR EMBL; U28406; AAA89155.1; --
 DR MGD; MG1:104616; Ccr3.
 DR GO; GO:0016493; F1C-C chemokine receptor activity; IDA.
 DR GO; GO:0005515; F1:protein binding; IPI.
 DR GO; GO:0006935; P1:chemotaxis; IDA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN

DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 38
 FT TRANSMEM 39 64
 FT DOMAIN 65 68
 FT TRANSMEM 69 95
 FT DOMAIN 96 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 150
 FT TRANSMEM 151 175
 FT DOMAIN 176 201
 FT TRANSMEM 202 227
 FT DOMAIN 228 243
 FT TRANSMEM 244 268
 FT DOMAIN 269 285
 FT TRANSMEM 286 309
 FT DOMAIN 310 359
 FT DISULFID 110 187
 FT CONFLICT 270 270 R -> S (IN REF. 2).
 SQ SEQUENCE 359 AA; 41825 MW; AC11ED6E283CEAF CRC64;

Query Match 40.7%; Score 48; DB 1; Length 359;
 Best Local Similarity 45.0%; Pred. No. 4.3;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNCC 21
 ||::||:|:|:|
 Db 259 PYNVLVLSAFHRTLETSC 277

RESULT 40

CC ACN4_XENLA
 ID ACN4_XENLA STANDARD; PRT; 484 AA.
 AC P30524;
 DT 01-APR-1993 (Rel. 25; Created)
 DT 01-APR-1993 (Rel. 25; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Muscarinic acetylcholine receptor M4.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95010703; PubMed=7925970;
 RA Herrera L., Carvallo P., Antonelli M., Olate J.;
 RT "Cloning of a Xenopus laevis muscarinic receptor encoded by an
 RT intronless gene.";
 RL FEBS Lett. 352:175-179(1994).
 CC -1- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
 CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
 CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS

```
CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS
CC INHIBITION OF ADENYLATE CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X65865; CAA46694.1; --
CC PIR; S48657; S48657.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
CC Phosphorylation; Multigene family; G-protein coupled receptor.
CC DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 33 55 1 (POTENTIAL).
CC DOMAIN 56 69 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 70 90 2 (POTENTIAL).
CC DOMAIN 91 107 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 108 129 3 (POTENTIAL).
CC DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 150 172 4 (POTENTIAL).
CC DOMAIN 173 194 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 195 217 5 (POTENTIAL).
CC DOMAIN 218 406 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 407 427 6 (POTENTIAL).
CC DOMAIN 428 441 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 442 461 7 (POTENTIAL).
CC DOMAIN 462 484 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC DISULFID 106 186 BY SIMILARITY.
CC SEQUENCE 484 AA; 54135 MW; D83BD856DE302BE8 CRC64;

Query Match 40.7%; Score 48; DB 1; Length 484;
Best Local Similarity 63.6%; Pred. No. 5.8;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PYNIVLLINTF 12
Db 420 PYNVMVLINTF 430
||||:|:|:|
```

Search completed: September 28, 2004, 09:04:07
Job time : 7.875 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2004, 08:56:16 ; Search time 35.2 Seconds
(without alignments)
197.199 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APYNIVLLNTFQEFFGLNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	333	4	014694
2	118	100.0	334	6	Q9TUQ7
3	118	100.0	339	4	Q9UN24
4	118	100.0	339	4	Q9UN26
5	118	100.0	339	4	Q9UN23
6	118	100.0	339	4	Q9UN37
7	118	100.0	339	4	Q9UN25
8	118	100.0	339	4	Q9UN27
9	118	100.0	339	4	Q9UT9
10	118	100.0	339	6	Q9TQW0
11	118	100.0	339	6	Q9TUX1
12	118	100.0	339	6	Q9TUT9
13	118	100.0	339	6	Q9TUX8
14	118	100.0	339	6	Q9TUT4
15	118	100.0	339	6	Q9TUX9
16	118	100.0	339	6	Q9TSQ1

17	118	100.0	339	6	Q9TUUS	Q9tuus cercopithec
18	118	100.0	339	6	Q9TQW4	Q9tqw4 pan troglod
19	118	100.0	339	6	Q9TQW4	Q9tqw4 pan troglod
20	118	100.0	339	6	Q9TQW7	Q9tqw7 cercopithec
21	118	100.0	339	6	Q9TUQ5	Q9tuq5 erythrocebu
22	118	100.0	339	6	Q9TUR9	Q9tur9 saguinus sp
23	118	100.0	339	6	Q9TQT0	Q9tqt0 macaca fasc
24	118	100.0	339	6	Q9TUT9	Q9tut9 macaca mula
25	118	100.0	339	6	Q9TSN2	Q9tsn2 macaca fasc
26	118	100.0	339	6	Q9TUR6	Q9tur6 cercopithec
27	118	100.0	339	6	Q9TQV6	Q9tqv6 colobus gue
28	118	100.0	339	6	Q9TUQ9	Q9tuq9 cercopithec
29	118	100.0	339	6	Q9TSN3	Q9tsn3 macaca fasc
30	118	100.0	339	6	Q9TUU7	Q9tuu7 macaca fusc
31	118	100.0	339	6	Q9TQV0	Q9tqv0 papio papio
32	118	100.0	339	6	Q9TQUS	Q9tqus cercopithec
33	118	100.0	339	6	Q9TUS7	Q9tus7 papio papio
34	118	100.0	339	6	Q9TUT7	Q9tut7 pan troglod
35	118	100.0	339	6	Q9TUM3	Q9tum3 pongo pygma
36	118	100.0	339	6	Q9TUS5	Q9tus5 papio papio
37	118	100.0	339	6	Q9TUU0	Q9tuu0 macaca mula
38	118	100.0	339	6	Q9TQV2	Q9tqv2 papio papio
39	118	100.0	339	6	Q9TQV3	Q9tqv3 cercopithec
40	118	100.0	339	6	Q9TUQ8	Q9tuq8 cercopithec
41	118	100.0	339	6	Q9TUR3	Q9tur3 erythrocebu
42	118	100.0	339	6	Q9TQW2	Q9tqw2 pongo pygma
43	118	100.0	339	6	Q9TUU1	Q9tuu1 macaca mula
44	118	100.0	339	6	Q9TUT6	Q9tut6 macaca neme
45	118	100.0	339	6	Q9TQX2	Q9tqx2 erythrocebu

ALIGNMENTS

RESULT 1

014694 PRELIMINARY; PRT; 333 AA.

AC 014694;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011504; AAB65704.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 333
SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

Query Match 100.0%; Score 118; DB 4; Length 333;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22

|||||

Db 230 APYINVLLNTFQEPFGLNCS 251

RESULT 2

Q9TUQ7 PRELIMINARY; PRT; 334 AA.

AC Q9TUQ7; 1

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Erythrocybus patas (Red guenon) (Husar).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Erythrocybus.

OX NCBI_TaxID=9538;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

species."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF162049; AAD47804.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_Rhodpsn.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

DR Receptor.

FT NON_TER 1 1

FT NON_TER 334 334

SQ SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 334;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFQEPFGLNCS 22

Db 237 APYINVLLNTFQEPFGLNCS 258

RESULT 3

Q9UN24 PRELIMINARY; PRT; 339 AA.

AC Q9UN24; 1

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

species."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161919; AAD47676.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_Rhodpsn.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

DR Receptor.

FT NON_TER 1 1

FT NON_TER 334 334

SQ SEQUENCE 339 AA; 39162 MW; A5C369FB0529F4B CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFQEPFGLNCS 22

Db 242 APYINVLLNTFQEPFGLNCS 263

RESULT 5

Q9UN23 PRELIMINARY; PRT; 339 AA.

AC Q9UN23; 1

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

species."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161919; AAD47676.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_Rhodpsn.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

DR Receptor.

FT NON_TER 1 1

FT NON_TER 339 339

SQ SEQUENCE 339 AA; 39162 MW; A5C369FB0529F4B CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFQEPFGLNCS 22

Db 242 APYINVLLNTFQEPFGLNCS 263

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_Rhodpsn.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON_TER 1 1

FT NON_TER 339 339

SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFQEPFGLNCS 22

Db 242 APYINVLLNTFQEPFGLNCS 263

RESULT 4

Q9UN26 PRELIMINARY; PRT; 339 AA.

AC Q9UN26; 1

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

species."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161919; AAD47673.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_Rhodpsn.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON_TER 1 1

FT NON_TER 339 339

SQ SEQUENCE 339 AA; 39162 MW; A5C369FB0529F4B CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFQEPFGLNCS 22

Db 242 APYINVLLNTFQEPFGLNCS 263

RESULT 5

Q9UN23 PRELIMINARY; PRT; 339 AA.

AC Q9UN23; 1

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

species."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161919; AAD47673.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_Rhodpsn.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON_TER 1 1

FT NON_TER 339 339

SQ SEQUENCE 339 AA; 39162 MW; A5C369FB0529F4B CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFQEPFGLNCS 22

Db 242 APYINVLLNTFQEPFGLNCS 263


```

DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFOEFFGLNCS 22
DB 242 APYINVLLNTFOEFFGLNCS 263

RESULT 9
QY Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9;
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47687.1; -.
DR EMBL; AF161911; AAD47688.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO:00016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFOEFFGLNCS 22
DB 242 APYINVLLNTFOEFFGLNCS 263

RESULT 10
QY Q9TCW0 PRELIMINARY; PRT; 339 AA.
AC Q9TCW0;

```

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DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
CCRS.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.
DR GO:00016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAF2614D35C CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFOEFFGLNCS 22
DB 242 APYINVLLNTFOEFFGLNCS 263

RESULT 11
QY Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
CCRS.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO:00016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 1

```



```

FT NON TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257BF8B34C4AE CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
DB 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 12
Q9TUW8 PRELIMINARY; PRT; 339 AA.
AC Q9TUW8
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161948; AAD47704.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
DB 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 13
Q9TUW8 PRELIMINARY; PRT; 339 AA.
AC Q9TUW8
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161948; AAD47704.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
DB 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 14
Q9TUW8 PRELIMINARY; PRT; 339 AA.
AC Q9TUW8
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161979; AAD47734.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39092 MW; 84B51B9548E0703C CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
DB 242 APYNIVLLNTFQEFFGLNCS 263

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RESULT 15
Q9TUW9 PRELIMINARY; PRT; 339 AA.
AC Q9TUW9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agly M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161890; AAD47647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39024 MW; EC4CB48DEEEF107E CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFQEFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
DB 242 APYNIIVLLNTFQEFFGLNCS 263

RESULT 16
Q9TSQ1 PRELIMINARY; PRT; 339 AA.
AC Q9TSQ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agly M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162023; AAD47778.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.

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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39216 MW; 847E935FA403E52D CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFQEFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
DB 242 APYNIIVLLNTFQEFFGLNCS 263

RESULT 17
Q9TUU8 PRELIMINARY; PRT; 339 AA.
AC Q9TUU8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agly M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161949; AAD47705.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39049 MW; 6D1A933F66270F3ED CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFQEFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
DB 242 APYNIIVLLNTFQEFFGLNCS 263

RESULT 18
Q9TQW4 PRELIMINARY; PRT; 339 AA.
AC Q9TQW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

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OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161905; AAD47662.1; -.
DR EMBL; AF161898; AAD47655.1; -.
DR EMBL; AF161901; AAD47658.1; -.
DR EMBL; AF161904; AAD47661.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39129 MW; 4A88F8BB601D46A4 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.le-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFOEFFGLNCS 22
Db 242 APYNVLLNTFOEFFGLNCS 263

RESULT 19
Q9TUW4 PRELIMINARY; PRT; 339 AA.
AC Q9TUW4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39159 MW; 8B699B882BAC0E84 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.le-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 APYNVLLNTFOEFFGLNCS 22
Db 242 APYNVLLNTFOEFFGLNCS 263

RESULT 20
Q9TUW7 PRELIMINARY; PRT; 339 AA.
AC Q9TUW7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Cercopithecus nictitans (White-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -.
DR EMBL; AF162042; AAD47797.1; -.
DR EMBL; AF162044; AAD47799.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39150 MW; 847D5F92BB03E6E2 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.le-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFOEFFGLNCS 22
Db 242 APYNVLLNTFOEFFGLNCS 263

RESULT 21
Q9TUQ5 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";

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RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162054; AAD47809.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 339 AA; 39048 MW; 1A2E19E3A6A5A52A CRC64;

Query Match
Best Local Similarity 100.0%; Score 118; DB 6; Length 339;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
Db 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 22
Q9TUT9
ID Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161954; AAD47710.1; -.
DR EMBL; AF161950; AAD47706.1; -.
DR EMBL; AF161952; AAD47708.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
FT NON_TER
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match
Best Local Similarity 100.0%; Score 118; DB 6; Length 339;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
Db 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 24
Q9TUT9
ID Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161972; AAD47727.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

```

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39067 MW; 5BFCBCSBA96C2F9E CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 APYNIIVLLNTFOEFFGLNCS 22
Db 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 25
Q9TSN2 PRELIMINARY; PRT; 339 AA.
AC Q9TSN2;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161953; AAD47709.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39137 MW; 9B626ED3288607C1 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 APYNIIVLLNTFOEFFGLNCS 22
Db 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 26
Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.

OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162026; AAD47781.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39178 MW; 9DF2A6F446C55AED CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 APYNIIVLLNTFOEFFGLNCS 22
Db 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 27
Q9TOV6 PRELIMINARY; PRT; 339 AA.
AC Q9TOV6;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Colobus guereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Colobus.
OX NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162005; AAD47760.1; -
DR EMBL; AF162000; AAD47755.1; -
DR EMBL; AF162001; AAD47756.1; -
DR EMBL; AF162002; AAD47757.1; -
DR EMBL; AF162003; AAD47758.1; -
DR EMBL; AF162004; AAD47759.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39168 MW; 6A4BF72FEBFF566F CRC64;


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ID Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinæ; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162046; AAD47744.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39113 MW; 7F9803EA0E0AF9ED CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2,1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
Db 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 32
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinæ; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162046; AAD47801.1; -.
DR EMBL; AF162043; AAD47798.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 847F8F936B00E6E2 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2,1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
Db 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 33
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinæ; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161995; AAD47750.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39068 MW; 84EB018085DC0A62 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2,1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
Db 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 34
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

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OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161899; AAD47656.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39157 MW; 4A9EBAD183E8E72D CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFGLNCS 22
|||||
DB 242 APYNIVLLNTFQEFGLNCS 263

RESULT 35
Q9TUW3 PRELIMINARY; PRT; 339 AA.
ID Q9TUW3
AC Q9TUW3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161908; AAD47665.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39103 MW; 4350CA4625FB0657C CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFGLNCS 22
|||||
DB 242 APYNIVLLNTFQEFGLNCS 263

RESULT 36
Q9TUS5 PRELIMINARY; PRT; 339 AA.
ID Q9TUS5
AC Q9TUS5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161997; AAD47752.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39028 MW; 8C9C978FDB80B936 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFGLNCS 22
|||||
DB 242 APYNIVLLNTFQEFGLNCS 263

RESULT 37
Q9TUU0 PRELIMINARY; PRT; 339 AA.
ID Q9TUU0
AC Q9TUU0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161970; AAD47725.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

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FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39148 MW; 0CA289CDDDEDE831 CRC64;
 Query Match 100.0%; Score 118; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2.le-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
 ||||||||||||||||||
 Db 242 APYNIVLLNTFQEFFGLNCS 263

Search completed: September 28, 2004, 09:06:20
 Job time : 36.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:51:21 ; Search time 42.975 Seconds
(without alignments)
118.345 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YAFVGEKFRNLLVFFQK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	95	100.0	18	4 AAB88982	Aab88982 HIV gp120
2	95	100.0	18	4 AAB88997	Aab88997 HIV gp120
3	95	100.0	27	5 AAE14757	Aae14757 Human CCR
4	95	100.0	43	5 AAE14756	Aae14756 Human CCR
5	95	100.0	58	5 AAE14759	Aae14759 Human CCR
6	95	100.0	58	5 AAE14755	Aae14755 Human CCR
7	95	100.0	268	7 ADC10142	Adc10142 Human NOV
8	95	100.0	268	7 ADC10144	Adc10144 Human NOV
9	95	100.0	332	2 AAW26766	Aaw26766 Human che
10	95	100.0	332	2 AAW27407	Aaw27407 Human CCR
11	95	100.0	332	2 AAW27123	Aaw27123 Human che
12	95	100.0	352	2 AAW27125	Aaw27125 Macaque c
13	95	100.0	352	2 AAW07602	Aaw07602 Human G-p
14	95	100.0	352	2 AAW23835	Aaw23835 Human CC
15	95	100.0	352	2 AAW8232	Aaw8232 HIV-1 co-
16	95	100.0	352	3 AAY80128	Aay80128 Human G-p
17	95	100.0	352	4 AAG79089	Aag79089 Amino aci
18	95	100.0	352	4 AAE07046	Aae07046 Human G-p
19	95	100.0	352	4 AAE07048	Aae07048 Human G-p
20	95	100.0	352	4 AAG80111	Aag80111 Human CCR
21	95	100.0	352	4 AAE04321	Aae04321 Human che
22	95	100.0	352	4 AAE07037	Aae07037 Human G-p
23	95	100.0	352	4 AAE07039	Aae07039 Human G-p
24	95	100.0	352	4 AAB46858	Aab46858 Human HDG
25	95	100.0	352	4 ABB56342	Abb56342 Non-endog

26	95	100.0	352	4 AAB83354	Aab83354 Human CCR
27	95	100.0	352	4 AAB82948	Aab82948 Human HIV
28	95	100.0	352	5 AAU97150	Aau97150 Human G-p
29	95	100.0	352	5 AAU97152	Aau97152 Human G-p
30	95	100.0	352	5 AAM52829	Aam52829 Human CCR
31	95	100.0	352	5 AAM52828	Aam52828 Human CC
32	95	100.0	352	5 ABG70597	Abg70597 Human G-p
33	95	100.0	352	5 ABG92883	Abg92883 Human imm
34	95	100.0	352	5 ABG92880	Abg92880 Human G-p
35	95	100.0	352	5 AAE25808	Aae25808 Human G-p
36	95	100.0	352	5 AAE25811	Aae25811 Human G-p
37	95	100.0	352	5 ABB81054	Abb81054 G-protein
38	95	100.0	352	5 ABB08343	Abb08343 Human che
39	95	100.0	352	6 ABG75540	Abg75540 Human G-p
40	95	100.0	352	6 ABR58602	AbR58602 Human can
41	95	100.0	352	6 AAO29514	Aao29514 Human C-C
42	95	100.0	352	6 ABU61654	Abu61654 Human G-p
43	95	100.0	352	6 ABP97728	Abp97728 Amino aci
44	95	100.0	352	6 ABP81933	Abp81933 Human C-C
45	95	100.0	352	7 ADC03341	Adc03341 Human che

ALIGNMENTS

RESULT 1
ID AAB88982 standard; peptide; 18 AA.

AC AAB88982;
XX
DT 23-MAY-2001 (first entry)

DE HIV gp120 protein binding peptide #75.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.

XX WO200116182-A2.

XX 08-MAR-2001.

PF 25-AUG-2000; 2000WO-US0233505.

PR 27-AUG-1999; 99US-0151270P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions.

XX Example 1; Page 37; 114pp; English.

XX The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus.

XX The present sequence is an example of a peptide of the invention

XX Sequence 18 AA;

SQ Query Match 100.0%; Score 95; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 8e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

```

Db      1 YAFVGEKFRNLLVFFQK 18
|||||
RESULT 2
AAB88997
ID AAB88997 standard; peptide; 18 AA.
XX
AC AAB88997;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #90.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX
FN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023505.
XX
PR 27-AUG-1999; 99US-0151270P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions.
XX
PS Claim 21; Page 38; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the virus.
CC The present sequence is an example of a peptide of the invention
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||
Db 1 YAFVGEKFRNLLVFFQK 18
|||||
RESULT 3
AAE14757
ID AAE14757 standard; peptide; 27 AA.
XX
AC AAE14757;
XX
DT 04-OCT-2002 (first entry)
XX
DE Human CCR5 chemokine receptor deletion mutant fragment (aa 295-321).
XX
KW Chemokine receptor CCR5; P2 protein; HIV infection; AIDS;
KW human immunodeficiency virus; gene therapy; human; mutant; mutein.
XX
OS Homo sapiens.
XX
FN Synthetic.
XX
FH Key Location/Qualifiers

```

```

FT Misc-difference 27 /note= "Wild-type Cys replaced by Glx"
FT
XX
PN EP1207202-A1.
XX
PD 22-MAY-2002.
XX
PF 12-NOV-2001; 2001EP-00126500.
XX
PR 16-NOV-2000; 2000EP-00125052.
XX
PA (MOEL/) MOELLING K.
XX
PI Moelling K, Schweneker M;
XX
DR WPI; 2002-437464/47.
XX
PT Nucleic acid encoding a protein which interacts with the carboxy terminus
PT of the chemokine receptor CCR5 isolated from a human B cell cDNA library
PT is useful to detect, treat and prevent HIV infection.
XX
PS Example 2; Fig 2A; 28pp; English.
XX
CC The invention relates to nucleic acid encoding a protein which interacts
CC with the carboxy terminus of the chemokine receptor CCR5 or of other
CC chemokine receptor family members. Molecules of the invention are used to
CC detect, prevent and treat HIV infection and progression to AIDS. Any CCR5
CC -derived peptides, or compounds derived from the protein of the invention
CC (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein
CC of the invention would block HIV infection. The present sequence is human
CC chemokine receptor CCR5 C-terminal fragment deletion mutant which is
CC incapable of interacting with the protein of the invention
XX
SQ Sequence 27 AA;
Query Match 100.0%; Score 95; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||
Db 3 YAFVGEKFRNLLVFFQK 20
|||||
RESULT 4
AAE14756
ID AAE14756 standard; peptide; 43 AA.
XX
AC AAE14756;
XX
DT 04-OCT-2002 (first entry)
XX
DE Human CCR5 chemokine receptor deletion mutant fragment (aa 295-337).
XX
KW Chemokine receptor CCR5; P2 protein; HIV infection; AIDS;
KW human immunodeficiency virus; gene therapy; human; mutant; mutein.
XX
OS Homo sapiens.
XX
FN Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 43 /note= "Wild-type Ser replaced by Glx"
FT
XX
PN EP1207202-A1.
XX
PD 22-MAY-2002.
XX
PF 12-NOV-2001; 2001EP-00126500.
XX
PR 16-NOV-2000; 2000EP-00125052.
XX
PA (MOEL/) MOELLING K.

```

XX Moelling K, Schwenecker M;
XX WPI; 2002-437464/47.
XX Nucleic acid encoding a protein which interacts with the carboxy terminus
XX of the chemokine receptor CCR5 isolated from a human B cell cDNA library
XX is useful to detect, treat and prevent HIV infection.
XX Example 2; Fig 2A; 28pp; English.
XX The invention relates to nucleic acid encoding a protein which interacts
XX with the carboxy terminus of the chemokine receptor CCR5 or of other
XX chemokine receptor family members. Molecules of the invention are used to
XX detect, prevent and treat HIV infection and progression to AIDS. Any CCR5
XX -derived peptides, or compounds derived from the protein of the invention
XX (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein
XX of the invention would block HIV infection. The present sequence is human
XX chemokine receptor CCR5 C-terminal fragment deletion mutant which is
XX incapable of interacting with the protein of the invention
XX Sequence 43 AA;
XX Query Match 100.0%; Score 95; DB 5; Length 43;
XX Best Local Similarity 100.0%; Pred. No. 28-08;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNYLLVFFQK 18
DB 3 YAFVGEKFRNYLLVFFQK 20
|||||
RESULT 5
AAE14759
ID AAE14759 standard; peptide; 58 AA.
XX AC AAE14759;
XX 04-OCT-2002 (first entry)
XX Human CCR5 chemokine receptor C-terminal mutant fragment (aa 295-352).
XX Chemokine receptor CCR5; P2 protein; HIV infection; AIDS;
XX human immunodeficiency virus; gene therapy; human; mutant; mutein.
XX Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 58
XX /note= "Wild-type Leu replaced by Pro"
XX EPI207202-A1.
XX 22-MAY-2002.
XX 12-NOV-2001; 2001EP-00126500.
XX 16-NOV-2000; 2000EP-00125052.
XX (MOEL/) MOELLING K.
XX Moelling K, Schwenecker M;
XX WPI; 2002-437464/47.
XX Nucleic acid encoding a protein which interacts with the carboxy terminus
XX of the chemokine receptor CCR5 isolated from a human B cell cDNA library
XX is useful to detect, treat and prevent HIV infection.
XX Example 2; Fig 2A; 28pp; English.
XX The invention relates to nucleic acid encoding a protein which interacts

CC with the carboxy terminus of the chemokine receptor CCR5 or of other
CC chemokine receptor family members. Molecules of the invention are used to
CC detect, prevent and treat HIV infection and progression to AIDS. Any CCR5
CC -derived peptides, or compounds derived from the protein of the invention
CC (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein
CC of the invention would block HIV infection. The present sequence is human
CC chemokine receptor CCR5 C-terminal mutant fragment which is incapable of
CC interacting with the protein of the invention
XX Sequence 58 AA;
XX Query Match 100.0%; Score 95; DB 5; Length 58;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-08;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNYLLVFFQK 18
DB 3 YAFVGEKFRNYLLVFFQK 20
|||||
RESULT 6
AAE14755
ID AAE14755 standard; peptide; 58 AA.
XX AC AAE14755;
XX 04-OCT-2002 (first entry)
XX Human CCR5 chemokine receptor C-terminal fragment (residues 295-352).
XX Chemokine receptor CCR5; P2 protein; HIV infection;
XX human immunodeficiency virus; AIDS; gene therapy; human.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Binding-site 58
XX /note= "Essential for binding to human protein P2
XX (AAE14754)"
XX EPI207202-A1.
XX 22-MAY-2002.
XX 12-NOV-2001; 2001EP-00126500.
XX 16-NOV-2000; 2000EP-00125052.
XX (MOEL/) MOELLING K.
XX Moelling K, Schwenecker M;
XX WPI; 2002-437464/47.
XX Nucleic acid encoding a protein which interacts with the carboxy terminus
XX of the chemokine receptor CCR5 isolated from a human B cell cDNA library
XX is useful to detect, treat and prevent HIV infection.
XX Example 2; Fig 2A; 28pp; English.
XX The invention relates to nucleic acid encoding a protein which interacts
XX with the carboxy terminus of the chemokine receptor CCR5 or of other
XX chemokine receptor family members. Molecules of the invention are used to
XX detect, prevent and treat HIV infection and progression to AIDS. Any CCR5
XX -derived peptides, or compounds derived from the protein of the invention
XX (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein
XX of the invention would block HIV infection. The present sequence is human
XX chemokine receptor CCR5 C-terminal fragment
XX Sequence 58 AA;
XX Query Match 100.0%; Score 95; DB 5; Length 58;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-08;

PR 19-JUN-2001; 2001US-0299230P.
PR 21-JUN-2001; 2001US-0299949P.
PR 22-JUN-2001; 2001US-0300177P.
PR 26-JUN-2001; 2001US-0300883P.
PR 28-JUN-2001; 2001US-0301530P.
PR 28-JUN-2001; 2001US-0301530P.
PR 03-JUL-2001; 2001US-0302951P.
PR 31-JUL-2001; 2001US-0308990P.
PR 14-SEP-2001; 2001US-0322297P.
PR 25-SEP-2001; 2001US-0324569P.
PR 03-DEC-2001; 2001US-0337477P.
PR 14-DEC-2001; 2001US-0341562P.
PR 21-FEB-2002; 2002US-0358566P.
PR 21-FEB-2002; 2002US-0359122P.
PR 22-FEB-2002; 2002US-0358978P.
PR 22-FEB-2002; 2002US-0359034P.
PR 22-FEB-2002; 2002US-0359035P.
PR 22-FEB-2002; 2002US-0359121P.
PR 27-FEB-2002; 2002US-0359864P.
PR 01-MAR-2002; 2002US-0360858P.
PR 12-MAR-2002; 2002US-0363430P.
PR 12-MAR-2002; 2002US-0363676P.
PR 10-APR-2002; 2002US-0371346P.
PR 10-MAY-2002; 2002US-0379444P.
PR 04-JUN-2002; 2002US-00379444.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;
PI Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
PI Ott T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
PI Burgess CE, Lepley DM;
XX
XX WPI: 2003-210149/20.
DR N-PSDB; ADC10143.
DR
XX
XX New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.
XX
PS Claim 1; SEQ ID NO 164; 772pp; English.
XX
XX The invention relates to novel isolated polypeptides, mature form of the
CC polypeptide, a sequence that is 95% identical to the polypeptide or the
CC polypeptide comprising one or more conservative substitutions. The NOVX
CC polypeptide is useful for treating or preventing a pathology associated
CC with the polypeptide e.g. disorders associated with aberrant expression
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
CC endocrine, CNS and inflammatory disorders. They can also be used in
CC various detection and screening assays, chromosome mapping, tissue typing
CC and predictive medicine. This sequence corresponds to one of the
CC polypeptides of the invention.
XX
SQ Sequence 268 AA;
Query Match 100.0%; Score 95; DB 7; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
DB 213 YAFVGEKFRNLLVFFQK 230
RESULT 9
AAW26766
ID AAW26766 standard; protein; 332 AA.
XX

AC AAW26766;
XX
DT 21-MAY-1998 (first entry)
XX
DE Human chemokine receptor MMLR-CCR.
XX
XX Mammalian mixed lymphocyte receptor; Chemokine receptor; MMLR-CCR; human;
KW monocyte; macrophage; chemotaxis; haematopoiesis; infection; tumour;
KW inflammation; proliferative disease; cardiovascular disease; tumour;
KW rheumatoid arthritis; alveolitis; atherosclerosis;
KW chronic granulomatous disease; asthma; myasthenia gravis; diabetes;
KW inflammatory bowel disease; toxic shock syndrome; septic shock;
KW Chediak-Higashi syndrome; therapy; diagnosis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 107..128
FT /note= "conserved peptide"
FT Misc-difference 121
FT /note= "a claimed polypeptide has isoleucine at residue
FT 121"
XX
XX WO9741225-A2.
PN
XX 06-NOV-1997.
PD
XX
XX 25-APR-1997; 97WO-US006993.
PP
XX
XX 26-APR-1996; 96US-00638081.
PR (INCY-) INCYTE PHARM INC.
XX
XX Au-Young J, Bandman O, Coleman R, Wilde CG;
PI WPI; 1997-549729/50.
XX
DR N-PSDB; AAT9542.
XX
XX Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful
PT to study, diagnose and treat, e.g. infection, inflammation, solid tumour
PT and proliferative and cardiovascular disease.
XX
PS Claim 8; Page 37-38; 59pp; English.
XX
XX This protein comprises human MMLR-CCR, a novel C-C chemokine receptor
CC associated with monocyte/macrophage infiltration and chemotaxis and
CC haematopoiesis. The amino acid sequence was deduced from a cDNA clone
CC (see AAT99542) obtained from a cDNA library made from mononuclear cells
CC collected on day 2 of a mixed lymphocyte culture, i.e. cells associated
CC with inflammation and immunomodulation. Another novel chemokine receptor,
CC MPHG-CCR (see AAT36767), is also claimed. MMLR-CCR contains 7
CC transmembrane spanning segments connected by a series of intracellular
CC and extracellular loops. MMLR-CCR and MPHG-CCR can be used to study,
CC diagnose and treat disease states in which normal leukocyte function is
CC perturbed by normal leukopoiesis or inappropriate activation via
CC chemokine agonists or antagonists, such as infection, inflammation,
CC proliferative disease, tumourigenesis, autoimmune disease, abnormal cell
CC proliferation, solid tumours, cardiovascular disease, rheumatoid
CC arthritis, alveolitis, atherosclerosis, chronic granulomatous disease,
CC asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic
CC shock syndrome, septic shock and Chediak-Higashi syndrome
XX
SQ Sequence 332 AA;
Query Match 100.0%; Score 95; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
DB 277 YAFVGEKFRNLLVFFQK 294

RESULT 10
AAW27407
ID AAW27407 standard; protein; 352 AA.
XX AC AAW27407;
XX DT 14-APR-1998 (first entry)
XX DE Human CCR5.
XX KW Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
KW type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
KW atherosclerosis; autoimmune disorder.
XX OS Homo sapiens.
XX PN WO9732019-A2.
XX PD 04-SEP-1997.
XX PF 28-FEB-1997; 97WO-BE000023.
XX PR 01-MAR-1996; 96EP-00870021.
XX PR 06-AUG-1996; 96EP-00870102.
XX PA (EURO-) EUROSCREEN SA.
XX PI Samson M, Parmentier M, Vaseart G, Libert F;
XX WPI; 1997-479829/44.
XX DR N-PSDB; AAT90117.
XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
PT disease and viral infection.
XX PS Claim 4; Fig 1b-c; 94pp; English.
XX CC The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but
CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,
CC interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency
CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to
CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
CC atherosclerosis and autoimmune disorders
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 95; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314
RESULT 11
AAW27123
ID AAW27123 standard; protein; 352 AA.
XX AC AAW27123;
XX DT 14-DEC-1997 (first entry)
XX DE Human chemokine receptor 88C.
XX KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;

KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
KW modulator; antibody; human.
XX OS Homo sapiens.
XX Key Location/Qualifiers
XX Domain 1..32
XX FT /label= Extracellular_domain
XX FT 56..67
XX FT /label= Intracellular_domain
XX FT 89..112
XX FT /label= Extracellular_domain
XX FT 125..145
XX FT /label= Intracellular_domain
XX FT 166..191
XX FT /label= Extracellular_domain
XX FT 213..235
XX FT /label= Intracellular_domain
XX FT 259..280
XX FT /label= Extracellular_domain
XX FT 301..352
XX FT /label= Intracellular_domain
XX PN WO9722698-A2.
XX XX
XX PD 26-JUN-1997.
XX PF 20-DEC-1996; 96WO-US020759.
XX PR 20-DEC-1995; 95US-00575967.
XX PR 07-JUN-1996; 96US-00661393.
XX PA (ICOS-) ICOS CORP.
XX PI Gray PW, Schweickart VL, Raport CJ;
XX WPI; 1997-341689/31.
XX DR N-PSDB; AAT85161.
XX PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
PT tumours, viral infections, auto-immune diseases, etc.
XX PS Claim 16; Page 47-48; 65pp; English.
XX CC This polypeptide sequence comprises novel human chemokine receptor 88C, a
CC G protein coupled receptor that is involved in leukocyte trafficking. Its
CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
CC macrophage library. It shows 62% identity to CCKX1. Chemokine receptor
CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
CC and their polypeptide fragments can be produced in transformed host
CC cells. The receptors, peptides comprising one or more of the
CC extracellular or intracellular domains, and anti-receptor antibodies can
CC be used to modulate receptor activities, particularly ligand and G
CC protein binding, and are potentially potentially useful in the treatment
CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
CC infection, AIDS, inflammatory conditions, pathological immune response,
CC abnormal haematopoietic processes etc
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 95; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314
RESULT 12
AAW27125


```

ID AAW27125 standard; protein; 352 AA.
XX
AC AAW27125;
XX
XX
XX 14-DEC-1997, (first entry)
XX
XX Macaque chemokine receptor 88C.
XX
XX Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
XX asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
XX diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
XX modulator; antibody.
XX
XX Macaca sp.
XX
XX WO9722698-A2.
XX
XX 26-JUN-1997.
XX
XX 20-DEC-1996; 96WO-US020759.
XX
XX 20-DEC-1995; 95US-00575967.
XX
XX 07-JUN-1996; 96US-00661393.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray PW, Schweickart VL, Raport CJ;
XX
XX WPI; 1997-341689/31.
XX
XX N-PSDB; AAT85163.
XX
XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX tumours, viral infections, auto-immune diseases, etc.
XX
XX Claim 36; Page 57-58; 65pp; English.
XX
XX This polypeptide sequence comprises macaque chemokine receptor 88C, a G
XX protein coupled receptor that is involved in leukocyte trafficking. Its
XX amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR
XX amplification. It shows 97% identity to human 88C (AAW27123). 88C
XX receptors and their polypeptide fragments can be produced in transformed
XX host cells. The receptors, peptides comprising one or more of the
XX extracellular or intracellular domains, and anti-receptor antibodies can
XX be used to modulate receptor activities, particularly ligand and G
XX protein binding, and are potentially potentially useful in the treatment
XX of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX infection, AIDS, inflammatory conditions, pathological immune response,
XX abnormal haematopoietic processes etc. A hybridoma that produces an
XX antibody that specifically binds to macaque 88C is claimed
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 95; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YAFVGEKFRNLLVFFQK 18
XX |||||
XX Db 297 YAFVGEKFRNLLVFFQK 314
XX
XX RESULT 13
XX AAW07602
XX ID AAW07602 standard; protein; 352 AA.
XX
XX AC AAW07602;
XX
XX 26-FEB-1997 (first entry)
XX
XX Human G-protein chemokine receptor HDGNR10.
XX
XX G-protein chemokine receptor; HDGNR10; signal transduction;
XX
AAW27125 standard; protein; 352 AA.
therapY.
Homo sapiens.
WO9639437-A1.
12-DEC-1996.
06-JUN-1995; 95WO-US0071173.
06-JUN-1995; 95WO-US0071173.
(HUMA-) HUMAN GENOME SCI INC.
Li Y, Ruben SM;
WPI; 1997-043072/04.
N-PSDB; AAT44042.
Human G-protein chemokine receptor, HDGNR10 - useful to identify
(fant)agonists, for treatment of haematopoiesis, leukaemia, chronic and
acute inflammation, rheumatoid arthritis, etc.
Claim 1; Page 44-46; 61pp; English.
Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7
-transmembrane protein involved in signal transduction. Its amino acid
sequence was deduced from a cDNA clone (AAT44042) isolated from a human
monocyte library. Isolation of the cDNA allows prodn. of recombinant
CC HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant
CC receptor can be used to identify agonists or antagonists of the receptor;
CC such cpds. can be used to treat conditions related to the under- and over
CC -expression of G-protein chemokine receptors
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 95; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YAFVGEKFRNLLVFFQK 18
XX |||||
XX Db 297 YAFVGEKFRNLLVFFQK 314
XX
XX RESULT 14
XX AAW23835
XX ID AAW23835 standard; protein; 352 AA.
XX
XX AC AAW23835;
XX
XX 08-JUN-1998 (first entry)
XX
XX Human CC chemokine receptor 5 (CCR5).
XX
XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;
XX human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 29..55
XX /label= I
XX /note= "transmembrane domain"
XX Domain 104..126
XX /label= III
XX /note= "transmembrane domain"
XX Region 109..120
XX /note= "extracellular loop-1 (Claim 19)"
XX Domain 143..171
XX /label= IV
XX /note= "transmembrane domain"

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FT Region 187..210 /note="extracellular loop-2 (Claim 19)"
FT Domain 194..219 /label=V
FT Domain /note="transmembrane domain"
FT Domain 238..258 /label=VI
FT Region 261..276 /note="transmembrane domain"
FT Domain 277..300 /note="extracellular loop-3 (Claim 19)"
FT Domain /label=VII
FT Domain /note="transmembrane domain"
XX WO9745543-A2.
XX 04-DEC-1997.
XX 28-MAY-1997; 97WO-US009586.
XX 28-MAY-1996; 96US-0018508P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
XX Broder CC, Kennedy PE;
XX WPI; 1998-032650/03.
XX N-PSDB; AAT76920.
XX CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
XX between HIV and a target cell.
XX Claim 68; Fig 1C; 70pp; English.
XX This protein sequence comprises of a novel human macrophage-selective CC
XX chemokine receptor that has been designated CCR5. The sequence was
XX deduced from an isolated cDNA clone (see AAT76920). An Ala127Leu variant
XX (see W238340 of CCR5 was also identified. The susceptibility of human
XX macrophages to HIV infection depends on cell surface expression of CD4
XX and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
XX protein coupled cell surface molecules. It plays an essential role in the
XX membrane fusion step of infection by some HIV isolates. The establishment
XX of stable, non-human cell lines and transgenic mammals having cells that
XX coexpress human CD4 and CCR5 provides valuable tools for research of HIV
XX infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
XX agents capable of blocking membrane fusion between HIV and target cells
XX represent potential anti-HIV therapeutics for macrophage tropic strains
XX of HIV
XX Sequence 352 AA;
XX Query Match 100.0%; Score 95; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 YAFVGEKFRNLLVFFQK 18
XX 297 YAFVGEKFRNLLVFFQK 314
XX Db
XX RESULT 15
XX AA88232
XX ID AA88232 standard; protein; 352 AA.
XX AC AA88232;
XX DT 15-MAR-1999 (first entry)
XX DE HIV-1 co-receptor CCR5.
XX KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
XX gene therapy; human.
XX
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT Domain 32..56 /note="transmembrane domain 1"
XX FT Domain 67..87 /note="transmembrane domain 2"
XX FT Misc-difference 101 /note="corresponds to TGT (Cys) in wild-type CCR5, TGA
XX (stop) in Ccr5m303"
XX FT Domain 103..124 /note="transmembrane domain 3"
XX FT Domain 142..167 /note="transmembrane domain 4"
XX FT Domain 200..223 /note="transmembrane domain 5"
XX FT Domain 236..260 /note="transmembrane domain 6"
XX FT Domain 275..301 /note="transmembrane domain 7"
XX WO9854317-A1.
XX 03-DEC-1998.
XX 29-MAY-1998; 98WO-BF003437.
XX 30-MAY-1997; 97US-0048057P.
XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
XX Beretta A, Quillent C, Arenzana Siesdedos P, Braun J;
XX WPI; 1999-059835/05.
XX N-PSDB; AAV84126.
XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
XX resistance of CCR5-expressing cells to HIV-1 infection.
XX Disclosure; Page 34-35; 55pp; English.
XX This is the amino acid sequence of wild-type human CCR5, which serves as
XX a co-receptor for infection by macrophage-tropic (M-tropic) strains of
XX HIV-1. The invention relates to the identification of a CCR5 variant (see
XX AA88231), designated CCR5m303, comprising the first two transmembrane
XX domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
XX positive correlation with resistance to infection with M-tropic HIV-1
XX strains, and may indicate slower progression of the disease. The
XX detection of CCR5 variants may be used to identify individuals at lower
XX risk of infection relative to the general population who, if infected,
XX may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
XX 36) are provided for use in diagnostic methods for detecting the presence
XX of such variants. A method is provided for inhibiting HIV-1 infection of
XX a cell expressing the CCR5 receptor. This involves introducing a nucleic
XX acid encoding a CCR5 variant into the cell, thereby reducing the number
XX of functional CCR5 molecules present on the cell surface
XX Sequence 352 AA;
XX Query Match 100.0%; Score 95; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 YAFVGEKFRNLLVFFQK 18
XX 297 YAFVGEKFRNLLVFFQK 314
XX Db
XX RESULT 16
XX AA80128
XX ID AA80128 standard; protein; 352 AA.

```

XX AC AAY80128;
 XX DT
 XX DE
 XX DE 19-MAY-2000 (first entry)
 XX DE Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
 XX DE
 XX KW Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;
 XX KW diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
 XX KW tumour; infection; leukaemia; psoriasis; allergy;
 XX KW T-cell mediated autoimmune disease; atherosclerosis; anaphylaxis;
 XX KW inflammation; allergic reaction; silicosis; sarcoidosis;
 XX KW rheumatoid arthritis; hyper-eosinophilia syndrome.
 XX OS
 XX OS Homo sapiens.
 XX PN
 XX PN US6025154-A.
 XX PD
 XX PD 15-FEB-2000.
 XX PF
 XX PF 06-JUN-1995; 95US-00466343.
 XX PR
 XX PR 06-JUN-1995; 95US-00466343.
 XX PA
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI
 XX PI Li Y, Ruben SM;
 XX DR
 XX DR WPI; 2000-181807/16.
 XX DR N-PSDB; AAZ91481.
 XX PT
 XX PT Isolated nucleic acid encoding human G-protein chemokine receptor useful
 XX PT for diagnostic assays, scientific research and screening for compounds
 XX PT which bind to and activate or inhibit activation of the receptor
 XX PT polypeptides.
 XX PS
 XX PS Claim 1; Fig 1; 22pp; English.
 XX CC
 XX CC The present sequence represents a human G-protein chemokine receptor
 XX CC designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
 XX CC screening for compounds which bind to and either: (1) activate the
 XX CC HDGNR10 polypeptides causing stimulation of haematopoiesis, wound
 XX CC healing, coagulation, and angiogenesis; treatment of solid tumours,
 XX CC chronic infections, leukaemia, T-cell mediated autoimmune diseases,
 XX CC parasitic infections, psoriasis, and to stimulate growth factor activity;
 XX CC or (2) inhibit activation of the HDGNR10 polypeptides which is useful for
 XX CC preventing and/or treating allergy, atherosclerosis, anaphylaxis,
 XX CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
 XX CC E-mediated allergic reactions, prostaglandin-independent fever, bone
 XX CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
 XX CC hyper-eosinophilia syndrome. The polynucleotides are also useful for
 XX CC diagnostic assays for detecting diseases related to mutations in the
 XX CC nucleic acid sequences encoding the polypeptides and for detecting an
 XX CC altered level of the soluble form of the receptor polypeptides. The
 XX CC polynucleotides are also useful for in vitro purposes related to
 XX CC scientific research, synthesis of DNA and manufacture of DNA vectors
 XX SQ
 XX SQ Sequence 352 AA;
 XX Query Match 100.0%; Score 95; DB 3; Length 352;
 XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 YAFVGEKFRNLLVFFQK 18
 XX DB 297 YAFVGEKFRNLLVFFQK 314
 XX
 XX RESULT 17
 XX AAG79089
 XX ID AAG79089 standard; protein; 352 AA.
 XX XX
 XX AC AAG79089;

XX DT
 XX DE
 XX DE 10-DEC-2001 (first entry)
 XX DE Amino acid sequence of human CCR5 protein.
 XX KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
 XX KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
 XX OS
 XX OS Homo sapiens.
 XX PN
 XX PN WO200164752-A2.
 XX PD
 XX PD 07-SEP-2001.
 XX PF
 XX PF 28-FEB-2001; 2001WO-US006322.
 XX PR
 XX PR 02-MAR-2000; 2000US-00517605.
 XX PA
 XX PA (UYNX) UNIV NEW YORK STATE.
 XX PA (UYN1-) UNIV NIDMEGEN.
 XX PI
 XX PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
 XX DR
 XX DR WPI; 2001-602565/68.
 XX PT
 XX PT An antibody for the treatment or prevention of HIV-infection comprises a
 XX PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of
 XX PT DC-SIGN due to concomitant conformational change.
 XX PS
 XX PS Disclosure; Page 118-119; 131pp; English.
 XX CC
 XX CC The specification describes an antibody which is specific for an
 XX CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
 XX CC is exposed upon gp120 binding of DC-SIGN due to concomitant
 XX CC conformational change. DC-SIGN is a receptor that is specifically
 XX CC expressed on dendritic cells and facilitates infection of T lymphocytes
 XX CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
 XX CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
 XX CC with high affinity. The antibody of the invention inhibits the trans
 XX CC enhancement of HIV entry into a T cell or macrophage facilitated by
 XX CC dendritic cells. The antibody is useful to treat or prevent HIV
 XX CC infection. The present sequence represents a human CCR5 protein, which is
 XX CC a translocation promoting agent that interacts with CD4. This receptor
 XX CC functions in HIV-1 entry into cells
 XX SQ
 XX SQ Sequence 352 AA;
 XX Query Match 100.0%; Score 95; DB 4; Length 352;
 XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 YAFVGEKFRNLLVFFQK 18
 XX DB 297 YAFVGEKFRNLLVFFQK 314
 XX
 XX RESULT 18
 XX AAE07046
 XX ID AAE07046 standard; protein; 352 AA.
 XX XX
 XX AC AAE07046;
 XX XX
 XX DT 16-OCT-2001 (first entry)
 XX XX
 XX XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
 XX XX
 XX KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 XX KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
 XX KW cytosolic; immunosuppressive; neutropenic; neuroprotective; gene therapy;
 XX KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 XX KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 XX KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 XX KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;

KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

Key Location/Qualifiers

FT Domain 1..36 /label= Extracellular_domain
 FT Domain 37..305 /label= Transmembrane_domain
 FT Domain 37..58 /label= Transmembrane_domain
 FT /label= Transmembrane_domain
 FT /note= "Segment 1"
 FT Domain 59..67 /label= Intracellular_loop_1
 FT Domain 68..88 /label= Transmembrane_domain
 FT /note= "Segment 2"
 FT Domain 89..102 /label= Intracellular_loop_1
 FT Domain 103..124 /label= Transmembrane_domain
 FT /note= "Segment 3"
 FT Domain 125..141 /label= Intracellular_loop_2
 FT Domain 142..166 /label= Transmembrane_domain
 FT /note= "Segment 4"
 FT Domain 167..195 /label= Extracellular_loop_2
 FT Domain 196..223 /label= Transmembrane_domain
 FT /note= "Segment 5"
 FT Domain 224..235 /label= Intracellular_loop_3
 FT Domain 236..260 /label= Transmembrane_domain
 FT /note= "Segment 6"
 FT Domain 261..274 /label= Extracellular_loop_3
 FT Domain 287..305 /label= Transmembrane_domain
 FT /note= "Segment 7"
 FT Domain 306..352 /label= Intracellular_domain

PN WO200158916-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004153.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488966/53.

XX N-PSDB; AAD13282.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.

XX Claim 102; Fig 1; 518pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5)

CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder

CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC disease or disorder may be associated with aberrant CCR5 expression, lack
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGNR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The
 CC present sequence is human CCR5 HDGNR10 protein

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.9e-07; Mismatches 0; Gaps 0;

Matches 18; Conservative 0; Indels 0;

OY 1 YAPVGEKFRNLLVFPQK 18

Db 297 YAPVGEKFRNLLVFPQK 314
 |||||

RESULT 19

AAE07048

ID AAE07048 standard; protein; 352 AA.

XX AAE07048;

XX 16-OCT-2001 (first entry)

XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; neutrotic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX WO200158916-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004153.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488966/53.

XX N-PSDB; AAD13299.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune

PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 XX neurodegenerative disorders.

PS Example 40; Page 504-505; 518pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5)
 CC HDGMR10 polypeptides and polynucleotides. CCR5 HDGMR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder
 CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC disease or disorder may be associated with aberrant CCR5 expression, lack
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGMR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGMR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGMR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemia) and wound healing. The
 CC present sequence is human CCR5 HDGMR10 protein

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 20

AAAG80111
 ID AAG80111 standard; protein; 352 AA.

XX AAG80111;

DT 17-JAN-2002 (first entry)

XX Human CCR5 protein.

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.

XX Homo sapiens.

XX WO200172830-A2.

PD 04-OCT-2001.

PF 02-APR-2001; 2001WO-EP003708.

XX 31-MAR-2000; 2000DE-01016013.

XX (IPFP-) IPF PHARM GMBH.

XX (FORS/) FORSSMANN U.

PI Forssmann W, Adernann K, Heitland A, Spodsborg N;

XX WPI; 2001-626256/72.

XX

PT Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 XX inhibitors.

PS Disclosure; Page 10; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 21

AAE04321
 ID AAE04321 standard; protein; 352 AA.

XX AAE04321;

DT 04-SEP-2001 (first entry)

XX Human chemokine receptor (CKR), CC-CKR-5 related protein #2.

XX Human; transformed mammalian cell; CD4; reporter gene; translocation;
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
 KW chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor;
 KW CC-CKR-5; envelope glycoprotein; anti-HIV.

XX Homo sapiens.

XX US6258527-B1.

XX 10-JUL-2001.

XX 21-MAY-1997; 97US-00861105.

XX 20-MAY-1996; 96US-0017157P.

XX 19-JUN-1996; 96US-0020043P.

XX 19-MAY-1997; 97US-00858660.

XX (AARO-) AARON DIAMOND AIDS RES CENT.

XX (UNY) UNIV NEW YORK STATE.

XX Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;

XX WPI; 2001-417127/44.

XX N-PSDB; AAD08577.

XX

PT Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
 PT and HIV LTR for identification of drugs and antibodies for treatment of
 PT HIV.

XX

1 YAFVGEKFRNYLLVFFQK 18
Ov Ov

Db 297 YAFVGEKFRNYLLVFFQK 314
 |||||
 RESULT 23
 AAE07039
 ID AAE07039 standard; protein; 352 AA.
 XX AC AAE07039;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGMR10 protein #2.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
 KW cytosolic; immunosuppressive; neutropenic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200158915-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004152.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 XX
 PR 09-MAR-2000; 2000US-0187999P.
 XX
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2001-488965/53.
 XX
 DR N-PSDB; AAD13198.
 XX
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune
 diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 neurodegenerative disorders.
 XX
 PS Example 40; Page 486-487; 495pp; English.
 XX
 CC The present sequence is human G-protein chemokine receptor (CCR5) HDGMR10
 protein. CCR5 HDGMR10 antibodies are useful for treating, preventing or
 ameliorating a disease or disorder associated with inflammation, such as
 defective or aberrant chemotaxis of immune cells, HIV infection, (such as
 Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
 aberrant T-cell antigen presenting cell interaction. The disease or
 disorder may also be an infectious disease (e.g. a viral infection such
 as an early stage HIV infection, a cytomegalovirus infection, or a
 poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
 neurodegenerative disorder. The disease or disorder may be associated
 with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
 ligand expression, or lack of CCR5 ligand function. CCR5 HDGMR10 protein
 is used as a food additive or preservative to increase or decrease
 storage capabilities. CCR5 HDGMR10 DNA are useful for chromosome
 identification and in gene therapy. CCR5 HDGMR10 DNA, protein,
 antibodies, agonists and antagonists are also useful in the diagnosis,
 treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
 bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
 disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
 autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular
 disorders (myocardial ischaemias) and wound healing

SQ Sequence 352 AA;
 Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNYLLVFFQK 314
 |||||
 RESULT 24
 AAB46858
 ID AAB46858 standard; protein; 352 AA.
 XX AC AAB46858;
 XX
 DT 16-AUG-2001 (revised)
 DT 02-AUG-2001 (revised)
 DT 04-MAY-2001 (first entry)
 XX
 DE Human HDGMR10 protein.
 XX
 KW HDGMR10; human; G-protein chemokine receptor; antiinflammatory;
 KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
 KW cytosolic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;
 KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
 KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
 KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
 KW anaphylaxis; malignancy; inflammation; histamine; IGE; silicosis; shock;
 KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
 KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
 KW hyper-eosinophilic syndrome; vulnerary.
 XX
 OS Homo sapiens.
 XX
 PN US2001000241-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 29-NOV-2000; 2000US-00725285.
 XX
 PR 06-JUN-1995; 95US-00466343.
 PR 18-NOV-1998; 98US-00195662.
 PR 25-JUN-1999; 99US-00339912.
 XX
 PA (LIYY/) LI Y.
 PA (RUSE/) RUBEN S M.
 XX
 PI Li Y, Ruben SM;
 DR WPI; 2001-226317/23.
 DR N-PSDB; AAF26390.
 XX
 PT New human G-protein chemokine receptor polypeptides and polynucleotides,
 useful for identifying (antagonists to the G-protein chemokine receptor.
 XX
 PS Claim 1a; Page 15; 22pp; English.
 XX
 CC This invention describes a novel receptor polypeptide (I) selected from
 (i) a fully defined 329 amino acid sequence (II) fully disclosed in the
 specification; and (ii) a polypeptide encoded by the cDNA contained in a
 plasmid, and fragments, analogs and derivatives of the polypeptide. The
 products of the invention have antiinflammatory, immunomodulatory,
 anticoagulant, antiallergic, immunosuppressive, vulnerary, cytostatic,
 antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic
 activity and can be used for gene therapy. The G-protein chemokine
 receptors, HDGMR10, (I) are useful for screening for compounds which
 activate or inhibit activation of (I). The products of the invention can
 also be used for stimulating haematopoiesis, wound healing, coagulation,
 angiogenesis, treating solid tumours, chronic infections, leukemia, T-
 cell mediated autoimmune diseases, parasitic infections, psoriasis, and
 stimulating growth factor activity. HDGMR10 is useful for treating

CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
 CC reactions, prostaglandin-independent fever, bone marrow failure,
 CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
 CC errors in the keyword formatting)

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 25
 ABB56342
 ID ABB56342 standard; protein; 352 AA.

XX AC ABB56342;

XX DT 18-FEB-2002 (first entry)

XX DE Non-endogenous human GPCR protein, SEQ ID NO: 477.

XX KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 constitutively activated GPCR; agonist; disease.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200177172-A2.

XX PD 18-OCT-2001.

XX PF 05-APR-2001; 2001WO-US011098.

XX PR 07-APR-2000; 2000US-0195747P.

XX PA (AREN-) ARENA PHARM INC.

XX PI Lehmann-Bruinsma K, Liaw CW, Lin I;

XX WPI; 2001-648759/74.

XX N-PSDB; ABI97978.

XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 disease treatment, comprises contacting candidate compounds with versions
 of GPCRs.

XX Claim 1; Page 277-278; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which
 the endogenous ligand has been identified. Non-endogenous constitutively
 activated versions of known GPCRs are used in the invention for the
 direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists. Such agonists are useful as
 CC therapeutic agents for diseases or disorders associated with GPCRs. The
 CC present sequence is a non-endogenous version of a known human GPCR.

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 26
 AAB83354
 ID AAB83354 standard; protein; 352 AA.

XX AC AAB83354;

XX DT 09-OCT-2001 (first entry)

XX DE Human CCR5 protein sequence.

XX KW Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
 human immunodeficiency virus; anti-inflammatory disease; human.

XX OS Homo sapiens.

XX PN EP1118858-A2.

XX PD 25-JUL-2001.

XX PF 03-JAN-2001; 2001EP-00300020.

XX PR 12-JAN-2000; 2000GB-00000659.

XX PR 12-JAN-2000; 2000GB-00000661.

XX PR 12-JAN-2000; 2000GB-00000663.

XX (PF12) PFIZER LTD.

XX (PF12) PFIZER INC.

XX Dobbs S, Perros M, Rickett G;

XX WPI; 2001-477088/52.

XX N-PSDB; AAF87099.

XX Determining if an agent can modulate CCR5-gp120 interaction, comprises
 incubating the agent with CCR5 and gp120 and determining if the agent
 modulates the interaction.

XX Claim 1; Page 110; 113pp; English.

XX This sequence represents the human CCR5 protein sequence. The invention
 relates to a method for determining whether an agent is capable of
 CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
 CC with gp120, comprising incubating the agent with CCR5 and gp120 and
 CC determining whether the agent modulates the interaction, where gp120 is
 CC associated with CD4, and where the interaction is a low affinity binding.
 CC The method is used to identify an agent capable of modulating the
 CC interaction of CCR5 with gp120. An agent identified by the method is used
 CC to prepare a pharmaceutical composition for the treatment of a disease or
 CC condition associated with CCR5 and gp120 interaction, to treat a subject
 CC with a disease or condition associated with CCR5 and gp120 interaction,
 CC and for preparing a pharmaceutical for treating human immunodeficiency
 CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
 CC is commercially useful, amenable to high throughput screening, and
 CC detects interaction of gp120 with cells expressing only CCR5

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 27
 AAB82948
 ID AAB82948 standard; protein; 352 AA.

XX AC AAB82948;

DT 21-DEC-2001 (first entry)
 XX Human HIV-1 co-receptor CCR5.
 XX CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
 XX infection; therapy; vaccine; anti-HIV-1.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Binding-site 2..18
 FT /note= "binds to HIV-1 gp120"
 FT XX
 PN W0200164710-A2.
 XX 07-SEP-2001.
 XX 28-FEB-2001; 2001WO-US006699.
 XX 29-FEB-2000; 2000US-0185667P.
 PR 19-MAY-2000; 2000US-0205939P.
 PR 07-FEB-2001; 2001US-0267231P.
 XX (PROG-) PROGENICS PHARM INC.
 PA (AARO-) AARON DIAMOND AIDS RES CENT.
 XX Dragic T, Olson WC;
 XX WPI; 2001-611273/70.
 DR N-PSDB; AAH26903.
 XX Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-
 PT receptor) amino terminal domain including negatively charged and two
 PT sulfated tyrosine residues is useful for treating HIV infection in
 PT humans.
 XX Claim 1; Page 30; 163pp; English.
 XX The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids
 XX 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding
 CC site that determines the specificity of the interaction between CCR5 and
 CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the
 CC CCR5 N-terminus is required for gp120 binding and may critically modulate
 CC the susceptibility of target cells to HIV-1 infection in vivo. The
 CC invention provides claimed sulfated peptides (see AAB82947) that are
 CC based on the CCR5 N-terminal region and which are effective for
 CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed
 CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+
 CC cells from becoming infected with HIV, of treating a subject whose CD4+
 CC cells are infected with HIV, and of identifying an agent which inhibits
 CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried
 CC out in a subject, especially a human, infected (therapeutic method), not
 CC infected with HIV (prophylactic method), or in a subject who is not
 CC infected with, but has been exposed to, HIV
 XX Sequence 352 AA;
 SQ Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEXFRNVLVFFQK 18
 |||||
 DB 297 YAFVGEXFRNVLVFFQK 314
 |||||
 RESULT 28
 AAU97150
 ID AAU97150 standard; protein; 352 AA.
 XX AAU97150;
 XX 13-AUG-2002 (first entry)
 DT

XX Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
 DE Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
 XX immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 KW hyperproliferative disease; neurological disease; receptor.
 XX Homo sapiens.
 OS US2002048786-A1.
 XX 25-APR-2002.
 PD 09-FEB-2001; 2001US-00779879.
 XX 09-FEB-2000; 2000US-0181259P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.
 PA (LIYY/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI: 2002-434754/46.
 XX N-PSDB; ABK51853.
 DR New nucleic acid encoding an antibody specific for the G-protein
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 PT inflammation.
 XX Claim 61; Fig 1; 180pp; English.
 XX The present invention relates to the isolation of a novel human G-protein
 CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
 CC sequences encoding it. The invention also describes antibodies that bind
 CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide
 CC sequences encoding the antibodies. The antibodies are useful for treating
 CC or preventing inflammation, defective or aberrant chemotaxis of immune
 CC cells and T-cell/antigen-presenting cell interactions, infections and
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 CC infections (especially early-stage human immune deficiency virus (HIV),
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 CC associated with aberrant or deficient expression of the CCR5 receptor or
 CC its ligands. The antibodies are also useful to determine CCR5 expression,
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other
 CC hyperproliferative diseases. The polynucleotide sequences encoding human
 CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
 CC recombinant receptor, and in the treatment of a wide range of diseases
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 CC present sequence represents human G-protein chemokine receptor (CCR5)
 CC HDGNR10 #1
 XX Sequence 352 AA;
 SQ Query Match 100.0%; Score 95; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEXFRNVLVFFQK 18
 |||||
 DB 297 YAFVGEXFRNVLVFFQK 314
 |||||
 RESULT 29
 AAU97152
 ID AAU97152 standard; protein; 352 AA.
 XX AAU97152;
 AC

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XX DT 13-AUG-2002 (first entry)
XX DE Human G-protein chemokine receptor (CCR5) HDGNR10 #2.
XX KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
XX KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
XX KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
XX KW hyperproliferative disease; neurological disease; receptor.
XX OS Homo sapiens.
XX PN US2002048786-A1.
XX PD 25-APR-2002.
XX PF 09-FEB-2001; 2001US-00779879.
XX PR 09-FEB-2000; 2000US-0181258P.
XX PR 09-MAR-2000; 2000US-0187999P.
XX PR 22-SEP-2000; 2000US-0234336P.
XX PA (ROSE/) ROSEN C A.
XX PA (ROSC/) ROSCHKE V.
XX PA (LIYY/) LI Y.
XX PA (RUBE/) RUBEN S M.
XX PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX XX
XX DR WPI: 2002-434754/46.
XX DR N-PSDB; ABK51870.
XX PT New nucleic acid encoding an antibody specific for the G-protein
XX PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
XX PT inflammation.
XX PS Disclosure; Page 165-166; 180pp; English.
XX CC The present invention relates to the isolation of a novel human G-protein
XX CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
XX CC sequences encoding it. The invention also describes antibodies that bind
XX CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide
XX CC sequences encoding the antibodies. The antibodies are useful for treating
XX CC or preventing inflammation, defective or aberrant chemotaxis of immune
XX CC cells and T-cell/antigen-presenting cell interactions, infections and
XX CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
XX CC infections (especially early-stage human immunodeficiency virus (HIV),
XX CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
XX CC associated with aberrant or deficient expression of the CCR5 receptor or
XX CC its ligands. The antibodies are also useful to determine CCR5 expression,
XX CC e.g. for diagnosis, prognosis and monitoring of cancer and other
XX CC hyperproliferative diseases. The polynucleotide sequences encoding human
XX CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
XX CC recombinant receptor, and in the treatment of a wide range of diseases
XX CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
XX CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
XX CC present sequence represents human G-protein chemokine receptor (CCR5)
XX CC HDGNR10 #2
XX SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 297 YAFVGEKFRNYLLVFFQK 314

RESULT 30
AAM52829
ID AAM52829 standard; protein; 352 AA.

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XX AC AAM52829;
XX DT 22-FEB-2002 (first entry)
XX DE Human CCR5 Gln 55 variant.
XX KW CCR5; CC chemokine receptor 5; human; HIV infection;
XX KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
XX KW drug screening; identification; variant.
XX OS Homo sapiens.
XX PN WO200171346-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009155.
XX PR 21-MAR-2000; 2000US-0190946P.
XX PR 21-MAR-2000; 2000US-0190996P.
XX PR 21-MAR-2000; 2000US-0191299P.
XX PR 20-MAR-2001; 2001US-00813448.
XX PR 20-MAR-2001; 2001US-00813651.
XX PR 20-MAR-2001; 2001US-00813653.
XX PA (CONS-) CONSENSUS PHARM INC.
XX PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX DR WPI: 2002-010610/01.
XX DR N-PSDB; ABA02318.
XX PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,
XX PT comprises binding a molecule from library to a molecule having binding
XX PT property corresponding to CCR5 and identifying bound molecule.
XX PS Example 3; Fig 4B; 50pp; English.
XX CC The invention relates to a method for identifying a binding compound for
XX CC chemokine receptor 5 (CCR5). The method involves screening a library
XX CC of test molecules (particularly peptides) with immobilised CCR5, and then
XX CC identifying those molecules which bind. The invention also relates to
XX CC CCR5-binding molecules identified using the method of the invention,
XX CC methods for identifying consensus motifs for CCR5-binding peptides, a
XX CC transfer vector encoding tagged CCR5, a computer-aided methods for
XX CC determining the relative binding affinity of a test molecule to CCR5 and
XX CC a computer aided drug screening assay that utilises the three-dimensional
XX CC structure of CCR5. Compounds identified using the methods of the
XX CC invention are useful for treating or preventing HIV (human
XX CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
XX CC syndrome) in a patient. The methods of the invention may also be used to
XX CC identify agonists or antagonists of the interaction of CCR5 with its
XX CC natural ligand, and to determine a binding motif for CCR5. The present
XX CC sequence represents a naturally occurring variant of human CCR5 in which
XX CC there is a glutamine, rather than a leucine, at position 55
XX SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 297 YAFVGEKFRNYLLVFFQK 314

```

RESULT 31

AAM52828
ID AAM52828 standard; protein; 352 AA.

XX AC AAM52828;

XX AC

DT 22-FEB-2002 (first entry)

XX Human CC chemokine receptor 5 (CCR5).

XX CCR5; CC chemokine receptor 5; human; HIV infection;
KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
KW drug screening; identification.

XX OS Homo sapiens.

XX WO200171346-A2.

XX PD 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009155.

XX 21-MAR-2000; 2000US-0190946P.

XX 21-MAR-2000; 2000US-0190996P.

XX 21-MAR-2000; 2000US-0191299P.

XX 20-MAR-2001; 2001US-00813448.

XX 20-MAR-2001; 2001US-00813651.

XX 20-MAR-2001; 2001US-00813653.

XX (CONS-) CONSENSUS PHARM INC.

XX Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;

XX WPI; 2002-010610/01.

XX N-PSDB; ABA02317.

PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,
PT comprises binding a molecule from library to a molecule having binding
PT property corresponding to CCR5 and identifying bound molecule.

XX Example 3; Fig 4A; 50pp; English.

XX The invention relates to a method for identifying a binding compound for
CC chemokine receptor 5 (CCR5). The method involves screening a library
CC of test molecules (particularly peptides) with immobilised CCR5, and then
CC identifying those molecules which bind. The invention also relates to
CC CCR5-binding molecules identified using the method of the invention, a
CC methods for identifying consensus motifs for CCR5-binding peptides, a
CC transfer vector encoding tagged CCR5, a computer-aided methods for
CC determining the relative binding affinity of a test molecule to CCR5 and
CC a computer aided drug screening assay that utilises the three-dimensional
CC structure of CCR5. Compounds identified using the methods of the
CC invention are useful for treating or preventing HIV (human
CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
CC syndrome) in a patient. The methods of the invention may also be used to
CC identify agonists or antagonists of the interaction of CCR5 with its
CC natural ligand, and to determine a binding motif for CCR5. The present
CC sequence represents human CCR5

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||

DB 297 YAFVGEKFRNLLVFFQK 314
|||||

RESULT 32

ABG70597

ABG70597 standard; protein; 352 AA.

XX ABG70597;

XX 03-DEC-2002 (first entry)

XX Human G-protein chemokine receptor, HDGNR10.

XX Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;

XX haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour;

XX chronic infection; leukaemia; T-cell mediated autoimmune disease;

XX parasitic infection; psoriasis; growth factor activity; allergy;

XX atherogenesis; anaphylaxis; malignancy; inflammation; histamine;

XX immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis;

XX prostaglandin-independent fever; bone marrow failure; shock;

XX rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic;

XX immunosuppressive; antiparasitic; antipsoriatic; antiallergic;

XX antiarteriosclerotic; antiinflammatory; antirheumatic; antiarthritic;

XX antipyretic; receptor.

XX Homo sapiens.

XX US2002099176-A1.

XX 25-JUL-2002.

XX 25-JUN-1999; 99US-00339912.

XX 06-JUN-1995; 95US-00466343.

XX (LIYY/) LI Y.

XX (RUBE/) RUBEN S M.

XX Li Y, Ruben SM;

XX WPI; 2002-690494/74.

XX N-PSDB; ABS54272.

XX Novel human G-protein chemokine receptor polypeptide useful for

XX identifying modulators for stimulating hematopoiesis, wound healing,

XX leukemia, for treating allergy, rheumatoid arthritis, shock and as

XX research agents.

XX Claim 7; Fig 1; 22pp; English.

XX The present invention relates to the isolation of human G-protein

XX chemokine receptor, HDGNR10 (CCR5 receptor), and the polynucleotide

XX sequence encoding it. HDGNR10 polypeptide and polynucleotide sequences

XX are or useful for diagnosing a disease or a susceptibility to a disease

XX related to underexpression of HDGNR10. They are useful for identifying

XX modulators for stimulating haematopoiesis, wound healing, coagulation,

XX angiogenesis, to treat solid tumours, chronic infections, leukaemia, T-

XX cell mediated autoimmune diseases, parasitic infections, psoriasis, or

XX for stimulating growth factor activity. The sequences are also useful for

XX preventing and/or treating allergy, atherogenesis, anaphylaxis.

XX malignancy, chronic and acute inflammation, histamine and immunoglobulin

XX E (IgE)-mediated allergic reactions, prostaglandin-independent fever,

XX bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-

XX eosinophilic syndrome. Polynucleotide sequences encoding HDGNR10 can be

XX used in gene therapy to treat conditions related to underexpression of

XX HDGNR10. The present sequence represents human G-protein chemokine

XX receptor, HDGNR10

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||

DB 297 YAFVGEKFRNLLVFFQK 314
|||||

RESULT 33
ID ABG92883 standard; protein; 352 AA.

XX AC ABG92883;
XX DT 19-NOV-2002 (first entry)
XX DE Human immunoglobulin variable heavy domain #1.
XX
XX Immunoglobulin; variable heavy chain; variable light chain; human;
KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
KW immunologic deficiency syndrome; blood protein disorder; nephritis;
KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
KW lymphocytopenia.

XX OS Homo sapiens.

XX PN WO200264612-A2.

XX PD 22-AUG-2002.

XX PF 08-FEB-2002; 2002WO-US003634.

XX PR 09-FEB-2001; 2001US-00779880.

XX PR 09-FEB-2001; 2001WO-US004153.

XX PR 12-JUN-2001; 2001US-0297257P.

XX PR 08-AUG-2001; 2001US-0310458P.

XX PR 12-OCT-2001; 2001US-0328447P.

XX PR 21-DEC-2001; 2001US-0341725P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Roschke V, Rosen CA, Ruben SM;

XX PF WPI; 2002-643455/69.

XX DR N-PSDB; ABS68606.

XX XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for

XX PT treating, preventing, ameliorating or monitoring diseases or disorders

XX PT associated with aberrant expression of HDGNR10 e.g. cancer.

XX PS Example 55; Fig 4; 562pp; English.

XX CC The invention describes an isolated polynucleotide encoding a first

XX CC antibody at least 95-100% identical to a second antibody consisting of an

XX CC amino acid sequence comprising at least one, two or three CDR regions of

XX CC a variable heavy (VH) or variable light (VL) domain of the antibody

XX CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,

XX CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,

XX CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody

XX CC is useful treating, preventing, ameliorating, prognosing or monitoring

XX CC cancers or other diseases or disorders e.g. immunologic deficiency

XX CC syndromes such as blood protein disorders and ataxia telangiectasia,

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9E-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YAFVGEKFRNYLLVFFQK 18
|||||
DB 297 YAFVGEKFRNYLLVFFQX 314
|||||

RESULT 34

ABG92880

ID ABG92880 standard; protein; 352 AA.

XX AC ABG92880;

XX DT 19-NOV-2002 (first entry)

XX DE Human G-protein chemokine receptor (CCRS) HDGNR10 #1.

XX
KW Immunoglobulin; variable heavy chain; variable light chain; human;

KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;

KW immunologic deficiency syndrome; blood protein disorder; nephritis;

KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;

KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;

KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;

KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;

KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;

KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;

KW lymphocytopenia.

XX OS Homo sapiens.

XX XX WO200264612-A2.

XX PD 22-AUG-2002.

XX PF 08-FEB-2002; 2002WO-US003634.

XX PR 09-FEB-2001; 2001US-00779880.

XX PR 09-FEB-2001; 2001WO-US004153.

XX PR 12-JUN-2001; 2001US-0297257P.

XX PR 08-AUG-2001; 2001US-0310458P.

XX PR 12-OCT-2001; 2001US-0328447P.

XX PR 21-DEC-2001; 2001US-0341725P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Roschke V, Rosen CA, Ruben SM;

XX PF WPI; 2002-643455/69.

XX DR N-PSDB; ABS68653.

XX XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for

XX PT treating, preventing, ameliorating or monitoring diseases or disorders

XX PT associated with aberrant expression of HDGNR10 e.g. cancer.

XX PS Disclosure; Fig 1A-B; 562pp; English.

XX CC The invention describes an isolated polynucleotide encoding a first

XX CC antibody at least 95-100% identical to a second antibody consisting of an

XX CC amino acid sequence comprising at least one, two or three CDR regions of

XX CC a variable heavy (VH) or variable light (VL) domain of the antibody

XX CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,

XX CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,

XX CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody

XX CC is useful treating, preventing, ameliorating, prognosing or monitoring

XX CC cancers or other diseases or disorders e.g. immunologic deficiency

XX CC syndromes such as blood protein disorders and ataxia telangiectasia,

XX CC inflammation associated disorders such as endotoxin lethality, nephritis

XX CC and inflammatory bowel disease, conditions associated with an increase in

CC certain haematopoietic cells such as histiocytosis, defective or aberrant
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
 CC an infectious disease, an autoimmune disease such as Addison's disease,
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
 CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
 CC disease or disorder associated with aberrant expression of novel human G-
 CC protein chemokine receptor (CCR5) HDGNR10. This is an amino acid sequence
 CC of Human G-protein chemokine receptor (CCR5) HDGNR10 #1
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLYLVFFQK 314

RESULT 35
 AAE25808
 ID AAE25808 standard; protein; 352 AA.
 XX
 AC AAE25808;
 XX
 DT 24-FEB-2003 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5), HDGNR10 #1.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
 KW inflammation; viral infection; autoimmune disease; neurodegeneration;
 KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
 KW hyperproliferative disease; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002061834-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 09-FEB-2001; 2001US-00779880.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 PA (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.
 PA (LIY/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Rosen CA, Roschke V, Li Y, Ruben SM;
 XX
 WPI; 2002-499674/53.
 DR N-PSDB; AAD42409.
 XX
 PT New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,
 PT useful for treatment, prevention and diagnosis of e.g. cancer, also
 PT related antibodies.
 XX
 PS Claim 61; Page 163-164; 186pp; English.
 XX
 CC The invention relates to human G-protein chemokine receptor (CCR5),
 CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
 CC antibodies are used for the treatment or prevention of inflammation,
 CC defective or aberrant chemotaxis of immune cells or T cell antigen-
 CC presenting cell interaction, viral infections (specifically human immune
 CC deficiency (including its early stages), cytomegalovirus or pox viruses),
 CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
 CC carinii infection, Kaposi's sarcoma or any condition associated with
 CC the present sequence is human G-protein

CC aberrant expression of CCR5 or their ligands. They are also used for the
 CC detection, diagnosis, prognosis and monitoring of cancers or other
 CC hyperproliferative diseases. The present sequence is human G-protein
 CC chemokine receptor (CCR5), HDGNR10 DNA
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLYLVFFQK 314

RESULT 36
 AAE25811
 ID AAE25811 standard; protein; 352 AA.
 XX
 AC AAE25811;
 XX
 DT 24-FEB-2003 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5), HDGNR10 #2.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
 KW inflammation; viral infection; autoimmune disease; neurodegeneration;
 KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
 KW hyperproliferative disease; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002061834-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 09-FEB-2001; 2001US-00779880.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 PA (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.
 PA (LIY/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Rosen CA, Roschke V, Li Y, Ruben SM;
 XX
 WPI; 2002-499674/53.
 DR N-PSDB; AAD42426.
 XX
 PT New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,
 PT useful for treatment, prevention and diagnosis of e.g. cancer, also
 PT related antibodies.
 XX
 PS Disclosure; Page 170; 186pp; English.
 XX
 CC The invention relates to human G-protein chemokine receptor (CCR5),
 CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
 CC antibodies are used for the treatment or prevention of inflammation,
 CC defective or aberrant chemotaxis of immune cells or T cell antigen-
 CC presenting cell interaction, viral infections (specifically human immune
 CC deficiency (including its early stages), cytomegalovirus or pox viruses),
 CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
 CC carinii infection, Kaposi's sarcoma or any condition associated with
 CC the present sequence is human G-protein
 CC detection, diagnosis, prognosis and monitoring of cancers or other
 CC hyperproliferative diseases. The present sequence is human G-protein
 CC chemokine receptor (CCR5), HDGNR10 DNA
 XX
 SQ Sequence 352 AA;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 39
 ABG75540
 ID ABG75540 standard; protein; 352 AA.

XX AC ABG75540;
 XX DT 16-APR-2003 (first entry)
 XX DE Human G-protein chemokine receptor, HDGNR10, protein.
 XX KW Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor;
 KW HDGNR10; signal transduction; gene therapy; haematopoiesis;
 KW wound healing; coagulation; angiogenesis; tumour; chronic infection;
 KW leukaemia; T-cell mediated auto-immune disease; parasitic infection;
 KW psoriasis; growth factor; allergy; atherogenesis; anaphylaxis;
 KW malignancy; inflammation; histamine; IgE-mediated;
 KW prostaglandin-independent fever; bone marrow failure; silicosis;
 KW sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.
 XX OS Homo sapiens.
 XX PN US2002132269-A1.
 XX PD 19-SEP-2002.
 XX PF 11-FEB-2000; 2000US-00502783.
 XX PR 06-JUN-1995; 95US-00466343.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Li Y, Ruben SM;
 XX WPI; 2003-208944/20.
 XX DR N-PSDB; ABX10635.
 XX PT Novel human G-protein chemokine receptor polypeptide useful for
 PT diagnostic purposes and for identifying modulators of the polypeptide
 PT useful for treating leukemia, autoimmune diseases, psoriasis and allergic
 PT reactions.
 XX Claim 7; Fig 1; 22pp; English.

The invention discloses a G-protein chemokine receptor (sometimes referred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the polynucleotide encoding it. G-protein chemokine receptors are involved in signal transduction pathways. The polynucleotide and polypeptide can be used to identify compounds which activate or inhibit activation of the protein and these compounds are useful for treating a patient having need to activate or inhibit a G-protein chemokine receptor. The compound is administered by providing to the patient DNA encoding the agonist or antagonist and expressing them in vivo (gene therapy). The polynucleotides and polypeptide are also useful for diagnosing a disease or susceptibility to a disease related to an under-expression of the protein. Agonists are useful in stimulating haematopoiesis, wound healing, coagulation, angiogenesis, to treat solid tumours, chronic infections, leukaemia, T-cell mediated auto-immune diseases, parasitic infections, psoriasis and to stimulate growth factor activity. Antagonists are useful in the prevention and treatment of allergy. Atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-eosinophilic syndrome. The sequence presented is the human HDGNR10 protein

SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 6; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 40
 ABR58602
 ID ABR58602 standard; protein; 352 AA.

XX AC ABR58602;

XX DT 09-JUL-2003 (first entry)

XX DE Human cancer related protein SEQ ID NO:259.

XX KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 KW heart disease; atherosclerosis; endometriosis.

XX OS Homo sapiens.

XX PN WO2003025138-A2.

XX PD 27-MAR-2003.

XX PF 17-SEP-2002; 2002WO-US029560.

XX PR 17-SEP-2001; 2001US-0323469P.

XX PR 20-SEP-2001; 2001US-0323887P.

XX PR 13-NOV-2001; 2001US-0350666P.

XX PR 08-FEB-2002; 2002US-0355145P.

XX PR 08-FEB-2002; 2002US-0355257P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
 Zlotnick A;

XX WPI; 2003-354600/33.

XX DR N-PSDB; ACC72740.

XX PT New genes that are up-regulated or down-regulated in cancers, useful as
 PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
 PT therapeutic targets for screening drugs for treating these diseases.

XX Claim 12; Page 745; 767pp; English.

XX The present invention describes an isolated nucleic acid molecule, which
 CC comprises the sequence of any of the genes that are up-regulated or down-
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
 CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
 CC related gene nucleotide sequences which encode the proteins given in
 CC ABR58521 to ABR58709. Also described: (1) determining the presence or
 CC absence of a pathological cell in a patient; (2) an expression vector
 CC comprising a nucleic acid molecule described above; (3) a host cell
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
 CC of (4); (6) specifically targeting a compound to a pathological cell in a
 CC patient by administering to the patient the antibody above; and (7) a
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or
 CC therapeutic targets. In particular, the nucleic acid is useful for
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
 CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in
 CC drug screening, particularly for identifying agents for treating these
 CC pathologies

XX
SQ Sequence 352 AA;
Query Match 100.0%; Score 95; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKPRNYLLVFFQK 18
Db 297 YAFVGEKPRNYLLVFFQK 314

Search completed: September 28, 2004, 09:03:39
Job time : 43.975 secs

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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:00:23 ; Search time 16.2 Seconds
(without alignments)
57.362 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95
Sequence: 1 YAFVGEKFRNYLLVFFQK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep.*
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5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	352	3	US-08-466-343D-2
2	95	100.0	352	3	US-09-087-232A-13
3	95	100.0	352	3	US-08-861-105-14
4	95	100.0	352	3	US-08-575-967A-2
5	95	100.0	352	3	US-09-045-583-52
6	95	100.0	352	4	US-09-517-605-5
7	95	100.0	352	4	US-09-534-185-52
8	95	100.0	352	4	US-08-833-752-5
9	95	100.0	352	4	US-09-502-783A-2
10	95	100.0	352	4	US-09-796-202-1
11	80	84.2	354	4	US-08-724-984A-2
12	79	83.2	347	1	US-08-461-244-3
13	79	83.2	360	1	US-08-450-393A-4
14	79	83.2	360	3	US-08-446-669-4
15	79	83.2	360	3	US-09-045-583-50
16	79	83.2	360	4	US-09-534-185-50
17	79	83.2	360	4	US-09-131-827A-2
18	79	83.2	360	4	US-09-131-827A-20
19	79	83.2	360	5	PCT-US95-00476-4
20	77	81.1	360	4	US-08-833-752-7
21	76	80.0	360	3	US-09-045-583-51
22	76	80.0	360	4	US-09-534-185-51
23	65	68.4	355	3	US-08-575-967A-4
24	65	68.4	355	3	US-08-847-296B-1
25	65	68.4	355	3	US-09-045-583-54
26	65	68.4	355	4	US-09-534-185-54
27	65	68.4	355	4	US-08-720-565-2

28 65 68.4 355 4 US-08-720-565-4 Sequence 4, Appli
29 65 68.4 356 4 US-08-567-882-7 Sequence 7, Appli
30 63 66.3 355 1 US-08-461-244-2 Sequence 2, Appli
31 63 66.3 355 3 US-09-045-583-56 Sequence 56, Appli
32 63 66.3 355 4 US-09-534-185-56 Sequence 5, Appli
33 63 66.3 355 4 US-08-833-752-8 Sequence 8, Appli
34 61 64.2 365 4 US-09-503-219B-8 Sequence 8, Appli
35 61 64.2 374 3 US-09-045-583-48 Sequence 48, Appli
36 61 64.2 374 4 US-09-534-185-48 Sequence 48, Appli
37 60 63.2 355 1 US-08-012-988A-2 Sequence 2, Appli
38 60 63.2 355 1 US-08-450-393A-5 Sequence 5, Appli
39 60 63.2 355 3 US-08-446-669-5 Sequence 5, Appli
40 60 63.2 355 4 US-09-239-938-1 Sequence 1, Appli
41 60 63.2 355 4 US-09-856-319A-14 Sequence 14, Appli
42 60 63.2 355 5 PCT-US95-00476-5 Sequence 5, Appli
43 58 61.1 355 4 US-08-720-565-6 Sequence 6, Appli
44 57 60.0 355 1 US-08-153-848-28 Sequence 28, Appli
45 57 60.0 355 1 US-08-153-848-32 Sequence 32, Appli

ALIGNMENTS

RESULT 1
US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-466-343D-2

Query Match 100.0%; Score 95; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 297 YAFVGEKFRNYLLVFFQK 314

RESULT 2

US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-13
Query Match 100.0%; Score 95; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314
RESULT 3
US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-861-105-14
Query Match 100.0%; Score 95; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314
RESULT 4
US-08-575-967A-2
; Sequence 2, Application US/08575967A
; Patent No. 6265184
; GENERAL INFORMATION:
; APPLICANT: Gray et al.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,967A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6265184and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32918
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: 206-485-1900
; TELEFAX: 206-485-1662
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: /= "88c amino acid sequence"
US-08-575-967A-2

Query Match 100.0%; Score 95; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. NO. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
| | | | | | | | | | | | | | | | | |
DB 297 YAFVGEKFRNYLLVFFQK 314

RESULT 5
US-09-045-583-52
; Sequence 52, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-52

Query Match 100.0%; Score 95; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. NO. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
| | | | | | | | | | | | | | | | | |
DB 297 YAFVGEKFRNYLLVFFQK 314
```

```
RESULT 6
US-09-517-605-5
; Sequence 5, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeek, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-605-5

Query Match 100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. NO. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
| | | | | | | | | | | | | | | | | |
DB 297 YAFVGEKFRNYLLVFFQK 314

RESULT 7
US-09-534-185-52
; Sequence 52, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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```
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

Query Match          100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 8
US-08-833-752-5
; Sequence 5, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-752-5

Query Match          100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 9
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
; TITLE OF INVENTION: HDGNR10
; FILE REFERENCE: 1488.1150006
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; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match          100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 10
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match          100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 11
US-08-984A-2
; Sequence 2, Application US/08724984A
; Patent No. 6388055
; GENERAL INFORMATION:
; APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
; TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-
; TITLE OF INVENTION: CCR5 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,984A
; FILING DATE: October 3, 1996
```

```

; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; FILING DATE:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATGS0023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-724-984A-2

; Query Match 84.2%; Score 80; DB 4; Length 354;
; Best Local Similarity 83.3%; Pred. No. 3.5e-06;
; Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNVLVFFQK 18
   |||||:|||||
Db 299 YAFVGEKFRSVLSVFFRK 316
   |||||:|||||

RESULT 12
US-08-461-244-3
; Sequence 3, Application US/08461244
; Patent No. 5778729
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,244
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-244-3

; Query Match 83.2%; Score 79; DB 1; Length 347;
; Best Local Similarity 83.3%; Pred. No. 5.2e-06;
; Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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; Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNVLVFFQK 18
   |||||:|||||
Db 292 YAFVGEKFRSVLSVFFRK 309
   |||||:|||||

RESULT 13
US-08-450-393A-4
; Sequence 4, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserit, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-4

; Query Match 83.2%; Score 79; DB 1; Length 360;
; Best Local Similarity 83.3%; Pred. No. 5.4e-06;
; Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNVLVFFQK 18
   |||||:|||||
Db 305 YAFVGEKFRSVLSVFFRK 322
   |||||:|||||

RESULT 14
US-08-446-669-4
; Sequence 4, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California

```

```

? COUNTRY: USA
? ZIP: 94306-2155
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/446,669
? Filing Date: May 25, 1995
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Neeley, Richard
? REGISTRATION NUMBER: 30,092
? REFERENCE/DOCKET NUMBER: UCAL-237/01US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-843-5000
? TELEFAX: 415-857-0663
? TELEX: 380816COOLEYPA
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 360 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-446-669-4
?
? Query Match 83.2%; Score 79; DB 3; Length 360;
? Best Local Similarity 83.3%; Fred. No. 5.4e-06;
? Matches 15; Conservative 1; Mismatches 2; Indels
?
? QY 1 YAFVGEKFRNYLLVFFQK 18
?
? Db 305 YAFVGEKFRYLSVFFRK 322

```

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-50

Query Match      83.2%; Score 79; DB 3; Length 360;
Best Local Similarity 83.3%; Pred: No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels

QY      1 YAFVGEKFRNYLLVFFQK 18
      |||||
Db      305 YAFVGEKFRYLSVFFRK 322
      |||||

RESULT 16
US-09-534-185-50
; Sequence 50, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: NO. 6403767el Molecules of the G P
; Heptahelical Receptor Superfamily
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

Query Match      83.2%; Score 79; DB 4; Length 360;
Best Local Similarity 83.3%; Pred: No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels

QY      1 YAFVGEKFRNYLLVFFQK 18
      |||||
Db      305 YAFVGEKFRYLSVFFRK 322
      |||||

RESULT 17
US-09-131-827A-2
; Sequence 2, Application US/09131827A

```

```

; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-00476-4

Query Match 83.2%; Score 79; DB 5; Length 360;
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps

QY 1 YAFVGEKFRNLLVFFQK 18
Db 305 YAFVGEKFRNLLSVFFRK 322

RESULT 20
US-833-752-7
; Sequence 7, Application US/08933752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CG-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

```

LENGTH: 360 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6448375e
US-08-833-752-7

Query Match 81.1%; Score 77; DB 4; Length 360;
Best Local Similarity 77.8%; Pred. No. 1.2e-05;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
|||||:|:|:|
Db 305 YAFVGEKFRYISVFFRK 322

RESULT 21
US-09-045-583-51
Sequence 51, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 51:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-534-185-51

Query Match 80.0%; Score 76; DB 3; Length 360;
Best Local Similarity 77.8%; Pred. No. 1.8e-05;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
|||||:|:|:|
Db 305 YAFVGEKFRYISVFFRK 322

RESULT 22
US-09-534-185-51
Sequence 51, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-534-185-51

Query Match 80.0%; Score 76; DB 4; Length 360;
Best Local Similarity 77.8%; Pred. No. 1.8e-05;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
|||||:|:|:|
Db 305 YAFVGEKFRYISVFFRK 322

RESULT 23
US-08-575-967A-4
Sequence 4, Application US/08575967A
Patent No. 6285184
GENERAL INFORMATION:
APPLICANT: Gray et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:


```
;
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6265184and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32918
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-485-1900
; TELEFAX: 206-485-1662
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88-2B amino acid sequence"
US-08-575-967A-4

Query Match 68.4%; Score 65; DB 3; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
Db 301 YAFVGERFRKYLRRHFFHR 318

RESULT 24
US-08-847-296B-1
; Sequence 1, Application US/08847296B
; Patent No. 6271347
; GENERAL INFORMATION:
; APPLICANT: DAUGHERTY, BRUCE L.
; APPLICANT: DEMARTINO, JULIE A.
; APPLICANT: SICILIANO, SALVATORE J.
; APPLICANT: SPRINGER, MARTIN J.
; TITLE OF INVENTION: EOSINOPHIL EOTAXIN RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,296B
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/016,158
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 60/017,113
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Thies, J. Eric
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19634Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3904
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-847-296B-1

Query Match 68.4%; Score 65; DB 3; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
Db 301 YAFVGERFRKYLRRHFFHR 318

RESULT 25
US-09-045-583-54
; Sequence 54, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-54

Query Match 68.4%; Score 65; DB 3; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
Db 301 YAFVGERFRKYLRRHFFHR 318

RESULT 26
US-09-534-185-54
; Sequence 54, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
```

Therefor
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-09-534-185-54
Query Match 68.4%; Score 65; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 YAFVGEKERNYLLVFPQK 18
DB 301 YAFVGERFRKYLRFHFR 318
RESULT 27
US-08-720-565-2
Sequence 2, Application US/08720565
Patent No. 6537764
GENERAL INFORMATION:
APPLICANT: Gerard, Craig J.
APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Mackay, Charles R.
APPLICANT: Ponath, Paul D.
APPLICANT: Post, Theodore W.
APPLICANT: Qin, Shixin
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
TITLE OF INVENTION: ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-565-2
Query Match 68.4%; Score 65; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 YAFVGEKERNYLLVFPQK 18
DB 301 YAFVGERFRKYLRFHFR 318
RESULT 28
US-08-720-565-4
Sequence 4, Application US/08720565
Patent No. 6537764
GENERAL INFORMATION:
APPLICANT: Gerard, Craig J.
APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Mackay, Charles R.
APPLICANT: Ponath, Paul D.
APPLICANT: Post, Theodore W.
APPLICANT: Qin, Shixin
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
TITLE OF INVENTION: ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.

REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-565-4

Query Match 68.4%; Score 65; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 301 YAFVGERPKYLRHFFHR 318

RESULT 29
US-08-567-882-7
Sequence 7, Application US/08567882
Patent No. 6512103
GENERAL INFORMATION:
APPLICANT: Dairaghi, Daniel J.
APPLICANT: Hara, Takahiko
APPLICANT: Miyajima, Atsushi
APPLICANT: Schall, Thomas J.
APPLICANT: Wang, Wei
APPLICANT: Yoshimura, Akihiko
TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,882
FILING DATE: 08-DEC-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0506
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-567-882-7

Query Match 68.4%; Score 65; DB 4; Length 356;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 302 YAFVGERPKYLRHFFHR 319

RESULT 30
US-08-461-244-2
Sequence 2, Application US/08461244
Patent No. 5776729
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Yi, Li
APPLICANT: Ruben, Steven M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-445
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-244-2

Query Match 66.3%; Score 63; DB 1; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0034;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 300 YAFVGEKPKHLSEIFQK 317

RESULT 31
US-09-045-583-56
Sequence 56, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-56

Query Match 66.3%; Score 63; DB 3; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0034;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 300 YAFVGEKFKHLSEIFQK 317

RESULT 32
US-09-534-185-56
Sequence 56, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-534-185-56

Query Match 66.3%; Score 63; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0034;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 300 YAFVGEKFKHLSEIFQK 317

RESULT 33
US-08-833-752-8
Sequence 8, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92860
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 8:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6448375e
US-08-833-752-8

Query Match 66.3%; Score 63; DB 4; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.0034;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 301 YAFVGERFRKRIHFFHR 318

RESULT 34
US-09-503-219B-8
Sequence 8, Application US/09503219B
Patent No. 6645491
GENERAL INFORMATION:
APPLICANT: Oldham, Elizabeth R.
APPLICANT: Horney, Bernhard
APPLICANT: Dieu-No. 6645491Jean, Marie C.

APPLICANT: Caux, Christophe
APPLICANT: Zlotnick, Albert
TITLE OF INVENTION: CHEMOKINE USES; COMPOSITIONS; METHODS
FILE REFERENCE: DR0934KI
CURRENT APPLICATION NUMBER: US/09/503,219B
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: US 60/118,335
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (579)..(579)
OTHER INFORMATION: unknown nucleotide
US-09-503-219B-8

Query Match 64.2%; Score 61; DB 4; Length 365;
Best Local Similarity 76.9%; Pred. No. 0.0079;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
|||:|||||
Db 307 YAFIGQKFRNYFL 319

RESULT 35
US-09-045-583-48
; Sequence 48, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-045-583-48

Query Match 64.2%; Score 61; DB 3; Length 374;
Best Local Similarity 76.9%; Pred. No. 0.0079;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
|||:|||||
Db 307 YAFIGQKFRNYFL 319

RESULT 36
US-09-534-185-48
; Sequence 48, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-534-185-48

Query Match 64.2%; Score 61; DB 4; Length 374;
Best Local Similarity 76.9%; Pred. No. 0.0081;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
|||:|||||
Db 316 YAFIGQKFRNYFL 328

RESULT 37
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; Macrophage Inflammatory Protein-1 alpha (MIP-1
; alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
; US-08-012-988A-2

Query Match 64.2%; Score 61; DB 4; Length 374;
Best Local Similarity 76.9%; Pred. No. 0.0081;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
|||:|||||
Db 316 YAFIGQKFRNYFL 328

US-09-534-185-48
; Query Match 64.2%; Score 61; DB 4; Length 374;
; Best Local Similarity 76.9%; Pred. No. 0.0081;
; Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
; Qy 1 YAFVGEKFRNYLL 13
; |||:|||||
; Db 316 YAFIGQKFRNYFL 328
; RESULT 37
; US-08-012-988A-2
; ; Sequence 2, Application US/08012988A
; ; Patent No. 5652133
; ; GENERAL INFORMATION:
; ; APPLICANT: Murphy, Philip M.
; ; TITLE OF INVENTION: Cloning and Expression of Human
; ; Macrophage Inflammatory Protein-1 alpha (MIP-1
; ; alpha)/RANTES Receptor
; ; NUMBER OF SEQUENCES: 2
; ; US-08-012-988A-2

Query Match 64.2%; Score 61; DB 3; Length 374;
Best Local Similarity 76.9%; Pred. No. 0.0079;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
|||:|||||
Db 307 YAFIGQKFRNYFL 319

US-09-045-583-48
; APPLICANT: Caux, Christophe
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: CHEMOKINE USES; COMPOSITIONS; METHODS
; FILE REFERENCE: DR0934KI
; CURRENT APPLICATION NUMBER: US/09/503,219B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/118,335
; PRIOR FILING DATE: 1999-02-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (579)..(579)
; OTHER INFORMATION: unknown nucleotide
; US-09-503-219B-8

Query Match 64.2%; Score 61; DB 4; Length 374;
Best Local Similarity 76.9%; Pred. No. 0.0079;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
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Db 307 YAFIGQKFRNYFL 319

RESULT 40
US-09-239-938-1
; Sequence 1, Application US/09239938
; Patent No. 6329510
; GENERAL INFORMATION:
; APPLICANT: Qin, Shixin
; APPLICANT: Newman, Walter
; APPLICANT: Kassam, Nasim
; APPLICANT: LeukoSite, Inc.
; TITLE OF INVENTION: ANTI-CCR1 ANTIBODIES AND METHODS OF USE
; FILE REFERENCE: LKS97-13
; CURRENT APPLICATION NUMBER: US/09/239,938
; CURRENT FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-239-938-1

Query Match 63.2%; Score 60; DB 4; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YAFVGEFRNYLLVFFOK 18
| | | | | | | | | | | | | | | | | | | | | |
Db 301 YAFVGERFRKYLROLFHR 318

Search completed: September 28, 2004, 09:21:33
Job time : 16.2 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:06:23 ; Search time 59.625 Seconds
(without alignments)
97.074 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95
Sequence: 1 YAFVGEKFRNLLVFFQK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 2: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 5: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 6: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 7: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 8: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 9: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 11: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	18	14	US-10-084-813-15
2	95	100.0	18	14	US-10-084-813-105
3	95	100.0	332	14	US-10-095-876A-2
4	95	100.0	352	9	US-09-725-285-2
5	95	100.0	352	9	US-09-759-841-2
6	95	100.0	352	9	US-09-779-879A-2
7	95	100.0	352	9	US-09-779-879A-22
8	95	100.0	352	9	US-09-779-880A-2
9	95	100.0	352	9	US-09-779-880A-22
10	95	100.0	352	9	US-09-813-653-15
11	95	100.0	352	9	US-09-813-653-17
12	95	100.0	352	9	US-09-796-202-1
13	95	100.0	352	9	US-09-195-662A-2
14	95	100.0	352	9	US-09-339-912A-2
15	95	100.0	352	9	US-09-938-719-5

16	95	100.0	352	9	US-09-938-726-5	Sequence 5, Appli
17	95	100.0	352	9	US-09-938-703-5	Sequence 5, Appli
18	95	100.0	352	9	US-09-502-783A-2	Sequence 2, Appli
19	95	100.0	352	10	US-09-734-221A-14	Sequence 14, Appli
20	95	100.0	352	11	US-09-826-509-477	Sequence 477, App
21	95	100.0	352	12	US-10-151-274-5	Sequence 5, Appli
22	95	100.0	352	13	US-10-106-623-2	Sequence 2, Appli
23	95	100.0	352	13	US-10-106-623-20	Sequence 20, Appli
24	95	100.0	352	14	US-10-232-686-2	Sequence 2, Appli
25	95	100.0	352	14	US-10-086-814-1	Sequence 1, Appli
26	95	100.0	352	14	US-10-067-800-2	Sequence 2, Appli
27	95	100.0	352	14	US-10-067-800-22	Sequence 22, Appli
28	95	100.0	352	14	US-10-290-058A-6	Sequence 6, Appli
29	95	100.0	352	14	US-10-225-567A-352	Sequence 352, App
30	95	100.0	352	14	US-10-323-314-1	Sequence 1, Appli
31	95	100.0	352	14	US-10-072-301-1	Sequence 1, Appli
32	95	100.0	352	14	US-10-164-649-52	Sequence 52, Appli
33	95	100.0	352	14	US-10-071-866-1	Sequence 1, Appli
34	95	100.0	352	14	US-10-135-839-2	Sequence 2, Appli
35	95	100.0	352	14	US-10-135-839-22	Sequence 22, Appli
36	95	100.0	352	14	US-10-339-423-67	Sequence 67, Appli
37	95	100.0	352	14	US-10-439-845-2	Sequence 2, Appli
38	95	100.0	352	14	US-10-439-845-4	Sequence 4, Appli
39	95	100.0	352	15	US-10-360-828-1	Sequence 1, Appli
40	95	100.0	352	16	US-10-661-798-5	Sequence 5, Appli
41	95	100.0	352	16	US-10-791-905-2	Sequence 2, Appli
42	95	100.0	352	16	US-10-612-791-5	Sequence 5, Appli
43	79	83.2	347	9	US-09-104-792-3	Sequence 3, Appli
44	79	83.2	347	14	US-10-176-078-3	Sequence 3, Appli
45	79	83.2	360	9	US-09-131-827A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-084-813-15
; Sequence 15, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-15

Query Match 100.0%; Score 95; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||
Db 1 YAFVGEKFRNLLVFFQK 18
|||||

RESULT 2
US-10-084-813-105
; Sequence 105, Application US/10084813
; Publication No. US20030068615A1

GENERAL INFORMATION:
APPLICANT: SAXINGER, CARL
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
FILE REFERENCE: 215875
CURRENT APPLICATION NUMBER: US/10/084,813
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/US00/23505
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,270
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: PatentIn version 3.1
SEQ ID NO 105
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-105

Query Match 100.0%; Score 95; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 1 YAFVGEKFRNLLVFFQK 18

RESULT 3
US-10-095-876A-2
Sequence 2, Application US/10095876A
Patent No. US20030148294A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice; Bandman, Olga
APPLICANT: Coleman, Roger; Wilde, Craig G.
TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
FILE REFERENCE: PP-0060-1 CON
CURRENT APPLICATION NUMBER: US/10/095,876A
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 08/638,081
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 332
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-2

Query Match 100.0%; Score 95; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 277 YAFVGEKFRNLLVFFQK 294

RESULT 4
US-09-725-285-2
Sequence 2, Application US/09725285
Patent No. US20010000241A1
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
TITLE OF INVENTION: (CCR5 Receptor)
FILE REFERENCE: 1488.1150003

CURRENT APPLICATION NUMBER: US/09/725,285
CURRENT FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 09/339,912
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Artificial Sequence: Genomic
FEATURE:
OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 5
US-09-759-841-2
Sequence 2, Application US/09759841
Patent No. US20010039026A1
GENERAL INFORMATION:
APPLICANT: Rickett, Graham A
APPLICANT: Dobbs, Susan
APPLICANT: Perros, Manoussos
TITLE OF INVENTION: Assay Method
FILE REFERENCE: PC10348ADME
CURRENT APPLICATION NUMBER: US/09/759,841
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: GB 0000661.9
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GB 0000663.5
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GB 0000659.3
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-759-841-2

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 6
US-09-779-879A-2
Sequence 2, Application US/09779879A
Patent No. US20020048786A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Roschke, Viktor
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
FILE REFERENCE: 1488.115000A

; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-2

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 7

US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-22

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 8

US-09-779-880A-2
; Sequence 2, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A

; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-2

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 9

US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-22

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 10

US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-15

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 11
US-09-813-653-17
; Sequence 17, Application US/098113653
; Patent No. US20020084770A1
; GENERAL INFORMATION:

; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-17

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 12
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US2002008813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1

; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 13
US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:

; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGMR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 14
US-09-339-912A-2
; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:

; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2

Query Match 100.0%; Score 95; DB 9; Length 352;

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Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
      |||
Db      297 YAFVGEKFRNYLLVFFQK 314
      |||

RESULT 15
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-AUG-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
;
US-09-938-719-5

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
      |||
Db      297 YAFVGEKFRNYLLVFFQK 314
      |||

RESULT 16
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;
; NUMBER OF SEQUENCES: 17

```

```
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: <Unknown>
/ INFORMATION FOR SEQ ID NO: 5:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 352 amino acids
/     TYPE: amino acid
/     TOPOLOGY: linear
/   MOLECULE TYPE: protein
/   SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5

Query Match      100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 18
US-09-502-783A-2
/ Sequence 2, Application US/09502783A
/ Patent No. US20020132269A1
/ GENERAL INFORMATION:
/   APPLICANT: Li, Yi
/   APPLICANT: Ruben, Steven M.
/   TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS
/   FILE REFERENCE: 1498.1150006
/   CURRENT APPLICATION NUMBER: US/09/502,783A
/   CURRENT FILING DATE: 2001-08-23
/   PRIOR FILING DATE: 1995-06-06
/   NUMBER OF SEQ ID NOS: 9
/   SOFTWARE: PatentIn version 3.0
/   SEQ ID NO 2
/   LENGTH: 352
/   TYPE: PRT
/   ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match      100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 19
US-09-734-221A-14
/ Sequence 14, Application US/09734221A
/ Publication No. US20030096221A1
/ GENERAL INFORMATION:
/   APPLICANT: LITWAN, DAN R.
/   APPLICANT: DENG, HONGKUI
/   APPLICANT: ELMELIER, WILFRIED
/   APPLICANT: LANDAU, NATHANIEL R.
/   APPLICANT: LIU, RONG
/   TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
/   MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
/   USES THEREOF
/   NUMBER OF SEQUENCES: 14
/   CORRESPONDENCE ADDRESS:
/   ADDRESSEE: David A. Jackson, Esq.
/   STREET: 411 Hackensack Ave, Continental Plaza, 4th
/   Floor
/   CITY: Hackensack
/   STATE: New Jersey
/   COUNTRY: USA
```

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/ ZIP: 07601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/09/734,221A
/   FILING DATE: 11-Dec-2000
/   CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 08/666,020
/   FILING DATE: 19-JUN-1996
/   APPLICATION NUMBER: US 08/227,319
/   FILING DATE: 13-APR-1994
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Jackson Esq., David A.
/   REGISTRATION NUMBER: 26,742
/   REFERENCE/DOCKET NUMBER: 1049-1-004 N2
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: 201-487-5800
/   TELEFAX: 201-343-1684
/ INFORMATION FOR SEQ ID NO: 14:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 352 amino acids
/     TYPE: amino acid
/     STRANDEDNESS: single
/     TOPOLOGY: linear
/   MOLECULE TYPE: protein
/   HYPOTHETICAL: NO
/   ORIGINAL SOURCE:
/     ORGANISM: Homo sapiens
/     SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14

Query Match      100.0%; Score 95; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 20
US-09-826-509-477
/ Sequence 477, Application US/09826509
/ Publication No. US20030204073A1
/ GENERAL INFORMATION:
/   APPLICANT: Lehmann-Bruinsma, Karin
/   APPLICANT: Liaw, Chen W.
/   APPLICANT: Lin, I-Lin
/   TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
/   FILE REFERENCE: AREN-207
/   CURRENT APPLICATION NUMBER: US/09/826,509
/   CURRENT FILING DATE: 2001-04-05
/   PRIOR APPLICATION NUMBER: 60/195,747
/   PRIOR FILING DATE: 2000-04-07
/   PRIOR APPLICATION NUMBER: 09/170,496
/   PRIOR FILING DATE: 1998-10-13
/   NUMBER OF SEQ ID NOS: 589
/   SOFTWARE: PatentIn Version 2.1
/   SEQ ID NO 477
/   LENGTH: 352
/   TYPE: PRT
/   ORGANISM: Homo sapiens
US-09-826-509-477

Query Match      100.0%; Score 95; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      297 YAFVGEKFRNYLLVFFQK 314
|||||
RESULT 24
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCRS) HDGMR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
|||||
DB      297 YAFVGEKFRNYLLVFFQK 314

RESULT 25
US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana C.
; APPLICANT: Olson, William A.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
|||||
DB      297 YAFVGEKFRNYLLVFFQK 314

RESULT 26
US-10-067-800-2
; Sequence 2, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGMR10
; FILE REFERENCE: 1488.115000I
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-2

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
|||||
DB      297 YAFVGEKFRNYLLVFFQK 314

RESULT 27
US-10-067-800-22
; Sequence 22, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGMR10
; FILE REFERENCE: 1488.115000I
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-22

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
|||||
DB      297 YAFVGEKFRNYLLVFFQK 314
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RESULT 28
US-10-290-058A-6
; Sequence 6, Application US/10290058A
; Publication No. US20030104455A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
; FILE REFERENCE: MP101-289P1RM
; CURRENT APPLICATION NUMBER: US/10/290,058A
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/344,552
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-058A-6

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 29
US-10-225-567A-352
; Sequence 352, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-352

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 30
US-10-323-314-1
; Sequence 1, Application US/10323314
; Publication No. US20030139571A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010-1/JPW/MAF/DJK
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; CURRENT APPLICATION NUMBER: US/10/323,314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-10-323-314-1

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 31
US-10-072-301-1
; Sequence 1, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-301-1

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 32
US-10-164-649-52
; Sequence 52, Application US/10164649
; Publication No. US20030162943A1
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/10/164,649
; FILING DATE: 07-Jun-2002
; CLASSIFICATION: <Unknown>
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/045,583
/ FILING DATE: 20-MAR-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mandragouras, Amy E.
/ REGISTRATION NUMBER: 36,207
/ REFERENCE/DOCKET NUMBER: MNI-044
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)742-4214
/ INFORMATION FOR SEQ ID NO: 52:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 352 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FRAGMENT TYPE: internal
/ SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-164-649-52

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 33
US-10-071-866-1
/ Sequence 1, Application US/10071866
/ Publication No. US20030165988A1
/ GENERAL INFORMATION:
/ APPLICANT: Hua, Shao-bing
/ APPLICANT: Pauling, Michelle H.
/ APPLICANT: Zhu, Li
/ TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST E
/ TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
/ FILE REFERENCE: 25636-717
/ CURRENT APPLICATION NUMBER: US/10/071,866
/ CURRENT FILING DATE: 2002-02-08
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-071-866-1

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 34
US-10-135-839-2
/ Sequence 2, Application US/10135839
/ Publication No. US20030166024A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen, Craig A.
/ APPLICANT: Roschke, Viktor
/ APPLICANT: Li, Yi
/ TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
/ TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
/ FILE REFERENCE: 1488.115000A
/ CURRENT APPLICATION NUMBER: US/10/135,839
/ CURRENT FILING DATE: 2002-05-01
/ PRIOR APPLICATION NUMBER: US/09/779,879A

/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: US 60/187,999
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: US 60/234,336
/ PRIOR FILING DATE: 2000-09-22
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-135-839-2

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 35
US-10-135-839-22
/ Sequence 22, Application US/10135839
/ Publication No. US20030166024A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen, Craig A.
/ APPLICANT: Roschke, Viktor
/ APPLICANT: Li, Yi
/ APPLICANT: Ruben, Steven, M.
/ TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
/ FILE REFERENCE: 1488.115000A
/ CURRENT APPLICATION NUMBER: US/10/135,839
/ CURRENT FILING DATE: 2002-05-01
/ PRIOR APPLICATION NUMBER: US/09/779,879A
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: US 60/187,999
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: US 60/234,336
/ PRIOR FILING DATE: 2000-09-22
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 22
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-135-839-22

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 36
US-10-239-423-67
/ Sequence 67, Application US/10239423
/ Publication No. US20030186889A1
/ GENERAL INFORMATION:
/ APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMAN, Knut;
/ APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
/ TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
/ TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
/ TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases;
/ TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
/ TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
/ FILE REFERENCE: 022217us
/ CURRENT APPLICATION NUMBER: US/10/239,423
/ CURRENT FILING DATE: 2002-09-23
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; PRIOR APPLICATION NUMBER: DEL0016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-67
Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
      |||
Db      297 YAFVGEKFRNLLVFFQK 314

RESULT 37
US-10-439-845-2
; Sequence 2, Application US/10439845
; Publication No. US20030195348A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-439-845-2

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
      |||
Db      297 YAFVGEKFRNLLVFFQK 314

RESULT 38
US-10-439-845-4
; Sequence 4, Application US/10439845
; Publication No. US20030195348A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-439-845-4

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
      |||
Db      297 YAFVGEKFRNLLVFFQK 314

RESULT 39
US-10-360-828-1
; Sequence 1, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
;
QY      1 YAFVGEKFRNLLVFFQK 18
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```

      |||
Db      297 YAFVGEKFRNLLVFFQK 314

RESULT 38
US-10-439-845-4
; Sequence 4, Application US/10439845
; Publication No. US20030195348A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-439-845-4

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
      |||
Db      297 YAFVGEKFRNLLVFFQK 314

RESULT 39
US-10-360-828-1
; Sequence 1, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
;
QY      1 YAFVGEKFRNLLVFFQK 18
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; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-360-828-1

Query Match 100.0%; Score 95; DB 15; Length 352;
Best Local Similarity 100.0%; Pred.No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
|||
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 40
US-10-661-798-5
; Sequence 5, Application US/10661798
; Publication No. US20040110127A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; APPLICANT: Frederic, Libert
; TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV En
; TITLE OF INVENTION: a Cell
; FILE REFERENCE: 9409/2023F
; CURRENT APPLICATION NUMBER: US/10/661,798
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: 09/938,703
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/626,939
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 08/833,752
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: 08/810,028
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: EP 96870021.1
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: EP 96870102.9
; PRIOR FILING DATE: 1996-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-798-5

Query Match 100.0%; Score 95; DB 16; Length 352;
Best Local Similarity 100.0%; Pred.No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
|||
Db 297 YAFVGEKFRNYLLVFFQK 314

Search completed: September 28, 2004, 09:44:42
Job time : 59.625 secs

A/Accession: A45177
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-355 <NEO>
 A/Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 A/Experimental source: HU60 cells
 A/Note: sequence extracted from NCBI backbone (NCBIP:124876)
 R:Gao, J.
 J. Exp. Med. 177, 1421-1427, 1993
 A/Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
 A/Reference number: I55671; MUID:92240122; PMID:7683036
 A/Accession: I55671
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-355 <RES>
 A/Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 C/Genetics:
 A/Gene: GDB:CMKBR1; CMKR-1
 A/Cross-references: GDB:I38446; OMIM:601159
 A/Map position: 3p21-3p21
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tm
 F:36-60/Domain: transmembrane #status predicted <TM1>
 F:71-91/Domain: transmembrane #status predicted <TM2>
 F:108-129/Domain: transmembrane #status predicted <TM3>
 F:147-171/Domain: transmembrane #status predicted <TM4>
 F:203-223/Domain: transmembrane #status predicted <TM5>
 F:240-264/Domain: transmembrane #status predicted <TM6>
 F:288-305/Domain: transmembrane #status predicted <TM7>
 F:5/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:24-273.106-183/disulfide bonds: #status predicted
 F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 Query Match 63.2%; Score 60; DB 2; Length 355;
 Best Local Similarity 61.1%; Pred. No. 0.024;
 Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 DB 301 YAFVGEKFRNLLVFFQK 318
 RESULT 9
 I58186
 Probable G protein-coupled receptor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
 C/Accession: I58186
 R:Harrison, J.K.; Barber, C.M.; Lynch, K.R.
 Neurosci. Lett. 169, 85-89, 1994
 A/Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and B
 A/Reference number: I58186; MUID:94323113; PMID:8047298
 A/Accession: I58186
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-354 <RES>
 A/Cross-references: EMBL:U04808; NID:g2558635; PIDN:AA87093.1; PID:g439861
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor
 Query Match 61.1%; Score 58; DB 2; Length 354;
 Best Local Similarity 61.1%; Pred. No. 0.053;
 Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 DB 294 YAFVGEKFRNLLVFFQK 311
 RESULT 10
 JC4304
 orphan G protein-coupled receptor - human
 N/Alternate names: V28 protein
 C/Species: Homo sapiens (man)
 C/Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
 C/Accession: JC4304
 R:Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
 Gene 163, 295-299, 1995
 A/Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to ge
 A/Reference number: JC4304; MUID:96011651; PMID:7590284
 A/Accession: JC4304
 A/Molecule type: mRNA
 A/Residues: 1-355 <RAP>
 A/Cross-references: GB:U03050; NID:g665580; PIDN:AAA91783.1; PID:g665581
 A/Experimental source: peripheral blood mononuclear cell
 C/Comment: This protein is a cell-surface receptor which recognizes extracellular signals;
 C/Comment: This protein is a key regulator of many immune and homeostatic responses, and
 C/Genetics:
 A/Gene: v28
 A/Map position: 3pter-p21
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
 F:35-57/Domain: transmembrane #status predicted <TM1>
 F:66-88/Domain: transmembrane #status predicted <TM2>
 F:104-125/Domain: transmembrane #status predicted <TM3>
 F:146-165/Domain: transmembrane #status predicted <TM4>
 F:197-217/Domain: transmembrane #status predicted <TM5>
 F:230-254/Domain: transmembrane #status predicted <TM6>
 F:275-296/Domain: transmembrane #status predicted <TM7>
 Query Match 60.0%; Score 57; DB 2; Length 355;
 Best Local Similarity 61.1%; Pred. No. 0.078;
 Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 DB 293 YAFVGEKFRNLLVFFQK 310
 RESULT 11
 A57160
 Chemokine (C-C) receptor 4 - human
 N/Alternate names: C-C CKR-4
 C/Species: Homo sapiens (man)
 C/Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C/Accession: A57160
 R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogwerf, A.J.; Proudfoot, A.E.I.; We
 J. Biol. Chem. 270, 19495-19500, 1995
 A/Title: Molecular cloning and functional expression of a novel CC chemokine receptor cbr
 A/Reference number: A57160; MUID:95370289; PMID:7642634
 A/Accession: A57160
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-360 <POW>
 A/Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
 A/Note: source clone K5-5
 C/Genetics:
 A/Gene: GDB:CMKBR4
 A/Cross-references: GDB:677463
 A/Map position: 3p21-3p21
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
 F:40-65/Domain: transmembrane #status predicted <TM1>
 F:76-97/Domain: transmembrane #status predicted <TM2>
 F:112-133/Domain: transmembrane #status predicted <TM3>
 F:151-175/Domain: transmembrane #status predicted <TM4>
 F:208-226/Domain: transmembrane #status predicted <TM5>
 F:243-264/Domain: transmembrane #status predicted <TM6>
 F:291-308/Domain: transmembrane #status predicted <TM7>
 F:29-276.110-187/disulfide bonds: #status predicted
 F:72.350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:183.194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 Query Match 60.0%; Score 57; DB 2; Length 360;


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Best Local Similarity 58.8%; Pred. No. 0.079;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 17
      | : ||||| : | :
Db      304 YFELGEKFRKYLQLFK 320

RESULT 12
I49339
Macrophage inflammatory protein-1 alpha receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I49339
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokines
A:Reference number: I49339; MUID:95340546; PMID:7542241
A:Accession: I49339
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <RES>
A:Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
C:Superfamily: vertebrate rhodopsin

Query Match          55.8%; Score 53; DB 2; Length 355;
Best Local Similarity 55.6%; Pred. No. 0.37;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
      | : ||||| : | :
Db      301 YFVGERFWKYLQLFQR 318

RESULT 13
I49340
MIP-1 alpha receptor like-1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I49340
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokines
A:Reference number: I49339; MUID:95340546; PMID:7542241
A:Accession: I49340
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <RES>
A:Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
C:Superfamily: vertebrate rhodopsin

Query Match          55.8%; Score 53; DB 2; Length 356;
Best Local Similarity 50.0%; Pred. No. 0.37;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
      | : ||||| : | :
Db      302 YFVGEKFRKYLWQLFRR 319

RESULT 14
JC4587
Chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: JC4587
R;Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A:Reference number: JC4587; MUID:96136324; PMID:8573157
A:Accession: JC4587
A:Molecule type: mRNA
A:Residues: 1-360 <HOO>

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A:Molecule type: mRNA
A:Residues: 1-356 <GOB>
A:Cross-references: EMBL:X77797
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match      52.6%; Score 50; DB 2; Length 356;
Best Local Similarity 69.2%; Pred. No. 1.2;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKPRNYLL 13
DB 310 YAFIQGKFRHGILL 322

RESULT 17
A48921
interleukin-8 receptor type B - mouse
N:Alternate names: G-protein coupled receptor GPCR16
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text change 05-Nov-1999
C:Accession: A48921; A53677; I49348; I55421; H48909; I53774
R:Carretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert,
Genomics 18, 410-413, 1993
A:Title: The murine homologue of the human interleukin-8 receptor type B maps near the
A:Reference number: A48921; MUID:94117014; PMID:8288247
A:Accession: A48921
A:Molecule type: DNA
A:Residues: 1-359 <CEB>
A:Cross-references: GB:L23637; NID:9435093; PIDN:AAA39305.1; PID:G435094
R:Suruki, H.; Prado, G.N.; Wilkenson, N.; Navarro, J.
J. Biol. Chem. 269, 18263-18266, 1994
A:Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding
A:Reference number: A53677; MUID:94308043; PMID:7518426
A:Accession: A53677
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-359 <SUZ>
A:Cross-references: GB:L26549
A>Note: sequence extracted from NCBI backbone (NCBIP:149812)
R:Lee, J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
J. Immunol. 155, 2158-2164, 1995
A:Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
A:Reference number: I49348; MUID:95363183; PMID:7636264
A:Accession: I49348
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <RES>
A:Cross-references: EMBL:U31207; NID:9550174; PIDN:AAC52239.1; PID:G950175
R:Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
J. Biol. Chem. 269, 23355-23358, 1994
A:Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression
A:Reference number: I55421; MUID:95050766; PMID:7961909
A:Accession: I55421
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <REZ>
A:Cross-references: GB:L13239; NID:G293665; PIDN:AAA62109.1; PID:G293666
R:Winkie, T.M.; Chen, Y.; Gilbert, D.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.
Genomics 18, 175-184, 1993
A:Title: Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptor
A:Reference number: A48909; MUID:94116980; PMID:8288218
A:Accession: A48909
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 145-258 <MIL>
A:Cross-references: GB:L20337; NID:G438800; PIDN:AAA16853.1; PID:G438801
R:Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.
Gene 142, 297-300, 1994
A:Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.
A:Reference number: I53774; MUID:94252584; PMID:8194768
A:Accession: I53774
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-359 <RE3>
A:Cross-references: GB:D17630; NID:G493671; PIDN:BA04536.1; PID:G493672
C:Genetics:
A:Gene: IL8rb
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:49-74/Domain: transmembrane #status predicted <TM1>
F:84-106/Domain: transmembrane #status predicted <TM2>
F:120-141/Domain: transmembrane #status predicted <TM3>
F:163-182/Domain: transmembrane #status predicted <TM4>
F:213-234/Domain: transmembrane #status predicted <TM5>
F:251-271/Domain: transmembrane #status predicted <TM6>
F:308-328/Domain: transmembrane #status predicted <TM7>

Query Match      52.6%; Score 50; DB 2; Length 359;
Best Local Similarity 69.2%; Pred. No. 1.2;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKPRNYLL 13
DB 313 YAFIQGKFRHGILL 325

RESULT 18
A53611
interleukin-8 receptor type B - human
C:Species: Homo sapiens (man)
C>Date: 07-Oct-1994 #sequence revision 12-Apr-1996 #text change 05-Nov-1999
C:Accession: I37898; I38712; A53611; A39446
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for human interleukin-8
A:Reference number: I37898; MUID:95014476; PMID:7929358
A:Accession: I37898
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <RES>
A:Cross-references: EMBL:U11869; NID:G511801; PIDN:AAB60656.1; PID:G511803
A:Accession: I38712
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <RE2>
A:Cross-references: EMBL:U11872; NID:G511808; PIDN:AAA4380.1; PID:G511809; EMBL:U11873;
I1876; NID:G511816; PID:G511817; EMBL:U11877; NID:G511818; PID:G511819; EMBL:U11878; NID:
R:Sprengr, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J. Biol. Chem. 269, 11065-11072, 1994
A:Title: Structure, genomic organization, and expression of the human interleukin-8 receptor
A:Reference number: A53611; MUID:94209273; PMID:7512557
A:Accession: A53611
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 6-360 <SPR>
A:Cross-references: GB:M99412; GB:L19593
R:Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor.
A:Reference number: A39446; MUID:91368200; PMID:1891716
A:Accession: A39446
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 6-360 <MUR>
A:Cross-references: GB:M73969
C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, inc
C:Genetics:
A:Gene: GDB:IL8RB; IL8RA
A:Cross-references: GDS:127868; OMIM:146928
A:Map position: 2q35-2q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match      52.6%; Score 50; DB 2; Length 360;

```

```
Best Local Similarity 59.2%; Pred. No. 1.2;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
    |||:||||:
Db 314 YAFVGEKFRHGLL 326

RESULT 19
A45680
G protein-coupled peptide receptor EBI 1 - human
C:Species: Homo sapiens (man)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45680
R:Birkenbach, M.; Josefsen, K.; Yalanianchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled R
A:Reference number: A45680; MUID:93188173; PMID:8383238
A:Accession: A45680
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-378 <BR>
A:Cross-references: GB:L08176; NID:g183484; PID:g183485
A:Experimental source: B-lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBIP:127095)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 52.6%; Score 50; DB 2; Length 378;
Best Local Similarity 52.9%; Pred. No. 1.2;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQ 17
    |||:||||:
Db 326 YAFVGVKFRNDIFKLFK 342

RESULT 20
E95247
hypothetical protein SP2115 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: E95247
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-76 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK76174.1; PID:g14973627; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP2115

Query Match 51.6%; Score 49; DB 2; Length 76;
Best Local Similarity 62.5%; Pred. No. 0.37;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFF 16
    |||:||||:
Db 24 YAFKGDFFNYLAVVF 39

RESULT 21
E98112
Hypothetical protein spr1925 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
```

```
C:Accession: B98112
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Es
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: B98112
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-76 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAL00727.1; PID:g15459622; GSPDB:GN00174
C:Genetics:
A:Gene: spr1925

Query Match 51.6%; Score 49; DB 2; Length 76;
Best Local Similarity 62.5%; Pred. No. 0.37;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFF 16
    |||:||||:
Db 24 YAFKGDFFNYLAVVF 39

RESULT 22
I38450
chemokine (C-C) receptor 2, splice form A - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C:Accession: I38450
R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant prot
A:Reference number: A53477; MUID:94195821; PMID:8146186
A:Accession: I38450
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601257
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
F:44-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:244-265/Domain: transmembrane #status predicted <TM6>
F:292-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:32-277,113-190/Disulfide bonds: #status predicted

Query Match 51.6%; Score 49; DB 2; Length 374;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRN 10
    |||:||||:
Db 305 YAFVGEKFRS 314

RESULT 23
JF0349
interferon-inducible protein 10 (IP-10) receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C:Accession: JF0349
R:Tamaru, M.; Tominaga, Y.; Yatsunami, K.; Narumi, S.
```

Biochem. Biophys. Res. Commun. 251, 41-48, 1998
 A>Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its
 A;Reference number: J50349; MUID:9909219; PMID:9790904
 A;Accession: J50349
 A;Molecule type: mRNA
 A;Residues: 1-367 <TAN>
 A;Cross-references: DBJ:AB003174; NID:G3798731; PIDN:BA434045.1; PID:G3798732
 A;Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
 C;Superfamily: vertebrate rhodopsin

Query Match 50.5%; Score 48; DB 2; Length 367;
 Best Local Similarity 50.0%; Pred. No. 2.6;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||:||||:|
 DB 317 YAFVGVKFRQWMLFTR 334

RESULT 24
 A53752
 interleukin-8 receptor (clone 5B1a) - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C;Accession: A53752
 R;Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navar-
 J. Biol. Chem. 269, 12391-12394, 1994
 A;Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
 A;Reference number: A53752; MUID:94230294; PMID:8175642
 A;Accession: A53752
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-358 <PRA>
 A;Cross-references: GB:L24445; NID:G437661; PIDN:AAA31378.1; PID:G437662
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 49.5%; Score 47; DB 2; Length 358;
 Best Local Similarity 69.2%; Pred. No. 3.8;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
 |||||:|||||
 DB 312 YAFIGQKFRYGLL 324

RESULT 25
 A55735
 G protein-coupled receptor EB11 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
 C;Accession: A55735
 R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
 Genomics 23, 643-650, 1994
 A;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
 A;Reference number: A55735; MUID:95154835; PMID:7851893
 A;Accession: A55735
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-378 <SCH>
 A;Cross-references: GB:L31580; NID:G468340; PIDN:AAA74232.1; PID:G468341
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor

Query Match 49.5%; Score 47; DB 2; Length 378;
 Best Local Similarity 52.9%; Pred. No. 4;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQ 17
 |||||:||||:|
 DB 326 YAFIGVKFRSLFKLFK 342

RESULT 26

A23669
 interleukin-8 receptor, high affinity - rabbit
 N;Alternate names: fMLP receptor
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
 C;Accession: A23669
 R;Thomas, K.M.; Pyun, H.Y.; Navarro, J.
 J. Biol. Chem. 265, 20061-20064, 1990
 A;Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
 A;Reference number: A23669; MUID:91056034; PMID:1700779
 A;Accession: A23669
 A;Molecule type: mRNA
 A;Residues: 1-354 <THO>
 A;Cross-references: GB:M58021; GB:J05705; NID:G165442; PIDN:AAA31377.1; PID:G165443
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 48.4%; Score 46; DB 2; Length 354;
 Best Local Similarity 61.5%; Pred. No. 5.5;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
 |||||:|||||
 DB 309 YAFIQGNFRNGFL 321

RESULT 27

JQ1231
 interleukin-8 receptor - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
 C;Accession: JQ1231; A46483
 R;Beckmann, M.P.; Mungar, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Garat-
 Biochem. Biophys. Res. Commun. 179, 784-789, 1991
 A;Title: Molecular characterization of the interleukin-8 receptor.
 A;Reference number: JQ1231; MUID:91378994; PMID:1898400
 A;Accession: JQ1231
 A;Molecule type: DNA
 A;Residues: 1-355 <BEC>
 A;Cross-references: GB:M74240; NID:G165438; PIDN:AAA31375.1; PID:G165439
 R;Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
 J. Immunol. 148, 1261-1264, 1992

Query Match 48.4%; Score 46; DB 2; Length 355;
 Best Local Similarity 61.5%; Pred. No. 5.5;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
 |||||:|||||
 DB 310 YAFIQGNFRNGFL 322

RESULT 28

B97185
 glycosyltransferase [imported] - Clostridium acetobutylicum
 C;Species: Clostridium acetobutylicum
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C;Accession: B97185
 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001

X48857
angiotensin II receptor type 1 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A48857
R:Burns, K.D.; Inagami, T.; Harris, R.C.
Am. J. Physiol. 264, F645-F654, 1993
A:Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is present i
A:Reference number: A48857; MUID:93236091; PMID:7916579
A:Accession: A48857
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-359

A:Cross-references: GB:S59041; NID:9299614; PIDN:AAB26239.1; PID:9299615
A:Experimental source: proximal tubule cells
A:Note: sequence extracted from NCBI backbone (NCBIN:129600, NCBIIP:129601)

A.Note: The authors translated the codon AGC for residue 120 as Thr, GTC for residue 225
A.Residues: 1-359 <ELT>
A.R.Kakar, S.S.; Sellers, J.C.; Devor, D.C.; Musgrove, L.C.; Neill, J.D.
Biochem. Biophys. Res. Commun. 183, 1090-1096, 1992
A.Title: Angiotensin II type-1 receptor subtype cDNAs: differential tissue expression and
A.Reference number: JH0578; MUID:92231868; PMID:1567388
A.Accession: JH0578
A.Molecule type: mRNA
A.Residues: 1-74, 'L', '76-119, 'T', 121-224, 'A', 226-359 <KAK>
A.Cross-references: GB:M7003; NID:q202920; PIDN:AAA40739.1; PID:g202921

A; Experimental source: anterior pituitary
R; Ye, M.Q.; Healy, D.P.
Biochem. Biophys. Res. Commun. 185, 204-210, 1992
A; Title: Characterization of an angiotensin type-1 receptor partial cDNA from rat kidney
A; Reference number: PH0850; MUID:92287094; PMID:1599457
A; Accession: PH0850
A; Molecule type: mRNA
A; Residues: 84-119, T', 121-224, A', 226-259 <YEM>
A; Cross-references: GB:S37461; NID:G249938; PIDN:AAB22267.1; PID:G249939
A; Experimental source: kidney
C; Genetics:
A; Gene: AVTB
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F; 27-53/Domain: transmembrane #status predicted <TM1>
F; 65-90/Domain: transmembrane #status predicted <TM2>
F; 103-125/Domain: transmembrane #status predicted <TM3>
F; 145-166/Domain: transmembrane #status predicted <TM4>
F; 194-216/Domain: transmembrane #status predicted <TM5>
F; 240-264/Domain: transmembrane #status predicted <TM6>
F; 278-304/Domain: transmembrane #status predicted <TM7>
F; 4,176,188,344/Binding site: carboxylate (Asn) (covalent) #status predicted
F; 232,323/Binding site: phosphate (Thr) (covalent) #status predicted
F; 331,338/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 47.4%; Score 45; DB 2; Length 359;
Best Local Similarity 53.8%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
| | : | : | |
DB 302 YGFLGKKFKKYFL 314

RESULT 36
S15403
angiotensin II receptor type 1 - bovine
C; Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C; Accession: S15403
R; Sasaki, K.; Yanano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Y.
Nature 351, 230-233, 1991
A; Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiotensin II receptor
A; Reference number: S15403; MUID:91251900; PMID:2041569
A; Accession: S15403
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-359 <SAS>
A; Cross-references: GB:X62294; NID:G43; PIDN:CAA44182.1; PID:G44
C; Superfamily: vertebrate rhodopsin

Query Match 47.4%; Score 45; DB 2; Length 359;
Best Local Similarity 53.8%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
| | : | : | |
DB 302 YGFLGKKFKKYFL 314

RESULT 37
JH0621
angiotensin II receptor 1A - mouse
C; Species: Mus musculus (house mouse)
C; Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Nov-1999
C; Accession: JH0621; JCI193
R; Sasamura, H.; Hein, L.; Krieger, J.E.; Pratt, R.E.; Kobilka, B.K.; Dzau, V.J.
Biochem. Biophys. Res. Commun. 185, 253-259, 1992
A; Title: Cloning, characterization, and expression of two angiotensin receptor (AT-1) is
A; Reference number: JH0621; MUID:92287102; PMID:1599461
A; Accession: JH0621
A; Molecule type: DNA
A; Residues: 1-359 <SAS>

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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:55:11 ; Search time 5.625 Seconds
(without alignments)
166.624 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YAFVGEKFRNYLLVFFQK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	95	100.0	352	1	CKR5_CERAE
2	95	100.0	352	1	CKR5_CERP
3	95	100.0	352	1	CKR5_CERTO
4	95	100.0	352	1	CKR5_GORGO
5	95	100.0	352	1	CKR5_HUMAN
6	95	100.0	352	1	CKR5_HYLLE
7	95	100.0	352	1	CKR5_HYLM
8	95	100.0	352	1	CKR5_HYLSY
9	95	100.0	352	1	CKR5_MACMU
10	95	100.0	352	1	CKR5_PANTR
11	95	100.0	352	1	CKR5_PAPHA
12	95	100.0	352	1	CKR5_PONPY
13	95	100.0	352	1	CKR5_PYGHI
14	95	100.0	352	1	CKR5_PYGNE
15	95	100.0	352	1	CKR5_TRAFR
16	95	100.0	352	1	CKR5_TRAPH
17	85	89.5	354	1	CKR5_RAT
18	80	84.2	354	1	CKR5_MOUSE
19	78	82.1	373	1	CKR2_MOUSE
20	78	82.1	373	1	CKR2_RAT
21	76	80.0	360	1	CKR2_MACMU
22	65	68.4	355	1	CKR3_CERAE
23	65	68.4	355	1	CKR3_HUMAN
24	65	68.4	355	1	CKR3_MACMU
25	64	67.4	353	1	CKR8_MOUSE
26	64	67.4	359	1	CKR3_MOUSE
27	64	67.4	359	1	CKR3_RAT
28	63	66.3	355	1	CKR8_HUMAN
29	63	66.3	356	1	CKR8_MACMU
30	61	64.2	374	1	CKR6_HUMAN
31	60	63.2	355	1	CKR1_HUMAN
32	59	62.1	367	1	CKR6_MOUSE
33	58	61.1	354	1	C3X1_RAT

ALIGNMENTS

```

RESULT 1
CKR5_CERAE
ID _CKR5_CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CCR5R5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses."
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "cDNA sequence of African green monkey CCR-5 chemokine receptor
RT gene."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U83324; AAC51795.1; -.
CC EMBL; U83325; AAC51796.1; -.
CC EMBL; AB015944; BAA31328.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1, 1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
CC Polymorphism.
CC -----
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

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34 57 60.0 354 1 C3X1_MOUSE Q920d9 mus musculus
35 57 60.0 355 1 C3X1_HUMAN P49238 homo sapien
36 57 60.0 360 1 CKR4_HUMAN P51679 homo sapien
37 56 58.9 355 1 CKR1_MACMU P56482 macaca mula
38 55 57.9 358 1 CKR3_CAVPO Q922i3 cavia porce
39 53 55.8 355 1 CKR1_MOUSE P51675 mus musculus
40 53 55.8 356 1 CKR1_MOUSE P51676 mus musculus
41 52 54.7 360 1 CKR4_MOUSE P51680 mus musculus
42 52 54.7 378 1 CKR7_HUMAN P32488 homo sapien
43 50 52.6 353 1 IL8B_MACMU Q28519 macaca mula
44 50 52.6 353 1 IL8B_PANTR Q28807 pan troglod
45 50 52.6 356 1 IL8B_CANFA O97571 canis famil

```

FT TRANSMEM 31 58 1 (POTENTIAL).

FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 69 89 2 (POTENTIAL).

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).

FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 142 166 4 (POTENTIAL).

FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 199 218 5 (POTENTIAL).

FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 236 260 6 (POTENTIAL).

FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 278 301 7 (POTENTIAL).

FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).

FT DISULFID 101 178 BY SIMILARITY.

FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

FT VARIANT 14 14 N -> Y.

FT VARIANT 352 352 F -> L.

SQ SEQUENCE 352 AA; 40561 MW; 7852E690C72EC29A CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 2

ID CKR5_CERP STANDARD; PRT; 352 AA.

AC Q9TV42;

DT 15-VAR-2004 (Rel. 43, Created)

DT 15-VAR-2004 (Rel. 43, Last sequence update)

DT 15-VAR-2004 (Rel. 43, Last annotation update)

DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCRS-5) (CCRS).

GN CCR5 OR CMKBR5.

OS Cercopithecus pygerythrus (Vervet monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Cercopithecus.

OX NCBI_TaxID=60710;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=100;

RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,

RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;

RT "Mutations in CCR5-coding sequences are not associated with SIV

RT carrier status in African nonhuman primates.";

RL AIDS Res. Hum. Retroviruses 15:931-939 (1999).

CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC MIP-1-beta and RANTES and subsequently transduces a signal by

CC increasing the intracellular calcium ions level. May play a role

CC in the control of granulocytic lineage proliferation or

CC differentiation.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL; AF035222; AAD44015.1; -

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PRO0237; GPCRHOOPS.

DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.

DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 31 58 1 (POTENTIAL).

FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 69 89 2 (POTENTIAL).

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).

FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 142 166 4 (POTENTIAL).

FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 199 218 5 (POTENTIAL).

FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 236 260 6 (POTENTIAL).

FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 278 301 7 (POTENTIAL).

FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).

FT DISULFID 101 178 BY SIMILARITY.

FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCCC3DB0 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 3

ID CKR5_CERTO STANDARD; PRT; 352 AA.

AC 062743; 062744; 062745; 062746;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCRS).

GN CCR5 OR CMKBR5.

OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Cercopithecus.

OX NCBI_TaxID=9531;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Isolate 079, 085, 087, and 089;

RA MEDLINE=98321155; PubMed=9656999;

RA Chen Z., Gattie A., Ho D.D., Marx P.A.;

RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys

RT naturally infected in west Africa: a comparison of coreceptor usage

RT of primary SIVsm, HIV-2, and SIVmac.";

RL Virology 246:113-124 (1998).

CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC MIP-1-beta and RANTES and subsequently transduces a signal by

CC increasing the intracellular calcium ions level. May play a role

CC in the control of granulocytic lineage proliferation or

CC differentiation.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL; AF035222; AAD44015.1; -

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

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DR EMBL; AF051902; AAC39830.1; -
DR EMBL; AF051903; AAC39831.1; -
DR EMBL; AF051904; AAC39832.1; -
DR EMBL; AF051905; AAC39833.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECF F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECF F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT VARIANT 1 2
FT VARIANT 2 3
FT VARIANT 25 25
FT VARIANT 100 100
FT VARIANT 107 107
FT VARIANT 134 134
FT VARIANT 146 146
FT VARIANT 340 340
FT VARIANT 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 4
CKR5 GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9726687; PubMed=9108095;
RA Edinger A.L., Amadee A., Miller K., Doranz B.J., Murphy M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CKR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; AF005659; AAB62553.1; -
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm1.1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
PROSITE; PS00237; G-PROTEIN RECF F1.1; 1.
PROSITE; PS0262; G-PROTEIN RECF F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT VARIANT 1 2
FT VARIANT 2 3
FT VARIANT 25 25
FT VARIANT 100 100
FT VARIANT 107 107
FT VARIANT 134 134
FT VARIANT 146 146
FT VARIANT 340 340
FT VARIANT 352 AA; 40515 MW; D0B6FCB9FE5EAC84 CRC64;
SQ SEQUENCE 352 AA; 40515 MW; D0B6FCB9FE5EAC84 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 5
CKR5 HUMAN STANDARD; PRT; 352 AA.
ID CKR5 HUMAN STANDARD; PRT; 352 AA.
AC P51881; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
AC O14708; O15538; Q9UPA4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
GN CKR5 OR CMKR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96241590; PubMed=8639485;
RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
RA "Molecular cloning and functional expression of a new human

```

CC-chemokine receptor gene.";
RA Biochemistry 35:3362-3367 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96291862; PubMed=8663314;
RA Report C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
RT "Molecular cloning and functional characterization of a novel human
CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";
RL J. Biol. Chem. 271:17161-17166 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96295970; PubMed=8699119;
RA Combadere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
RT "Cloning and functional expression of CC CR5, a human monocyte CC
chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
RANTES.";
RL J. Leukoc. Biol. 60:147-152 (1996).
RN [4]
RP SEQUENCE FROM N.A.
RX McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses.";
RL J. Virol. 71:8642-8656 (1997).
RN [6]
RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366 (1997).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=98049523; PubMed=9388201;
RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
with 5'-end heterogeneity, dual promoter usage, and evidence for
polymorphisms within the regulatory regions and noncoding exons.";
RL J. Biol. Chem. 272:30662-30671 (1997).
RN [8]
RP SEQUENCE FROM N.A., AND VARIANT ARG-178.
RX Medierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
RA Debre P.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RX Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [10]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE=96260017; PubMed=8649511;
RA Deng H., Liu R., Ellmeier W., Choe S., Unutmak D., Burkhardt M.,
RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
RT "Identification of a major co-receptor for primary isolates of
HIV-1.";
RL Nature 381:661-666 (1996).
RN [11]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE=96260018; PubMed=8649512;
RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
RA Nagashima K.A., Cavanan C., Maddon P.J., Koup R.A., Moore J.P.,
RA Paxton W.A.;
RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
CC-CCR-5.";
RL Nature 381:667-673 (1996).
RN [12]
RP SULFATION
RX MEDLINE=99189752; PubMed=10089882;
RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
entry.";
RL Cell 96:667-676 (1999).
RN [13]
RP FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and rantes and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation. Acts as co-receptor with CD4 for primary non-
CC syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1
CC virus. It promotes Env-mediated fusion of the virus.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Found in promyelocytic cells.
CC -!- PTM: Sulfation contributes to the efficiency of HIV-1 entry.
CC -!- PTM: Modified by O-linked glycosylation, but not by N-linked
CC glycosylation.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X91492; CAA62796.1; -
CC EMBL; U54994; AAC50598.1; -
CC EMBL; U57840; AAB17071.1; -
CC EMBL; U95626; AAB57793.1; -
CC EMBL; U83326; AAC51797.1; -
CC EMBL; AF011500; AAB65700.1; -
CC EMBL; AF011501; AAB65701.1; -
CC EMBL; AF011502; AAB65702.1; -
CC EMBL; AF011503; AAB65703.1; -
CC EMBL; AF011505; AAB65705.1; -
CC EMBL; AF011506; AAB65706.1; -
CC EMBL; AF011507; AAB65707.1; -
CC EMBL; AF011508; AAB65708.1; -
CC EMBL; AF011509; AAB65709.1; -
CC EMBL; AF011510; AAB65710.1; -
CC EMBL; AF011511; AAB65711.1; -
CC EMBL; AF011512; AAB65712.1; -
CC EMBL; AF011513; AAB65713.1; -
CC EMBL; AF011514; AAB65714.1; -
CC EMBL; AF011515; AAB65715.1; -
CC EMBL; AF011516; AAB65716.1; -
CC EMBL; AF011517; AAB65717.1; -
CC EMBL; AF011518; AAB65718.1; -
CC EMBL; AF011519; AAB65719.1; -
CC EMBL; AF011520; AAB65720.1; -
CC EMBL; AF011521; AAB65721.1; -
CC EMBL; AF011522; AAB65722.1; -
CC EMBL; AF011523; AAB65723.1; -
CC EMBL; AF011524; AAB65724.1; -
CC EMBL; AF011525; AAB65725.1; -
CC EMBL; AF011526; AAB65726.1; -
CC EMBL; AF011527; AAB65727.1; -
CC EMBL; AF011528; AAB65728.1; -
CC EMBL; AF011529; AAB65729.1; -
CC EMBL; AF011530; AAB65730.1; -
CC EMBL; AF011531; AAB65731.1; -
CC EMBL; AF011532; AAB65732.1; -

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CC -----
 DR EMBL; AF177899; AAK43382.1; --
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1.1
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT TRANSMEM 90 102
 FT TRANSMEM 103 124
 FT TRANSMEM 125 141
 FT TRANSMEM 142 166
 FT TRANSMEM 167 198
 FT TRANSMEM 199 218
 FT TRANSMEM 219 235
 FT TRANSMEM 236 260
 FT TRANSMEM 261 277
 FT TRANSMEM 278 301
 FT TRANSMEM 302 352
 FT TRANSMEM 353 378
 FT TRANSMEM 379 403
 FT TRANSMEM 404 436
 FT TRANSMEM 437 470
 FT TRANSMEM 471 504
 FT TRANSMEM 505 538
 FT TRANSMEM 539 572
 FT TRANSMEM 573 606
 FT TRANSMEM 607 640
 FT TRANSMEM 641 674
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Genetically divergent strains of simian immunodeficiency virus use CCR5 as a coreceptor for entry." J. Virol. 71:2705-2714(1997).

SEQUENCE FROM N.A. SPECIES=M.mulatta; PubMed=11461684; MEDLINE=21354176; Hauer B.J., Clements J.E.; "Identification and comparison of eleven rhesus macaque chemokine receptors." Hum. Retroviruses 17:981-986(2001).

SEQUENCE FROM N.A. SPECIES=M.mulatta, M.fascicularis, and M.nemestrina; MEDLINE=97268687; PubMed=9108095; Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M., Peiper S.C., Parmentier M., Broder C.C., Doms R.W.; "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains." Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).

-1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; U77672; AAC51109.1; -
DR EMBL; U73739; AAC51158.1; -
DR EMBL; U96762; AAC34132.1; -
DR EMBL; AF005660; AAB62254.1; -
DR EMBL; AF005661; AAB62255.1; -
DR EMBL; AF005662; AAB62256.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7cm_1; -
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DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
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QY 1 YAFVGEKFRNLYLVFFQK 18
DB 297 YAFVGEKFRNLYLVFFQK 314

RESULT 10
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AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-CKR-5) (CC-CKR-5) (CCR-5) (CCRS).
GN CCR5 OR CWKBR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
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RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M., Peiper S.C., Parmentier M., Broder C.C., Doms R.W.; "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains." Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Zimmerman P.A., Buckler-White A., Alkhatib G.; Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B., Ho D.D.; "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism." AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97426118; PubMed=9282822;
RA Zacharova V., Zachar V., Goustin A.S.; "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural HIV type 1 host." AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.; "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1." AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RN [6]
RP SEQUENCE FROM N.A.
RX Zhang Y., Ryder O.A., Zhang Y.; "Sequence comparison of the CCR5 gene in primates and primate phylogeny." Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC EMBL; AF005663; AAB62557.1; -
 CC EMBL; U94329; AAB58446.1; -
 CC EMBL; AF011542; AAB65742.1; -
 CC EMBL; U97666; AAC51670.1; -
 CC EMBL; AF011540; AAB65740.1; -
 CC EMBL; U89797; AAC03717.1; -
 CC EMBL; AF177894; AAK43377.1; -
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm1; 1.
 CC PRINTS; PR00237; GPCR_RHODOPSIN.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 CC DOMAIN 1 30
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 31 58
 CC DOMAIN 59 68
 CC CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 69 89
 CC DOMAIN 90 102
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 103 124
 CC DOMAIN 125 141
 CC CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 142 166
 CC DOMAIN 167 198
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 199 218
 CC DOMAIN 219 235
 CC CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 236 260
 CC DOMAIN 261 277
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 278 301
 CC DOMAIN 302 352
 CC CYTOPLASMIC (POTENTIAL).
 CC DISULFID 101 178
 CC MOD_RES 3 3
 CC SULFATION (BY SIMILARITY).
 CC MOD_RES 10 10
 CC SULFATION (BY SIMILARITY).
 CC MOD_RES 14 14
 CC SULFATION (BY SIMILARITY).
 CC MOD_RES 15 15
 CC SULFATION (BY SIMILARITY).
 CC CARBOHYD 268 268
 CC N-LINKED (GLCNAC...) (POTENTIAL).
 CC CONFLICT 123 123
 CC T -> S (IN REF. 1.) (POTENTIAL).
 CC SEQUENCE 352 AA; 40539 MW; 4A338698B80FE34C CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 11
 ID_CKRS_PAPHA STANDARD; PRT; 352 AA.
 AC P5641.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-CR-5) (CC-CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Papio hamadryas (Hamadryas baboon), and
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OC NCBI_TaxID=9557, 9555;
 RN [1]

SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas;
 EX MEDLINE=97286868; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharpton M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;

"Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains";
 Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 [2]

SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas;
 RX MEDLINE=99210133; PubMed=10195758;
 RA Sakkena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
 RT "Species-specific changes in the CCR5 gene from African and Asian
 nonhuman primates";
 RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
 RN [3]

SEQUENCE FROM N.A.
 RC SPECIES=P.anubis;
 RA Bentton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC EMBL; AF005658; AAB62552.1; -
 CC EMBL; AF105287; AAD20556.1; -
 CC EMBL; AF105288; AAD20557.1; -
 CC EMBL; AF105289; AAD20558.1; -
 CC EMBL; AF105290; AAD20559.1; -
 CC EMBL; AF023452; AAC63830.1; -
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm1; 1.
 CC PRINTS; PR00237; GPCR_RHODOPSIN.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 CC DOMAIN 1 30
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 31 58
 CC DOMAIN 59 68
 CC CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 69 89
 CC DOMAIN 90 102
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 103 124
 CC DOMAIN 125 141
 CC CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 142 166
 CC DOMAIN 167 198
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 199 218
 CC DOMAIN 219 235
 CC CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 236 260
 CC DOMAIN 261 277
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 278 301
 CC DOMAIN 302 352
 CC CYTOPLASMIC (POTENTIAL).
 CC DISULFID 101 178
 CC MOD_RES 3 3
 CC SULFATION (BY SIMILARITY).
 CC MOD_RES 10 10
 CC SULFATION (BY SIMILARITY).
 CC MOD_RES 14 14
 CC SULFATION (BY SIMILARITY).
 CC MOD_RES 15 15
 CC SULFATION (BY SIMILARITY).
 CC CARBOHYD 268 268
 CC N-LINKED (GLCNAC...) (POTENTIAL).
 CC CONFLICT 123 123
 CC T -> S (IN REF. 1.) (POTENTIAL).
 CC SEQUENCE 352 AA; 40489 MW; 5E15049BA1FE8B2 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 11
 ID_CKRS_PAPHA STANDARD; PRT; 352 AA.
 AC P5641.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-CR-5) (CC-CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Papio hamadryas (Hamadryas baboon), and
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OC NCBI_TaxID=9557, 9555;
 RN [1]

SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas;
 EX MEDLINE=97286868; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharpton M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;


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Db      297 YAFVGEKFRNLYLVFFQK 314
RESULT 12
ID_CKRS_PONPY STANDARD; PRT; 352 AA.
AC 097881;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075446; AAD19858.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G-PROTEIN RECP FL 1; 1.
CC PROSITE; PS00262; G-PROTEIN RECP FL 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT TRANSMEM 302 352
FT DISULFID 101 178
FT MOD RES 3 3
FT MOD RES 10 10
FT MOD RES 14 14
FT MOD RES 15 15
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18
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Db      297 YAFVGEKFRNLYLVFFQK 314
RESULT 13
ID_CKRS_PYGBI STANDARD; PRT; 352 AA.
AC 097880;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKCR5.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075445; AAD19857.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G-PROTEIN RECP FL 1; 1.
CC PROSITE; PS00262; G-PROTEIN RECP FL 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT TRANSMEM 302 352
FT DISULFID 101 178
FT MOD RES 3 3
FT MOD RES 10 10
FT MOD RES 14 14
FT MOD RES 15 15
SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18
|||||

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Db 297 YAFVGEKFRNLLVFFQK 314
|||||

RESULT 14

CKR5_PYGNE STANDARD; PRT; 352 AA.
AC O97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075448; AAD19860.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsin.
CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58
FT DOMAIN 1 (POTENTIAL).
FT TRANSMEM 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT TRANSMEM 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT TRANSMEM 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT TRANSMEM 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT TRANSMEM 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40532 MW; FE4FD9D98D3B3E861 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||
Db 297 YAFVGEKFRNLLVFFQK 314
|||||

RESULT 15

CKR5_TRAFR STANDARD; PRT; 352 AA.
AC O97878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075442; AAD19854.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsin.
CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT TRANSMEM 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT TRANSMEM 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT TRANSMEM 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT TRANSMEM 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT TRANSMEM 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 16
 CKR5 TRAPH STANDARD; PRT; 352 AA.
 AC Q87879;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
 GN CKR5 OR CMKBR5
 OS Trachypithecus phayrei (Phayre's leaf monkey)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Trachypithecus
 OX NCBI_TaxID=61618;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -|- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL: AF075443; AAD19855.1; -;
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS: PR00237; GPCRHOPOPSN.
 CC PROSITE: PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
 CC PROSITE: PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 CC
 CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 31 58 1 (POTENTIAL).
 CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 69 89 2 (POTENTIAL).
 CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 103 124 3 (POTENTIAL).
 CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 142 166 4 (POTENTIAL).
 CC DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 199 218 5 (POTENTIAL).
 CC DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 236 260 6 (POTENTIAL).
 CC DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 278 301 7 (POTENTIAL).
 CC DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 CC BY SIMILARITY.
 CC DISULFID 101 178
 CC MOD RES 3 3 SULFATION (BY SIMILARITY).
 CC MOD RES 10 10 SULFATION (BY SIMILARITY).
 CC MOD RES 14 14 SULFATION (BY SIMILARITY).
 CC MOD RES 15 15 SULFATION (BY SIMILARITY).
 CC SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938F CRC64;
 SQ

Query Match 100.0%; Score 95; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 17
 CKR5 RAT STANDARD; PRT; 354 AA.
 AC Q08556;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1
 DE alpha receptor).
 GN CKR5 OR CMKBR5
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Wistar; TISSUE=Brain;
 RA MEDLINE=98334064; PubMed=9670389;
 RA Spieiss O., Gourmal N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
 RA Berger M., Gebicke-Haerter P.J.;
 RT "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
 RT upregulation of its mRNA in ischemic and endotoxemic rat brain.";
 RT J. Neurosci. Res. 53:16-28(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Sprague-Dawley;
 RA MEDLINE=98318173; PubMed=9655467;
 RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
 RA Defebbre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis".
 RT J. Neuroimmunol. 86:1-12(1998).
 CC -|- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL: Y12009; CAA72737.1; -;
 CC EMBL: U77350; AAC03243.1; -;
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS: PR00237; GPCRHOPOPSN.
 CC PROSITE: PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
 CC PROSITE: PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 CC
 CC DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 33 60 1 (POTENTIAL).
 CC DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 71 91 2 (POTENTIAL).
 CC DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 105 126 3 (POTENTIAL).
 CC DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 144 168 4 (POTENTIAL).
 CC DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 201 220 5 (POTENTIAL).
 CC DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 238 262 6 (POTENTIAL).
 CC

Qy 1 YAFVGEKFRNVLVFFQK 18
Db 299 YAFVGEKFRNVLVFFQK 316

RESULT 19
CKR2_MOUSE
ID CKR2_MOUSE STANDARD; PRT; 373 AA.
AC PS1683; Q61172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (JE/FIC receptor) (MCP-1 receptor).
GN CCR2 OR CMKSR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9."
RT J. Biol. Chem. 271:7551-7558 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RX MEDLINE=96216064; PubMed=8662823;
RA Kurihara T., Bravo R.;
RT "Cloning and functional expression of mCCR2, a murine receptor for
RT the C-C chemokines JE and FIC."
RT J. Biol. Chem. 271:11603-11606 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97026720; PubMed=8872898;
RX Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
RX Post T.W., Gerard C., Dorf M.E.;
RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
RT transcriptase-polymerase chain reaction does not detect mRNA for the
RT KC or new MCP-1 receptor."
RT J. Neurosci. Res. 45:382-391 (1996).
CC -|- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC but not in nonhematopoietic cell lines.
CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U47035; AAC52453.1; -;
CC EMBL; U51717; AAC52557.1; -;
CC EMBL; U56819; AAC52784.1; -;
CC GDB; MGI:106185; Ccr2.
CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
CC GO; GO:0019955; F:cytokine binding; IPI.
CC GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.
CC GO; GO:0030097; P:hemoiesis; IMP.
CC GO; GO:0006959; P:humoral immune response; IMP.
CC GO; GO:0006954; P:inflammatory response; IMP.

GO; GO:0030334; P:regulation of cell migration; IMP.
InterPro: IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm.1; 1.
DR PRINIS; PR000337; GPCRHOODPSN
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 55
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 56 83
FT DOMAIN 84 93
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 94 114
FT DOMAIN 115 127
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 128 149
FT DOMAIN 150 166
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 191
FT DOMAIN 192 219
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 239
FT DOMAIN 240 256
FT TRANSMEM 257 281
FT DOMAIN 282 298
FT TRANSMEM 299 322
FT DOMAIN 323 373
FT CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 203
FT CONFLICT 39 39
FT CONFLICT 184 184
FT CONFLICT 284 284
FT SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;
Query Match 82.1%; Score 78; DB 1; Length 373;
Best Local Similarity 77.8%; Pred. No. 6.4e-06;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNVLVFFQK 18
Db 318 YAFVGEKFRNVLVFFQK 335

RESULT 20
CKR2_MOUSE
ID CKR2_MOUSE STANDARD; PRT; 373 AA.
AC 055193;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2).
GN CCR2 OR CMKSR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=9818173; PubMed=9655467;
RA Jiang Y., Salafraza M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA deFiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis".
RT J. Neuroimmunol. 86:1-12 (1998).
CC -|- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level (by similarity).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
CC macrophages.
CC -|- INDUCTION: In animals in which experimental allergic
CC encephalomyelitis (EAE) has been induced.
CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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DR ENBL; Y13775; CAA74106.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
 DR PROSITE; PS00262; G PROTEIN RECP F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 35 62 1 (POTENTIAL).
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 73 93 2 (POTENTIAL).
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 204 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 SQ SEQUENCE 355 AA; 4467ASEFEEB978FF CRC64;

Query Match 68.4%; Score 65; DB 1; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.0011;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
 Dd 301 YAFVGEKFRNYLLVFFQK 318

RESULT 23

CC CR3_HUMAN STANDARD; PRT; 355 AA.
 AC P51677; Q15748; Q86WD2; Q9ULY8;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3) (CCR3)
 DE (CCR3) (Eosinophil eotaxin receptor).
 GN CCR3 OR CCR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Monocytes;
 RX MEDLINE=95348056; PubMed=7622448;
 RA Combadiere C., Ahuja S.K., Murphy P.M.;
 RT "Cloning and functional expression of a human eosinophil CC chemokine
 RT receptor";
 RL J. Biol. Chem. 270:16491-16494(1995).
 RN [2]
 RP ERRATUM.
 RA Combadiere C., Ahuja S.K., Murphy P.M.;
 RL J. Biol. Chem. 270:30235-30235(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96235044; PubMed=9642344;
 RA Daugherty B.B., Siciliano S.J., Demartino J.A., Malkowitz L.,
 RA Sirotna A., Springer M.S.;
 RT "Cloning, expression, and characterization of the human eosinophil
 RT eotaxin receptor";
 RL J. Exp. Med. 183:2349-2354(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RX MEDLINE=96281895; PubMed=8676064;
 RA Ponath P.D., Qin S., Post T.W., Wang J., Wu L., Gerard N.P.,
 RA Newman W., Gerard C., Mackay C.R.;
 RT "Molecular cloning and characterization of a human eotaxin receptor
 RT expressed selectively on eosinophils";
 RL J. Exp. Med. 183:2737-2748(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;
 RA "Partial resistance to infection by syncytium-inducing primary HIV-1
 RT in exposed uninfected individuals homozygous for CCR5 32bp deletion";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A., AND VARIANT SER-218.
 RX MEDLINE=21040311; PubMed=11196669;
 RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
 RA Hirai K., Tokunaga K.;
 RT "New variations of human CC-chemokine receptors CCR3 and CCR4";
 RL Genes Immun. 1:97-104(1999).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22074933; PubMed=12079287;
 RA Vijh S., Dayhoff D.E., Wang C.E., Imam Z., Ehrenberg P.K.,
 RA Michael N.L.;
 RT "Transcription regulation of human chemokine receptor CCR3: evidence
 RT for a rare TATA-less promoter structure conserved between Drosophila
 RT and humans";
 RL Genomics 80:86-95(2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RA "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org)";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Lung, and Testis;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
 CC eotaxin-3, MCP-3, MCP-4, RANTES and MIP-1 delta. Subsequently
 CC transduces a signal by increasing the intracellular calcium ions
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: In eosinophils as well as trace amounts in
 CC neutrophils and monocytes.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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DR EMBL; U28694; AAC50469.1; -.
DR EMBL; U51241; AAB16831.1; -.
DR EMBL; U49727; AAB09726.1; -.
DR EMBL; AF026535; AAB82589.1; -.
DR EMBL; AB023887; BAA86964.1; -.
DR EMBL; AF247361; AAL85154.1; -.
DR EMBL; AY221092; AAO65970.2; -.
DR EMBL; BC033514; AAB33514.1; -.
DR FIR; G02436; G02436.
DR GENE; HGNC:1604; CCR3.
DR MIM; 601268; -.
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0004950; F: chemokine receptor activity; TAS.
DR GO; GO:0007155; P: cell adhesion; TAS.
DR GO; GO:0006968; P: cellular defense response; TAS.
DR GO; GO:0006935; P: chemotaxis; TAS.
DR GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0007188; P: G-protein signaling, coupled to cAMP nucleoside; TAS.
DR GO; GO:0006954; P: inflammatory response; TAS.
DR GO; GO:0007125; P: invasive growth; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
DR G-protein coupled receptor; Transmembrane; Polymorphism.
KW DOMAIN 1 34
FT DOMAIN 1 34
FT TRANSMEM 35 62
FT DOMAIN 63 72
FT TRANSMEM 73 93
FT DOMAIN 94 107
FT TRANSMEM 108 129
FT DOMAIN 130 146
FT TRANSMEM 147 171
FT DOMAIN 172 203
FT TRANSMEM 204 223
FT DOMAIN 224 239
FT TRANSMEM 240 264
FT DOMAIN 265 281
FT TRANSMEM 282 305
FT DOMAIN 306 355
FT DISULFID 106 183
FT VARIANT 218 218
FT C -> S (polymorphism found in about 7% of the population; may show reduced activity).
FT FTID=VAR_010668.
SQ SEQUENCE 276 276
Query Match 68.4%; Score 65; DB 1; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0011;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLYLVFFQK 18
| | | | | | | | | | | | | | | | | | | | | |
DB 301 YAFVGERFRKYLRRHFFR 318
RESULT 24
ID_CKR3 MACMU STANDARD; PRT; 355 AA.
AC P56483;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 3 (C-CR-3) (CCR-3) (CCR3)
DE (CCR3).
GN CCR3 OR CCR3.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```


15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 8 (C-C CKR-8) (CC-CKR-8) (CCR-8).
CCR8 OR CMKBR8 OR TER1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
Zaballos A., Goya I.I., Gutierrez J., Varona R., Marquez G.;
Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
STRAIN=129/SV;
MEDLINE=98334001; PubMed=9670926;
Zingoni A., Soto H., Hedrick J.A., Stoppacciaro A., Storlazzi C.T.,
Sinigaglia F., D'Ambrosio D., O'Garra A., Robinson D., Kocchi M.,
Santoni A., Zlotnik A., Napolitano M.;
"The chemokine receptor CCR8 is preferentially expressed in Th2 but
not Th1 cells";
J. Immunol. 161:547-551 (1998).
CC -1- FUNCTION: Receptor for the TCA-3 chemokine.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL; Z98206; CAB10896.1; -;
CC EMBL; Z98205; CAB10895.1; -;
CC EXBL; AF001277; AAC97598.1; -;
CC MGD; MGI:1201402; Ccr8.
CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0006935; P:chemotaxis; IDA.
CC InterPro; IPR004068; CC 8 receptor.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR01530; CHEMOKINER8.
CC PRINTS; PR00237; GPCR_RHODOPSIN.
CC PROSITE; PS00237; G PROTEIN RECEPTOR F1_1; 1.
CC PROSITE; PS0262; G PROTEIN RECEPTOR F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 1 33
CC TRANSMEM 34 61
CC DOMAIN 62 71
CC TRANSMEM 72 91
CC DOMAIN 92 105
CC TRANSMEM 106 127
CC DOMAIN 128 144
CC TRANSMEM 145 169
CC DOMAIN 170 200
CC TRANSMEM 201 220
CC DOMAIN 221 236
CC TRANSMEM 237 261
CC DOMAIN 262 278
CC TRANSMEM 279 302
CC DOMAIN 303 353
CC DISULFID 104 181
CC CAREOHYD 8
CC SEQUENCE 353 AA; 40045 MW; 31EC4B642CDB9A5 CRC64;
Query Match 67.4%; Score 64; DB 1; Length 353;
Best Local Similarity 61.1%; Pred. No. 0.0016;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 YAFVGKFRNLLVFFQK 18

Db 298 YAFIGEKEFKKLMDFQK 315
|||||:|:|
ID CKR3 MOUSE STANDARD; PRT; 359 AA.
AC P51678;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3)
DE (CCR3) (CCR3) (Macrophage inflammatory protein-1 alpha receptor-like
DE 2) (MIP-1 alpha RL2).
DE CCR3 OR CMKBR3 OR CMKBR1L2.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
Gerard C.;
RT "Molecular characterization of two murine eosinophil beta chemokine
RT receptors";
RL J. Immunol. 155:5299-5305 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=95340546; PubMed=7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
RT beta chemokine receptor-like genes, including the gene for a
RT functional macrophage inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 270:17494-17501 (1995).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Detected in skeletal muscle and in trace
CC amounts in Leukocytes.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; U29677; AAA86118.1; -;
CC EMBL; U28406; AAA89155.1; -;
CC MGD; MGI:104616; Ccr3.
CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0006935; P:chemotaxis; IDA.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCR_RHODOPSIN.
CC PROSITE; PS00237; G PROTEIN RECEPTOR F1_1; 1.
CC PROSITE; PS0262; G PROTEIN RECEPTOR F1_2; 1.
CC G-protein coupled receptor; Transmembrane.
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 1 38
CC TRANSMEM 39 64
CC DOMAIN 65 68
CC TRANSMEM 69 95
CC DOMAIN 96 111
CC TRANSMEM 112 133
CC DOMAIN 134 150
CC TRANSMEM 151 175

[5] SEQUENCE FROM N.A.
 RP Nakajima T., Yoshida R., Harada S.;
 RA Nakajima T., Yoshida R., Harada S.;
 RL Nakajima T., Yoshida R., Harada S.;
 [6]
 RP LIGAND BINDING.
 RX MEDLINE=98180363; PubMed=9521068;
 RA Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;
 RT "Identification of the CC chemokines TARC and macrophage inflammatory
 protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 CC -!- FUNCTION: Receptor for the chemokines SCY1/I-309, SCY44/MIP-1-
 beta and SCY17/TARC. May regulate monocyte chemotaxis and thymic
 cell line apoptosis. Alternative coreceptor with CD4 for HIV-1
 infection.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U45983; AB61962.1; -;
 DR EMBL; U62556; AB05542.1; -;
 DR EMBL; Z79782; CAB02142.1; -;
 DR EMBL; Y08456; CAA69712.1; -;
 DR EMBL; D49919; BAA23387.1; -;
 DR EMBL; AF005210; AAB62547.1; -;
 DR PIR; JC5067; JC5067.
 DR GENE; HGNC:1609; CCR8.
 DR MIN; 601834; -;
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0004950; F: chemokine receptor activity; TAS.
 DR GO; GO:0010266; P: coreceptor activity; TAS.
 DR GO; GO:0007155; P: cell adhesion; TAS.
 DR GO; GO:0006935; P: chemotaxis; TAS.
 DR GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; TAS.
 DR GO; GO:0006955; P: immune response; TAS.
 DR InterPro; IPR004068; CC 8 receptor.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR01530; CHEMOKINER8.
 DR PROSITE; PS00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 35
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 36 63
 FT DOMAIN 64 73
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 74 93
 FT DOMAIN 94 107
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 108 129
 FT DOMAIN 130 146
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 147 171
 FT DOMAIN 172 202
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 203 222
 FT DOMAIN 223 238
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 239 263
 FT DOMAIN 264 280
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 281 304
 FT DOMAIN 305 355
 FT CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 183
 FT BY SIMILARITY.
 SQ SEQUENCE 355 AA; 40844 MW; BC14A153CF695361 CRC64;

Query Match 66.3%; Score 63; DB 1; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.0024;

Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLYLVFFQK 18
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 Db 300 YAFVGEKFKHLSEIFQK 317
 RESULT 29
 CCR8_MACMU
 ID CCR8 MACMU STANDARD; PRT; 356 AA.
 AC O97655;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 8 (C-C CCR-8) (CCR-8).
 GN CCR8.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Spleen;
 RC MEDLINE=21354176; PubMed=11461684;
 RX Margulies B.J., Hauer D.A., Clements J.E.;
 RA "Identification and comparison of eleven rhesus macaque chemokine
 receptors";
 RT
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 CC -!- FUNCTION: Receptor for the chemokines SCY1/I-309, SCY44/MIP-1-
 beta and SCY17/TARC. May regulate monocyte chemotaxis and thymic
 cell line apoptosis (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF100205; AAC72403.1; -;
 DR InterPro; IPR004068; CC 8 receptor.
 DR InterPro; IPR00276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR01530; CHEMOKINER8.
 DR PROSITE; PS00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 35
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 36 63
 FT DOMAIN 64 73
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 74 93
 FT DOMAIN 94 107
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 108 129
 FT DOMAIN 130 146
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 147 172
 FT DOMAIN 173 203
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 204 223
 FT DOMAIN 224 239
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 264
 FT DOMAIN 265 281
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 282 305
 FT DOMAIN 306 356
 FT CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 184
 FT BY SIMILARITY.
 SQ SEQUENCE 356 AA; 41210 MW; 1979628DEE44845B CRC64;
 Query Match 66.3%; Score 63; DB 1; Length 356;
 Best Local Similarity 66.7%; Pred. No. 0.0024;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVCEKERNVLLVFFQK 18
 DB 301 YAFVCEKPKHLEIFQK 318

RESULT 30

CKR6 HUMAN
 ID CKR6 HUMAN STANDARD; PRT; 374 AA.
 AC P51684; P78553; Q92846;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 6 (C-C CKR-6) (CCR-6) (IARC
 receptor) (GPR-CY4) (GPCY4) (Chemokine receptor-like 3) (CKR-L3)
 DE (DRY6).
 GN CCR6 OR CKR6 OR STRL22 OR GPR29 OR CKRL3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RX MEDLINE=97313465; PubMed=9169459;
 RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
 RA Nomiya H., Yoshie O.;
 RT "Identification of CCR6, the specific receptor for a novel
 RT lymphocyte-directed CC chemokine LARC.";
 RL J. Biol. Chem. 272:14893-14898 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lautens L.B., Modi W., Bonner T.I.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97040707; PubMed=8886020;
 RA Zaballos A., Varona R., Guierrez J., Lind P., Marquez G.;
 RT "Molecular cloning and RNA expression of two new human chemokine
 RT receptor-like genes.";
 RL Biochem. Biophys. Res. Commun. 227:846-853 (1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA McCoy R., Perlmutter D.H.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224503; PubMed=9070937;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180 (1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Warren C.N., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22935763; PubMed=14574404;
 RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
 RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
 RA Gilbert J.G.R., Clamp M.E., Bechler G., Milne S., Ainscough R.,
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
 RA Babbage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J.,
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
 RA Blakey S., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
 RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
 RA Chapman J.C., Clark S.Y., Clark G., Clegg S., Copley V.,
 RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
 RA Cullley K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,
 RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,

Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
 Gilby L.M., Gillson C.J., Griffiths R.J., Grafham D.V., Grant M.,
 Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Hallis K.S.,
 Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
 Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
 Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
 Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
 Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
 Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
 Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,
 McMurray A., Moore M.J.E., Mullikin J.C., Niblett D., Nickerson T.,
 Novik K.L., Oliver K., Overton-Latty E.K., Parker A., Patel R.,
 Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
 Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,
 Sehra H.K., Sheridan E., Skuce C.B., Smith S., Smith M., Spraggon L.,
 Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
 Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
 Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
 Whitaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
 Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
 Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
 RT "The DNA sequence and analysis of human chromosome 6.";
 RL Nature 425:805-811 (2003).
 RN [8]
 RP SEQUENCE FROM N.A.
 TISSUE=Pancreas;
 MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-3-
 CC alpha/LARC and subsequently transduces a signal by increasing the
 CC intracellular calcium ions level.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Spleen, lymph nodes, appendix, and fetal
 CC liver. Expressed in lymphocytes, T cells and B cells but not in
 CC natural killer cells, monocytes or granulocytes.
 CC -1- INDUCTION: By interleukin-2.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-6 is the initiator.
 CC
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 CC -----
 CC EMBL; U45984; AAB62714.1; -
 CC EMBL; U79784; CAB02144.1; ALT_INIT.
 CC EMBL; U68030; AAC51124.1; -
 CC EMBL; U68030; AAC51124.1; -
 CC EMBL; U68030; AAC51125.1; -
 CC EMBL; AY242126; AAC92293.1; -
 CC EMBL; AL121935; CAB99328.1; -

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DR EMBL; BC037960; AAH37960.1; -.
DR HSSP; P34996; 1DDD.
DR Genew; HGNC:1607; CCR6.
DR MIM; 601835; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004950; F:chemokine receptor activity; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0006960; F:antimicrobial humoral response (sensu Inver. . .); TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0006968; P:cellular defense response; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0006959; P:humoral immune response; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR004067; CC 6 receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01529; CHEMOKINER6.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 47
FT TRANSMEM 48 74
FT DOMAIN 75 83
FT TRANSMEM 84 104
FT DOMAIN 105 119
FT TRANSMEM 120 141
FT DOMAIN 142 159
FT TRANSMEM 160 180
FT DOMAIN 181 211
FT TRANSMEM 212 238
FT DOMAIN 239 254
FT TRANSMEM 255 279
FT DOMAIN 280 303
FT TRANSMEM 304 321
FT DOMAIN 322 374
FT DISULFID 118 197
FT CARBOHYD 7 7
FT CARBOHYD 23 23
FT CONFLICT 60 60
FT CONFLICT 74 74
FT CONFLICT 86 86
FT CONFLICT 164 164
FT CONFLICT 182 182
FT CONFLICT 192 192
FT CONFLICT 206 206
FT CONFLICT 225 225
FT CONFLICT 370 374
SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 64.2%; Score 61; DB 1; Length 374;
Best Local Similarity 75.9%; Pred. No. 0.0056;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEFRNYLL 13
Dd 316 YAFVGEFRNYFL 328

RESULT 31
ID - CKR1 HUMAN STANDARD; PRT; 355 AA.
AC P32246;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)
DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
DE (RANTES-R) (HM145) (LD78 receptor).
GN CKR1 OR CCKR1 OR CCR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=93161416; PubMed=7679328;
RA Neoe K., Digregorio D., Max J.Y., Horuk R., Schall T.J.;
RT "Molecular cloning, functional expression, and signaling
characteristics of a C-C chemokine receptor.";
RL Cell 72:415-425(1993).
RN [2]_SEQUENCE FROM N.A.
RP MEDLINE=93240122; PubMed=7683036;
RA Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
Murphy P.M.;
RT "Structure and functional expression of the human macrophage
inflammatory protein 1 alpha/RANTES receptor.";
RL J. Exp. Med. 177:1421-1427(1993).
RN [3]_SEQUENCE FROM N.A.
RP TISSUE=Monocytes;
RX MEDLINE=94092629; PubMed=7505609;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
leukocyte chemotactic peptide receptors.";
RL Int. Immunol. 5:1239-1249(1993).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-
beta or MCP-1 and subsequently transduces a signal by increasing
the intracellular calcium ions level. Responsible for affecting
stem cell proliferation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed in different hematopoietic
cells.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC EMBL; L09230; AAA58408.1; -.
CC EMBL; L10918; AAA36543.1; -.
CC EMBL; D10925; BAA01723.1; -.
CC F01; A45177; A45177.
CC Genew; HGNC:1602; CCR1.
CC MIM; 601159; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004950; F:chemokine receptor activity; TAS.
CC GO; GO:0007155; P:cell adhesion; TAS.
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0006935; P:chemotaxis; TAS.
CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
CC GO; GO:0006955; P:immune response; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC GO; GO:0007125; P:invasive growth; TAS.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_REC_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34
FT TRANSMEM 35 60
FT DOMAIN 61 64
FT TRANSMEM 65 91
FT DOMAIN 92 107
FT TRANSMEM 108 129
FT DOMAIN 130 146
FT CYTOPLASMIC (POTENTIAL).

```

FT TRANSMEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 197 5 (EXTRACELLULAR (POTENTIAL)).
 FT TRANSMEM 198 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 6 (EXTRACELLULAR (POTENTIAL)).
 FT TRANSMEM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 FT CONFLICT 337 337 E -> D (IN REF. 3).
 SQ SEQUENCE 355 AA; 41172 MW; B3C100FFED275985 CRC64;
 Query Match 63.2%; Score 60; DB 1; Length 355;
 Best Local Similarity 61.1%; Pred. No. 0.0079;
 Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 YAFVGEKERNVLPFQK 18
 |||||:|||||:
 Db 301 YAFVGERFKYLRQLFHR 318
 |||||:|||||:
 RESULT 32
 CKR6 MOUSE
 ID CKR6 MOUSE STANDARD; PRT; 367 AA.
 AC 054689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 6 (C-CR-6) (CCR-6) (KY411).
 GN CCR6 OR CMKCR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 analysis of the murine chemokine receptor CCR6 and its specific ligand
 MIP-3alpha.";
 RT MIP-3alpha.";
 RL FEBS Lett. 440:188-194 (1998).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-3-
 alpha/LARC and subsequently transduces a signal by increasing the
 intracellular calcium ions level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AB009369; BAA23776.1; -.
 CC EMBL; AJ222714; CAA10956.1; -.
 DR MGD; MGI:133797; Ccr6.
 DR GO; GO:0005515; F-protein binding; IPI.
 DR InterPro; IPR004067; CC-6_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR01529; CHEMOKINER6.
 DR PRINTS; PR00237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 40 66 1 (POTENTIAL).
 FT DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 76 96 2 (POTENTIAL).
 FT DOMAIN 97 111 2 (EXTRACELLULAR (POTENTIAL)).
 FT TRANSMEM 112 133 3 (POTENTIAL).
 FT DOMAIN 134 151 4 (POTENTIAL).
 FT TRANSMEM 152 172 4 (POTENTIAL).
 FT DOMAIN 173 203 5 (POTENTIAL).
 FT TRANSMEM 204 230 5 (POTENTIAL).
 FT DOMAIN 231 246 6 (POTENTIAL).
 FT TRANSMEM 247 271 6 (POTENTIAL).
 FT DOMAIN 272 295 7 (POTENTIAL).
 FT TRANSMEM 296 313 7 (POTENTIAL).
 FT DOMAIN 314 367 7 (POTENTIAL).
 FT DISULFID 110 189 BY SIMILARITY.
 FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF83B1117E CRC64;
 Query Match 62.1%; Score 59; DB 1; Length 367;
 Best Local Similarity 69.2%; Pred. No. 0.012;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YAFVGEKERNVLL 13
 |||||:|||||:
 Db 308 YAFVGEKERNVLL 320
 |||||:|||||:
 RESULT 33
 C3X1 RAT
 ID C3X1 RAT STANDARD; PRT; 354 AA.
 AC F35411;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CX3C chemokine receptor 1 (C-X3-C-CKR-1) (CX3CR1) (Fractalkine
 receptor) (GPR13) (RBS11).
 GN CX3CR1 OR GPR13.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Sprague-Dawley; TISSUE=Spinal cord;
 RX MEDLINE=94233113; PubMed=8047298;
 RA Harrison J.K., Barber C.M., Lynch K.R.;
 RT "cDNA cloning of a G-protein-coupled receptor expressed in rat spinal
 cord and brain related to chemokine receptors.";
 RL Neurosci. Lett. 169:85-89 (1994).
 CC -!- FUNCTION: Receptor for the CX3C chemokine fractalkine and mediates
 both its adhesive and migratory functions.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Most abundant in adult spinal cord, brain,
 kidney, gut, uterus and testes.
 CC -!- PFM: This protein is not N-glycosylated which is unusual for G-
 protein-coupled receptors.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U04808; AAB87093.1; -.
 DR PIR; I58186; I58186.
 DR InterPro; IPR005387; Fractalkiner.

```

DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR01562; FRACCTALKINER.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
DR PROSITE; PS00237; G PROTEIN RECP FL 2; 1.
DR PROSITE; PS02624; G-PROTEIN RECP FL 2; 1.
DR G-protein coupled receptor; Transmembrane.
KW DOMAIN 1 32
FT TRANSMEM 33 60
FT DOMAIN 61 70
FT TRANSMEM 71 91
FT DOMAIN 92 104
FT TRANSMEM 105 126
FT DOMAIN 127 143
FT TRANSMEM 144 168
FT DOMAIN 169 196
FT TRANSMEM 197 216
FT DOMAIN 217 232
FT TRANSMEM 233 257
FT DOMAIN 258 274
FT TRANSMEM 275 298
FT DOMAIN 299 354
FT DISULFID 103 176
SQ SEQUENCE 354 AA; 40327 MW; CFC4578095E577376 CRC64;

Query Match 61.1%; Score 58; DB 1; Length 354;
Best Local Similarity 61.1%; Pred. No. 0.017;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 YAFVGEKFRNYLVFFQK 18
DB 294 YAFAGEKFRNYLVHLYNK 311

RESULT 34
C3X1_MOUSE STANDARD; PRT; 354 AA.
ID C3X1_MOUSE
AC Q9Z0D9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C3X3 chemokine receptor 1 (C-X3-C CKR-1) (C3XCR1) (Fractalkine
DE receptor).
DE C3XCR1.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=99119076; PubMed=9918795;
RA Combadiere C., Gao J.-L., Tiffany H.L., Murphy P.M.;
ET "Gene cloning, RNA distribution, and functional expression of mCX3CR1,
ET a mouse chemotactic receptor for the CX3C chemokine fractalkine.";
RL Biochem. Biophys. Res. Commun. 253:728-732(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX Coultas L., McCall S.R.;
ET "Cloning and characterization of murine CX3CR1, a receptor for murine
ET fractalkine/neurotactin.";
RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary gland;
RX MEDLINE=23389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for the CX3C chemokine fractalkine and mediates
CC both its adhesive and migratory functions.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: This protein is not N-glycosylated which is unusual for
CC G-protein-coupled receptors.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF074912; AAD08665.1; -
DR EMBL; AF102269; AAC72408.1; -
DR EMBL; BC012653; AAH12653.1; -
DR MGD; MGI:133815; Cx3cr1.
DR InterPro; IPR00387; Fractalkiner.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR01562; FRACCTALKINER.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
DR PROSITE; PS02624; G-PROTEIN RECP FL 2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 32
FT TRANSMEM 33 60
FT DOMAIN 61 70
FT TRANSMEM 71 91
FT DOMAIN 92 104
FT TRANSMEM 105 126
FT DOMAIN 127 143
FT TRANSMEM 144 168
FT DOMAIN 169 196
FT TRANSMEM 197 216
FT DOMAIN 217 232
FT TRANSMEM 233 257
FT DOMAIN 258 274
FT TRANSMEM 275 298
FT DOMAIN 299 354
FT DISULFID 103 176
SQ SEQUENCE 354 AA; 40266 MW; 12C745E8E3755CA9 CRC64;

Query Match 60.0%; Score 57; DB 1; Length 354;
Best Local Similarity 61.1%; Pred. No. 0.026;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 YAFVGEKFRNYLVFFQK 18
DB 294 YAFAGEKFRNYLVHLYNK 311

RESULT 35
C3X1_HUMAN STANDARD; PRT; 355 AA.
ID C3X1_HUMAN
AC P49238;
DT 01-FEB-1996 (Rel. 33, Created)

```


01-FBE-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
CX3C chemokine receptor 1 (C-X3-C CR-1) (CX3CR1) (Fractalkine
DE receptor) (GPR13) (V28) (Beta chemokine receptor-like 1) (CWK-BRL-1)
DE (CWKBLR1).
GN CX3CR1 OR GPR13
ON Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96011651; PubMed=7590284;
RA Raport C.J., Schweickart V.L., Eddy R.L. Jr., Shows T.B., Gray P.W.;
RT "The orphan G-protein-coupled receptor-encoding gene V28 is closely
RT related to genes for chemokine receptors and is expressed in lymphoid
RT and neural tissues.";
RL Gene 163:295-299(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95374679; PubMed=7646814;
RA Combadiere C., Ahuja S.K., Murphy P.M.;
RT "Cloning, chromosomal localization, and RNA expression of a human
RT beta chemokine receptor-like gene.";
RL DNA Cell Biol. 14:673-680(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavent T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettanan M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=98050927; PubMed=9390561;
RA Imai T., Hieshima K., Haskell C., Baba M., Nagira M., Nishimura M.,
RA Kakiyaki M., Takagi S., Nomiyama H., Schall T.J., Yoshie O.;
RT "Identification and molecular characterization of fractalkine receptor
RT CX3CR1, which mediates both leukocyte migration and adhesion.";
RL Cell 91:521-530(1997).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=98395093; PubMed=9726990;
RA Combadiere C., Salzwedel K., Smith E.D., Tiffany H.L., Berger E.A.,
RA Murphy P.M.;
RT "Identification of CX3CR1. A chemotactic receptor for the human CX3C
RT chemokine fractalkine and a fusion coreceptor for HIV-1.";
RL J. Biol. Chem. 273:23799-23804(1998).
RN [6]
RP VARIANTS ALA-57; ILE-122; ILE-249 AND MET-280.
RX MEDLINE=20196025; PubMed=10731151;
RA Faure S., Meyer L., Costagliola D., Vaneensbergh C., Genin E.,
RA Autran B., Delraissy J.-F., McDermott D.H., Murphy P.M., Debre P.,
RA Theodorou I., Combadiere C.;
RT "Rapid progression to AIDS in HIV+ individuals with a structural
RT variant of the chemokine receptor CX3CR1.";
RN [7]

Db 293 YAFAGEKFRRLYHLYGK 310

RESULT 36

CKR4_HUMAN

ID CKR4_HUMAN STANDARD; PRT; 360 AA.

AC P51679; Q9ULY6; Q9ULY7;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE C-C chemokine receptor type 4 (C-C CKR-4) (CCR-4) (CCR4)

DE (X5-5).

GN CCR4 OR CMKBR4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spine;

RX MEDLINE=95370289; PubMed=7642634;

RA Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,

RA Proudfoot A.E.I., Wells T.N.C.;

RT "Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line.";

RL J. Biol. Chem. 270:19495-19500(1995).

RN [2]

RP SEQUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.

RX MEDLINE=21040311; PubMed=11196669;

RA Kato H., Tsuchiya N., Izumi S., Miyama M., Nakajima T., Kawasaki H.,

RA Hirai K., Tokunaga K.;

RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";

RL Genes Immun. 1:97-104(1999).

RN [3]

RP SEQUENCE FROM N.A.

RA Kopatz S.A., Aronstam R.S., Sharma S.V.;

RT "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RN [4]

RP FUNCTION.

RX MEDLINE=97313486; PubMed=9169480;

RA Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;

RT "The T cell-directed CC chemokine TARC is a highly specific biological ligand for CC chemokine receptor 4.";

RL J. Biol. Chem. 272:15036-15042(1997).

RN [5]

RP FUNCTION.

RX MEDLINE=98104169; PubMed=9430724;

RA Imai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska R.,

RA Yoshie O., Gray P.W.;

RT "Macrophage-derived chemokine is a functional ligand for the CC chemokine receptor 4.";

RL J. Biol. Chem. 273:1764-1768(1998).

RN [6]

RP FUNCTION.

RX MEDLINE=99394604; PubMed=10466728;

RA Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Ponath P.,

RA Andrew D.P., Warnke R., Ruffing N., Kassam N., Wu L., Butcher E.C.;

RT "The chemokine receptor CCR4 in vascular recognition by cutaneous but not intestinal memory T cells.";

RL Nature 400:776-780(1999).

RN [7]

RP FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.

RX MEDLINE=20219238; PubMed=10754297;

RA Ingjerdengen M., Damaj B., Maghazachi A.A.;

RT "Human NK cells express CC chemokine receptors 4 and 8 and respond to thymus and activation-regulated chemokine, macrophage-derived chemokine, and I-309.";

RL J. Immunol. 164:4048-4054(2000).

CC -!- FUNCTION: High affinity receptor for the C-C type chemokines TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is mediated by G(i) proteins which activate a phosphatidylinositol-

CC calcium second messenger system. Can function as a chemoattractant homing receptor on circulating memory lymphocytes and as a coreceptor for some primary HIV-2 isolates. In the CNS, could mediate hippocampal-neuron survival.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Predominantly expressed in the thymus, in peripheral blood leukocytes, including T cells, mostly cd4+ cells, and in monocytes. Detected also in macrophages, in-2-activated natural killer cells and skin-homing memory T cells, mostly the ones expressing the cutaneous lymphocyte antigen (CLA). Expressed in brain microvascular and coronary artery endothelial cells.

CC -!- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL; X85740; CAA59743.1; -

DR EMBL; AB023888; BAA86965.1; -

DR EMBL; AB023889; BAA86966.1; -

DR EMBL; AB023890; BAA86967.1; -

DR EMBL; AB023891; BAA86968.1; -

DR EMBL; AB023892; BAA86969.1; -

DR EMBL; AY322539; AAP84352.1; -

DR PIR; A57160; A57160.

DR Genes; HGNC:1605; CCR4.

DR MIM; 604836; -

DR GO; GO:0005887; C: integral to plasma membrane; TAS.

DR GO; GO:0004950; F: chemokine receptor activity; TAS.

DR GO; GO:0006935; P: chemotaxis; TAS.

DR GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.

DR GO; GO:0006955; P: immune response; TAS.

DR GO; GO:0006954; P: inflammatory response; TAS.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PRO0237; GPCRHHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Phosphorylation; Polymorphism

FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 40 67 1 (POTENTIAL).

FT DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 78 98 2 (POTENTIAL).

FT DOMAIN 99 111 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 112 133 3 (POTENTIAL).

FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 151 175 4 (POTENTIAL).

FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 207 226 5 (POTENTIAL).

FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 243 267 6 (POTENTIAL).

FT DOMAIN 268 284 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 285 308 7 (POTENTIAL).

FT DOMAIN 309 360 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 110 187 BY SIMILARITY.

FT VARIANT 130 130 L -> V.

FT VARIANT 178 178 /FTID=VAR_010669.

FT VARIANT 178 178 C -> S.

FT /FTID=VAR_010670.

SQ SEQUENCE 360 AA; 41402 MW; 51BE12AD1FAFBF CRC64;

Query Match 60.0%; Score 57; DB 1; Length 360;

Best Local Similarity 58.8%; Pred. No. 0.026;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKPRNYLLVFFQ 17
DB 304 YFGLGKPRKYLQLFK 320

RESULT 37
CKR1_MACMU STANDARD; PRT; 355 AA.
AC PS6482;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1).
GN CKR1 OR CMKBR1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine receptors";
RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, RANTES, MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND, SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL PROLIFERATION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC EMBL; AF017282; AAB70526.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 106 183 BY SIMILARITY.
FT DISULFID 106 183
SQ SEQUENCE 355 AA; 41198 MW; 41CAEA7CC19D23D4 CRC64;
Query Match 58.9%; Score 56; DB 1; Length 355;
Best Local Similarity 55.6%; Pred. No. 0.039;

Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKPRNYLLVFFQK 18
DB 301 YAFAGERFRKYLQLFHR 318

RESULT 38
CKR3_CAVPO STANDARD; PRT; 358 AA.
AC Q92213;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
GN CKR3 OR CMKBR3.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99049845; PubMed=9834099;
RA Sabroe I., Conroy D.M., Gerard N.P., Li Y., Collins P.D., Post T.W., Jose P.J., Williams T.J., Gerard C.J., Ponath P.D.;
RT "Cloning and characterization of the guinea pig eosinophil eotaxin receptor, C-C chemokine receptor-3: blockade using a monoclonal antibody in vivo";
RL J. Immunol. 161:6139-6147 (1998).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin, MCP-3, MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC EMBL; AF060698; AAC80428.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 64 POTENTIAL.
FT DOMAIN 65 74 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 75 95 POTENTIAL.
FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 113 133 POTENTIAL.
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 POTENTIAL.
FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 227 POTENTIAL.
FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 264 POTENTIAL.
FT DOMAIN 265 287 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 308 POTENTIAL.
FT DOMAIN 309 358 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 358 AA; 41623 MW; 7B73FAB7A3BC3670 CRC64;
Query Match 57.9%; Score 55; DB 1; Length 358;
Best Local Similarity 55.6%; Pred. No. 0.058;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKPRNYLLVFFQK 18

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:56:16 ; Search time 28.8 Seconds
(without alignments)
197.199 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95
Sequence: 1 YAFVGEKFRNLLVFFQK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	333	4	O14694
2	95	100.0	334	6	Q9TU07
3	95	100.0	339	4	Q9UN24
4	95	100.0	339	4	Q9UN26
5	95	100.0	339	4	Q9UN23
6	95	100.0	339	4	Q9UBJ7
7	95	100.0	339	4	Q9UN25
8	95	100.0	339	4	Q9UN27
9	95	100.0	339	4	Q9UBT9
10	95	100.0	339	4	Q9UN28
11	95	100.0	339	6	Q9TQW0
12	95	100.0	339	6	Q9TUX1
13	95	100.0	339	6	Q9TUU9
14	95	100.0	339	6	Q9TUN8
15	95	100.0	339	6	Q9TUT4
16	95	100.0	339	6	Q9TUN9

17	95	100.0	339	6	Q9TSQ1	Q9tsq1 cercopithec
18	95	100.0	339	6	Q9TUU8	Q9tuu8 cercopithec
19	95	100.0	339	6	Q9TQW4	Q9tqw4 pan troglod
20	95	100.0	339	6	Q9TUM4	Q9tum4 pan troglod
21	95	100.0	339	6	Q9TQU7	Q9tqu7 cercopithec
22	95	100.0	339	6	Q9TUU5	Q9tuu5 erythrocebu
23	95	100.0	339	6	Q9TUU3	Q9tuu3 macaca mula
24	95	100.0	339	6	Q9TUS9	Q9tus9 saguinus sp
25	95	100.0	339	6	Q9TQT0	Q9tqt0 macaca fasc
26	95	100.0	339	6	Q9TUN9	Q9tun9 macaca mula
27	95	100.0	339	6	Q9TSN2	Q9tsn2 macaca fasc
28	95	100.0	339	6	Q9TQV6	Q9tqv6 colobus gue
29	95	100.0	339	6	Q9TQV6	Q9tqv6 pan troglod
30	95	100.0	339	6	Q9TQW6	Q9tqw6 cercopithec
31	95	100.0	339	6	Q9TUU9	Q9tuu9 macaca fasc
32	95	100.0	339	6	Q9TSK3	Q9tsk3 macaca fusc
33	95	100.0	339	6	Q9TUN7	Q9tun7 erythrocebu
34	95	100.0	339	6	Q9TUR2	Q9tur2 papio papio
35	95	100.0	339	6	Q9TQV0	Q9tqv0 macaca fusc
36	95	100.0	339	6	Q9TUU6	Q9tuu6 macaca fusc
37	95	100.0	339	6	Q9TQU5	Q9tqu5 cercopithec
38	95	100.0	339	6	Q9TUS7	Q9tus7 papio papio
39	95	100.0	339	6	Q9TUM7	Q9tum7 pan troglod
40	95	100.0	339	6	Q9TUN3	Q9tun3 pongo pygma
41	95	100.0	339	6	Q9TUS5	Q9tus5 papio papio
42	95	100.0	339	6	Q9TUU0	Q9tuu0 macaca mula
43	95	100.0	339	6	Q9TQV2	Q9tqv2 papio papio
44	95	100.0	339	6	Q9TQV3	Q9tqv3 cercopithec
45	95	100.0	339	6	Q9TUD8	Q9tud8 cercopithec

ALIGNMENTS

RESULT 1

O14694 PRELIMINARY; PRT; 333 AA.
AC O14694;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RL "Hiv-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011504; AAB65704.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PFC0001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS02622; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 333 333
AEFA07A67893AEB CRC64;

Query Match 100.0%; Score 95; DB 4; Length 333;

Best Local Similarity 100.0%; Pred. No. 1.1e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

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Db      278 YAFVGEKFRNYLLVFFQK 295

RESULT 2
Q9TUQ7
ID Q9TUQ7 PRELIMINARY; PRT; 334 AA.
AC Q9TUQ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162049; AAD47804.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 334
FT NON_TER 334
SQ SEQUENCE 334 AA; 38460 MW; B19DOCEC667B69F0 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db      285 YAFVGEKFRNYLLVFFQK 302

RESULT 3
Q9UN24
ID Q9UN24 PRELIMINARY; PRT; 339 AA.
AC Q9UN24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161919; AAD47676.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4B CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db      290 YAFVGEKFRNYLLVFFQK 307

RESULT 5
Q9UN23
ID Q9UN23 PRELIMINARY; PRT; 339 AA.
AC Q9UN23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307
|||||

RESULT 6
Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR EMBL; AF161917; AAD47674.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39128 MW; 9C3369FF1F2F27A CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307
|||||

RESULT 7
Q9UN25 PRELIMINARY; PRT; 339 AA.
AC Q9UN25;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161919; AAD47675.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39146 MW; 10FE05FE5371D4B3 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307
|||||

RESULT 8
Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.

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FT NON TER 339 339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAF2614D35C CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
DB 290 YAFVGEKFRNLLVFFQK 307

RESULT 12
Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (Crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257FBFB834C4AE CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
DB 290 YAFVGEKFRNLLVFFQK 307

RESULT 13
Q9TUU9 PRELIMINARY; PRT; 339 AA.
AC Q9TUU9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,

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RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47704.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
DB 290 YAFVGEKFRNLLVFFQK 307

RESULT 14
Q9TUU8 PRELIMINARY; PRT; 339 AA.
AC Q9TUU8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47651.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
DB 290 YAFVGEKFRNLLVFFQK 307

RESULT 15

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Q9TUT4 PRELIMINARY; PRT; 339 AA.
 AC Q9TUT4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Macaca nemestrina (pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161979; AAD47734.1; --
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1.1.
 DR PRINTS; PR00237; GPCR_Rhodpsn.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 339
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39032 MW; 84B51B9548E0703C CRC64;
 Query Match 100.0%; Score 95; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 DB 290 YAFVGEKFRNLLVFFQK 307
 [1]
 SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161979; AAD47734.1; --
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1.1.
 DR PRINTS; PR00237; GPCR_Rhodpsn.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 339
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39032 MW; 84B51B9548E0703C CRC64;
 Query Match 100.0%; Score 95; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 DB 290 YAFVGEKFRNLLVFFQK 307
 [1]
 PRELIMINARY; PRT; 339 AA.
 AC Q9TUT9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Hylobates concolor (crested gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=29089;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161890; AAD47647.1; --
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1.1.
 DR PRINTS; PR00237; GPCR_Rhodpsn.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 339
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39032 MW; EC4CE48DEEF107E CRC64;
 Query Match 100.0%; Score 95; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 DB 290 YAFVGEKFRNLLVFFQK 307
 [1]
 PRELIMINARY; PRT; 339 AA.
 AC Q9TSQ1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercopithecoidea.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162023; AAD47778.1; --
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1.1.
 DR PRINTS; PR00237; GPCR_Rhodpsn.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 339
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39216 MW; 847E935FA403E52D CRC64;
 Query Match 100.0%; Score 95; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 DB 290 YAFVGEKFRNLLVFFQK 307
 [1]
 PRELIMINARY; PRT; 339 AA.
 AC Q9TUU8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Cercopithecus diana (Diana monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercopithecoidea.

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OK NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161949; AAD47705.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39049 MW; 6D1A93F66270F3ED CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 290 YAFVGEKFRNLLVFFQK 307
|||||
[1]

RESULT 19
Q9TQW4 PRELIMINARY; PRT; 339 AA.
AC Q9TQW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39159 MW; 8E699B882BAC0E84 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 290 YAFVGEKFRNLLVFFQK 307
|||||
[1]

RESULT 20
Q9TQW4 PRELIMINARY; PRT; 339 AA.
AC Q9TQW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39159 MW; 8E699B882BAC0E84 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 290 YAFVGEKFRNLLVFFQK 307
|||||
[1]

RESULT 21
Q9TQW4 PRELIMINARY; PRT; 339 AA.
AC Q9TQW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -.
DR EMBL; AF162042; AAD47797.1; -.

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DR EMBL; AF162044; AAD47799.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39150 MW; 8475F92BB03E6E2 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 22
Q9TU05 PRELIMINARY; PRT; 339 AA.
AC Q9TU05;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5
OS Erythrocybus, patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162054; AAD47809.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39048 MW; 1A2E19E3A6A5A52A CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 23
Q9TU03 PRELIMINARY; PRT; 339 AA.
AC Q9TU03;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5
OS Erythrocybus, patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162054; AAD47809.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39048 MW; 1A2E19E3A6A5A52A CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 24
Q9TUR9 PRELIMINARY; PRT; 339 AA.
AC Q9TUR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5
OS Saguinus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162015; AAD47770.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 1

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FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39063 MW; 78BC57A8AB877085 CRC64;

Query Match
Best Local Similarity 100.0%; Score 95; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 25
Q9TQTO PRELIMINARY; PRT; 339 AA.
AC Q9TQTO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161954; AAD47710.1; -.
DR EMBL; AF161950; AAD47706.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39067 MW; 5BFCB5BA96C2F9E CRC64;

Query Match
Best Local Similarity 100.0%; Score 95; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 26
Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161954; AAD47710.1; -.
DR EMBL; AF161950; AAD47706.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match
Best Local Similarity 100.0%; Score 95; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 27
Q9TSN2 PRELIMINARY; PRT; 339 AA.
AC Q9TSN2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161953; AAD47709.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39137 MW; 9E626ED3288607C1 CRC64;

Query Match
Best Local Similarity 100.0%; Score 95; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18

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[1]
RN RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161972; AAD47727.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39067 MW; 5BFCB5BA96C2F9E CRC64;

Query Match
Best Local Similarity 100.0%; Score 95; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 27
Q9TSN2 PRELIMINARY; PRT; 339 AA.
AC Q9TSN2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161953; AAD47709.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39137 MW; 9E626ED3288607C1 CRC64;

Query Match
Best Local Similarity 100.0%; Score 95; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18

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Db      290 YAFVGEKFRNLLVFFQK 307

RESULT 28
Q9TUR6
ID      PRELIMINARY;      PRT;      339 AA.
AC      Q9TUR6;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      C-C chemokine receptor 5 (Fragment).
CCRS.
GN      Cercopithecus aethiops vervet.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Cercopithecus.
OX      NCBI_TaxID=100936;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA      Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT      "Sequences of the CCR5 genes from diverse simian and prosimian
RT      species.";
RL      Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF162002; AAD47757.1; -.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR      GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      Pfam; PF00001; 7tm.1; 1.
DR      PRINTS; PR00237; GPCRHHODOPS.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW      Receptor.
FT      NON_TER
FT      NON_TER
SQ      SEQUENCE 339 AA; 39178 MW; 9DF2A6F446C55AED CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
Db      290 YAFVGEKFRNLLVFFQK 307

RESULT 29
Q9TOV6
ID      PRELIMINARY;      PRT;      339 AA.
AC      Q9TOV6;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      C-C chemokine receptor 5 (Fragment).
CCRS.
GN      Colobus guereza (Black-and-white colobus monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC      Colobus.
OX      NCBI_TaxID=33548;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA      Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT      "Sequences of the CCR5 genes from diverse simian and prosimian
RT      species.";
RL      Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF162005; AAD47760.1; -.
DR      EMBL; AF162000; AAD47755.1; -.
DR      EMBL; AF162001; AAD47756.1; -.
DR      EMBL; AF162002; AAD47757.1; -.

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DR      EMBL; AF162003; AAD47758.1; -.
DR      EMBL; AF162004; AAD47759.1; -.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR      GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      Pfam; PF00001; 7tm.1; 1.
DR      PRINTS; PR00237; GPCRHHODOPS.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW      Receptor.
FT      NON_TER
FT      NON_TER
SQ      SEQUENCE 339 AA; 39168 MW; 6A4BF72FEBFF566F CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
Db      290 YAFVGEKFRNLLVFFQK 307

RESULT 30
Q9TUM6
ID      PRELIMINARY;      PRT;      339 AA.
AC      Q9TUM6;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      C-C chemokine receptor 5 (Fragment).
CCRS.
GN      Pan troglodytes (Chimpanzee).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX      NCBI_TaxID=9598;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA      Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT      "Sequences of the CCR5 genes from diverse simian and prosimian
RT      species.";
RL      Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF161900; AAD47657.1; -.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR      GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      Pfam; PF00001; 7tm.1; 1.
DR      PRINTS; PR00237; GPCRHHODOPS.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW      Receptor.
FT      NON_TER
FT      NON_TER
SQ      SEQUENCE 339 AA; 39103 MW; 4038C132D024C5A4 CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
Db      290 YAFVGEKFRNLLVFFQK 307

RESULT 31
Q9TUQ9
ID      PRELIMINARY;      PRT;      339 AA.
AC      Q9TUQ9;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus mona.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36226;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162041; AAD47796.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39019 MW; 7176F940AF11F3ED CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307

RESULT 32
Q9TSN3
ID Q9TSN3 PRELIMINARY; PRT; 339 AA.
AC Q9TSN3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161951; AAD47707.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39019 MW; 7176F940AF11F3ED CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307

RESULT 33
Q9TUU7
ID Q9TUU7 PRELIMINARY; PRT; 339 AA.
AC Q9TUU7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161955; AAD47711.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39037 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307

RESULT 34
Q9TUR2
ID Q9TUR2 PRELIMINARY; PRT; 339 AA.
AC Q9TUR2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Erythrocebus patas (Red guenon) (Husar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]

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FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39098 MW; F0132B8BC44EF829 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307

RESULT 33
Q9TUU7
ID Q9TUU7 PRELIMINARY; PRT; 339 AA.
AC Q9TUU7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161955; AAD47711.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39037 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307

RESULT 34
Q9TUR2
ID Q9TUR2 PRELIMINARY; PRT; 339 AA.
AC Q9TUR2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Erythrocebus patas (Red guenon) (Husar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]

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RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162034; AAD47789.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39138 MW; AD31455EBBC69499 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 35
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161989; AAD47744.1; -.
DR EMBL; AF161988; AAD47743.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39113 MW; 7F9803EA0E0AF9ED CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 36
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161956; AAD47712.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39080 MW; 4DCA9C72B093216D CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 37
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162046; AAD47801.1; -.
DR EMBL; AF162043; AAD47798.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.

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GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
[1]
RN SEQUENCE FROM N.A.
RP Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161899; AAD47656.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39157 MW; 4A9EBAD183E8E72D CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. NO. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 YAFVGEKFRNYLLVFFQK 18
|||||
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 40
Q9TUW3 PRELIMINARY; PRT; 339 AA.
ID Q9TUW3 AC Q9TUW3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
[1]
RN SEQUENCE FROM N.A.
RP Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161908; AAD47665.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39103 MW; 4350C4625FB0657C CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. NO. 1.1e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 290 YAFVGEKFRNYLLVFFQK 307

Search completed: September 28, 2004, 09:06:20
Job time : 28.8 secs